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Tomato TFT1 Is Required for PAMP-Triggered Immunity and Mutations that Prevent T3S Effector XopN from Binding to TFT1 Attenuate Xanthomonas Virulence

Kyle W. Taylor1,†, Jung-Gun Kim1,†, Xue B. Su1,‡, Chris D. Aakre1,‡, Julie A. Roden1,‡, Christopher M. Adams2, Mary Beth Mudgett1,*

1 Department of Biology, Stanford University, Stanford, California, United States of America, 2 Stanford Mass Spectrometry, Stanford University, Stanford, California, United States of America

* E-mail: mudgett@stanford.edu
† These authors contributed equally to this work.
‡ Current address: Department of Biological Sciences, University of California, San Diego, California, United States of America
§ Current address: Department of Biology, College of the Holy Cross, Worcester, Massachusetts, United States of America

Abstract

XopN is a type III effector protein from Xanthomonas campestris pathovar vesicatoria that suppresses PAMP-triggered immunity (PTI) in tomato. Previous work reported that XopN interacts with the tomato 14-3-3 isoform TFT1; however, TFT1’s role in PTI and XopN virulence was not determined. Here we show that TFT1 functions in PTI and is a XopN virulence target. Virus-induced gene silencing of TFT1 mRNA in tomato leaves resulted in increased growth of Xcv. In vitro, XopN binding to TFT1 in plant extracts and inhibits XopN-dependent virulence in tomato, demonstrating that these residues are necessary for the XopN/TFT1 interaction. Phos-tag gel analysis and mass spectrometry showed that XopN is phosphorylated in plant extracts at serine 688 in a putative 14-3-3 recognition motif. Mutation of S688 reduced XopN's phosphorylation state but was not sufficient to inhibit binding to TFT1 or reduce XopN virulence. Mutation of S688 and two leucines (L64, L65) in XopN, however, eliminated XopN binding to TFT1 in plant extracts and XopN virulence. L64 and L65 are required for XopN to bind TARK1, a tomato atypical receptor kinase required for PTI. This suggested that TFT1 binding to XopN’s C-terminal domain might be stabilized via TARK1/XopN interaction. Pull-down and BiFC analyses show that XopN promotes TARK1/TFT1 complex formation in vitro and in planta by functioning as a molecular scaffold. This is the first report showing that a type III effector targets a host 14-3-3 involved in PTI to promote bacterial pathogenesis.

Introduction

Plant immunity to bacterial pathogens requires a complex detection and signaling network. Plants use pattern recognition receptors (PRRs) at the host cell surface to detect conserved microbial-associated molecular patterns (PAMPs) (e.g. flagellin and elongation factor EF-Tu) [1]. Activation of PRRs initiates downstream signaling events that lead to the production of reactive oxygen species, stimulation of mitogen-activated protein kinase (MAPK) cascades, defense gene induction, and callose deposition at the plant cell wall [2–6]. These host responses are sufficient to limit the growth of a broad range of potential pathogens and are collectively referred to as PAMP-triggered immunity or PTI [7].

In response, phytopathogenic bacteria evolved the type III secretion (T3S) to combat this layer of plant immunity [8–11]. T3S systems are widely conserved amongst bacteria and in most cases are critical virulence determinants [12,13]. The T3S apparatus mediates the secretion and translocation of effector proteins from the pathogen into eukaryotic host cells. Progress in understanding T3S effector function in plants has revealed that several proteins encode enzymes with different activities (e.g. SUMO protease, cysteine proteases, protein tyrosine phosphatase, E3 ligase, ADP-ribosyltransferase, phosphothreonine lyase and acetyltransferase) [14–21]. Some of these enzymes have been shown to target critical signaling components of the plant defense machinery [17,22–27]. In response, plants have evolved another layer of immune signaling known as effector-triggered immunity (ETI), which employs the use of resistance (R) proteins to monitor and amplify defense signal transduction to limit pathogen invasion and spread [7]. Plant immune signaling is thus complex and multilayered. Defining the mechanism(s) by which T3S effectors function in plants is critical for understanding pathogen evolution and the development of novel defense strategies.

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Author Summary

Bacterial pathogens of plants and animals employ the type III secretion system to secrete and translocate effector proteins into host cells to suppress defense responses. Biochemical analyses have revealed that several effector proteins mimic host enzyme activities to directly interfere with pathogen perception, defense signal transduction, and/or secretion of antimicrobial compounds. The XopN effector from Xanthomonas campestris pathovar vesicatoria, the causal agent of bacterial spot disease on tomato and pepper plants, suppresses PAMP-triggered immunity (PTI) but structural modeling predicts it encodes a unique scaffolding-like protein with no obvious enzymatic fold. We postulate that XopN mediates its virulence function by associating with host proteins regulating defense. XopN was previously shown to physically interact with the tomato 14-3-3 protein TFT1 in planta. The significance of TFT1 in plant immune signaling and the role of the XopN/TFT1 interaction were not determined. Here we show that TFT1 is a positive regulator of PTI in tomato required to inhibit Xcv growth. Moreover, we provide evidence that TFT1 is a bona fide target of XopN because mutations that disrupt XopN/TFT1 binding also eliminate XopN-dependent virulence in tomato. This is the first example of a bacterial effector targeting a 14-3-3 associated with host immunity.

TFT1 is a member of a large 14-3-3 family in tomato consisting of 12 isoforms [35,36]. 14-3-3s are acidic, phosphopeptide-binding proteins that are ubiquitously found among eukaryotes. 14-3-3s bind a diverse set of client proteins involved in distinct cellular processes (e.g., primary metabolism, signal transduction, transcription, protein trafficking, cell cycle, development, apoptosis, and stress responses), revealing that 14-3-3s are critical regulators of protein function [37–39]. Although 14-3-3s have no intrinsic enzymatic activity, they are known to regulate client activity by three principal mechanisms—clamping, masking, and scaffolding [37]. These mechanisms directly influence client stability, conformation, trafficking, and/or protein-protein interactions.

In terms of plant immunity, it has been known for some time that 14-3-3 mRNA levels are up-regulated in plants in response to pathogen attack [36]. The precise role of 14-3-3s in the regulation of plant defense signal transduction is not clear. Two recent biochemical studies indicate that 14-3-3s interact with central components of the plant defense machinery to positively regulate immunity. The Arabidopsis 14-3-3 isoform λ, (GF14A) binds to the atypical R protein RPW8.2 [40] and is implicated in the regulation of programmed cell death (PCD) and resistance to powdery mildew [40]. The tomato 14-3-3 isoform 7 (TFT7) interacts with two mitogen-activated protein kinases, MAPKKKz and MKK2, that function in multiple R protein signaling pathways revealing that this 14-3-3 coordinates the activity and possibly the assembly of multiple defense components [41]. Interestingly, host 14-3-3s have been shown to specifically interact with T3S effectors from animal and plant bacterial pathogens [28,42–44]. In the case of exoenzyme S (ExoS) from Pseudomonas aeruginosa, 14-3-3 binding is required for activation of ExoS-dependent ADP-ribosyltransferase activity [45] and cell death in the mouse model of pneumonia [46]. Host 14-3-3s are thus recruited during infection to promote ExoS virulence. Evidence showing that T3S effectors directly antagonize 14-3-3 function(s) to inhibit defense signaling has been lacking, although prime candidates include XopN from Xcv and HopM1 from Pseudomonas syringae. Both effectors are known to bind specific plant 14-3-3 isoforms and suppress PTI [28,44].

In this study, we characterized the role of the tomato 14-3-3 TFT1 in PTI and examined the biological relevance of the XopN/TFT1 interaction during Xcv infection in tomato. We performed virus-induced gene silencing (VIGS) in tomato to determine if TFT1 is required to inhibit Xcv growth. In addition, we performed structure-function analyses to identify the domains and amino acids in XopN that are required for TFT1 binding and XopN-dependent virulence in tomato. Our data indicate that TFT1 is a positive regulator of PTI in tomato required to inhibit Xcv pathogenesis and is a virulence target of the XopN effector.

Results

TFT1 mRNA levels increase in response to Xcv

To determine if Xcv infection alters TFT1 mRNA abundance, we monitored TFT1 mRNA levels in 4-week old VF36 tomato leaflets inoculated with 10 mM MgCl2 or a 10 mM MgCl2 suspension containing a low titer (1×107 colony forming units (CFU)/mL) of Xcv or Xcv ΔxopN. These conditions mirror those used in bacterial growth curves to monitor changes in pathogen multiplication and disease symptom development over a two-week period. Quantitative real-time RT-PCR (Q-PCR) revealed that the relative level of TFT1 mRNA was similar in all leaf samples at 2 and 4 days post-inoculation (DPI). At 6 and 8 DPI, TFT1 mRNA levels significantly increased in both the Xcv- and Xcv ΔxopN-infected leaf tissues (Figure 1A). This is the time period
**TFT1**-silenced tomatoes are more susceptible to infection with the Xcv ΔhrpF mutant

Considering that Xcv ΔhrpF inoculation significantly increases the level of **TFT1** mRNA (Figure 1B), we determined whether or not **TFT1** expression in tomato leaves was required to inhibit the growth of Xcv ΔhrpF. We performed transient virus-induced gene silencing (VIGS) using a tobacco rattle virus (TRV)-based system to reduce **TFT1** mRNA levels in susceptible VF36 tomato leaves. Growth curves were performed using the vector control and **TFT1**-silenced plants to determine if Xcv ΔhrpF growth increases when **TFT1** expression is reduced. Leaflets from the same fully expanded branch were inoculated with a 1×10^8 CFU/mL suspension of wild type Xcv or the Xcv ΔhrpF mutant. The number of bacteria in each leaflet was quantified at 0, 6, and 9 DPI (Figure 2A). Total RNA was isolated from the same leaflets at 0 DPI to measure **TFT1** mRNA levels by Q-PCR (Figure S1A). We also measured the mRNA levels of **TFT3** and **TFT6** to verify specificity for the VIGS construct (Figure S1B,C). These isoforms were chosen because they are highly homologous to **TFT1** at the nucleotide level and they were shown to only weakly interact with XopN [28].

Relative to the vector control plants (i.e. TRV2 lines), **TFT1** mRNA levels were reduced approximately 4-fold in leaflets from four independent **TFT1**-silenced tomato plants (i.e. TRV2-**TFT1** lines, Figure S1A). Reduced **TFT1** mRNA levels in the TRV2-**TFT1** leaves correlated with a significant increase in growth of Xcv ΔhrpF at 6 and 9 DPI relative to the growth of Xcv ΔhrpF detected in the TRV2 vector control leaves (Figure 2A). Growth of wild type Xcv was not significantly different in the TRV2-*TFT1* lines with significantly reduced levels of **TFT1** (Figure 2A). In the TRV2-**TFT1** leaves compared to the TRV2 vector control leaves (Figure 2A). Taken together, our data indicate that **TFT1** is required to inhibit Xcv ΔhrpF multiplication in tomato, further substantiating a role for this 14-3-3 in PTI.

**Silencing **TFT1** mRNA expression partially restores Xcv ΔxopN growth**

We hypothesized that XopN may directly bind to **TFT1** to suppress PTI during Xcv infection. If XopN binding to **TFT1** is critical for XopN-dependent virulence, then reduced **TFT1** levels in plants should increase and/or fully restore the growth of the Xcv ΔxopN null mutant [28] in tomato leaves. To test this, we quantified Xcv ΔxopN growth in the same set of control and **TFT1**-silenced tomato plants described above (Figure 2A). In the TRV2 vector control line containing **TFT1** mRNA (Figure S1A), the titer of Xcv was 5-fold higher than that of Xcv ΔxopN at 9 DPI (Figure 2A), consistent with the levels typically quantified in wild type VF36 tomato plants [28]. By contrast, in the **TFT1**-silenced lines with significantly reduced levels of **TFT1** mRNA (Figure S1A), the titer of Xcv in the TRV2-**TFT1** leaflets was only 2.4-fold higher than that of the Xcv ΔxopN in the TRV2-**TFT1** leaflets (Figure 2A). These data indicate that increased growth of the Xcv ΔxopN mutant correlates with reduced **TFT1** mRNA expression in tomato. This phenotype was observed in three independent **TFT1** silenced tomato leaves inoculated with Xcv ΔhrpF or Xcv ΔhrcV compared with those infected with Xcv or 10 mM MgCl2 (Figure 1B), revealing that **TFT1** is a PAMP-induced gene that is regulated in a T3S-dependent manner. Elevated **TFT1** mRNA levels in Xcv ΔhrpF-infected leaves in the high dose experiment (Figure 1B) are consistent with our findings in the low dose experiments (Figure 1A). The early induction of **TFT1** mRNA levels in response to a high dose of Xcv ΔhrcV suggests that **TFT1** plays a role in PTI and qualifies it as a PTI marker gene in tomato.

**Figure 1. TFT1 is a PTI-induced gene in tomato.** (A) Susceptible VF36 tomato leaves were inoculated with 10 mM MgCl2 (white bars), 1×10^6 CFU/mL of Xcv (black bars), or Xcv ΔxopN (grey bars). (B) Susceptible VF36 tomato leaves were inoculated with 10 mM MgCl2 (white bars), 2×10^6 CFU/mL of Xcv (black bars), Xcv ΔhrpF (yellow bars), or Xcv ΔhrcV (green bars). Total RNA was isolated at 2, 4, 6, and 8 DPI (A) or 6 HPI (B). Q-PCR was performed to monitor **TFT1** mRNA levels. Actin expression was used to normalize the expression value in each sample, and relative expression values were determined against the average value of the sample infiltrated with 10 mM MgCl2 at each time point. Error bars indicate SD for three (A) and four (B) plants. Asterisk indicates significant difference (t test, P<0.05) relative to the 10 mM MgCl2 control at 6 or 8 DPI (A) or 6 HPI (B). doi:10.1371/journal.ppat.1002768.g001

when Xcv and Xcv ΔxopN titers begin to differ significantly within the leaf tissue due to the impact of PTI in tomato [28]. It is also the time point when XopN-dependent suppression of PTI marker genes occurs [28]. These data indicate that Xcv infection induces **TFT1** mRNA levels tomato leaves in a XopN-independent manner. We next determined if **TFT1** is a PAMP-induced gene. Tomato leaflets were inoculated with 10 mM MgCl2 or a 10 mM MgCl2 suspension containing a high titer (2×10^6 CFU/mL) of Xcv, Xcv ΔhrpF, or Xcv ΔhrcV. The ΔhrpF mutant lacks the putative T3S translocon HrpF required for effector delivery into plant cells [47]. The ΔhrcV mutant lacks a structural membrane component of the T3S apparatus required for effector secretion from the pathogen [48]. Host responses to Xcv ΔhrcV represent the recognition of a collection of Xcv PAMPs that are not suppressed by Xcv T3S effectors. A high titer and short time course was used to ensure similar bacterial cell number within the leaves at the indicated time points because PTI inhibits Xcv ΔhrpF and Xcv ΔhrcV growth much more than wild type Xcv. Q-PCR was used to determine **TFT1** mRNA abundance in the inoculated leaves at 6 hours post-inoculation (HPI). **TFT1** mRNA levels were significantly higher in tomato leaves inoculated with Xcv ΔhrpF or Xcv ΔhrcV compared with those infected with Xcv or 10 mM MgCl2 (Figure 1B), revealing that **TFT1** is a PAMP-induced gene that is regulated in a T3S-dependent manner. Elevated **TFT1** mRNA levels in Xcv ΔhrpF-infected leaves in the high dose experiment (Figure 1B) are consistent with our findings in the low dose experiments (Figure 1A). The early induction of **TFT1** mRNA levels in response to a high dose of Xcv ΔhrcV suggests that **TFT1** plays a role in PTI and qualifies it as a PTI marker gene in tomato.
**A**

Xanthomonas XopN T3S Effector Targets Tomato 14-3-3

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VIGS experiments (data not shown). It is noteworthy to mention that symptom development was not dramatically affected in the TTF1-silenced lines. That is, Xcv-infected leaves generally collapsed before the Xcv ΔxopN-infected leaves, a phenotype typically observed in wild-type tomato plants [28]. Only slight differences in the onset and severity of tissue chlorosis and necrosis were observed in some TTF1 VIGS lines depending the severity of TTF1 silencing.

We also monitored the mRNA levels of PR-1b1, a tomato pathogenesis-related gene, in the same VIGS lines to determine if TTF1 expression is required for maximal PR-1b1 mRNA induction during Xcv ΔxopN infection. We previously showed that XopN is required to suppress PR-1b1 mRNA levels in tomato leaves during Xcv infection [28]. As expected, PR-1b1 mRNA levels (Figure 2B) increased at 6 DPI in TRV2 vector control leaflets infected with Xcv ΔxopN or Xcv ΔhrpF. The levels of PR-1b1 mRNA were however significantly lower in the TRV2-TTF1 leaflets infected with Xcv ΔxopN and Xcv ΔhrpF (Figure 2B). These data indicate that TTF1 mRNA expression is required for maximal expression of this defense marker gene during Xcv infection in tomato.

**TTF1 expression is required for Xcv-induced PTI mRNA accumulation**

Reduced PR-1b1 mRNA levels in TTF1-silenced tomato leaves suggested that TTF1 may be required for other PTI marker gene expression in tomato. To examine this, we generated an independent set of control and TTF1-silenced tomato plants using VIGS. The plants were inoculated with a high titer (2 × 10⁶ CFU/mL) of Xcv or Xcv ΔhrpF. Total RNA was isolated at 6 HPI and then the level of four mRNAs (i.e. PTI5, GRAS4, WRKY28, and LRR22) known to be associated with PTI in tomato [28,49] was quantified by Q-PCR. TTF1 mRNA levels were significantly reduced (~4-fold lower) in the TRV2-TTF1 leaves relative to the TRV2 control leaves (Figure S2). The mRNA levels for PTI5, GRAS4, WRKY28, and LRR22 were significantly higher in TRV2 control leaves inoculated with Xcv ΔhrpF compared to those inoculated with Xcv ΔhrpF (Figure 3). This indicates that TTF1 suppresses the accumulation of these PTI marker mRNAs in a type III-dependent manner. PTI5, GRAS4, WRKY28, and LRR22 mRNA levels in the TRV2-TTF1 leaves inoculated with Xcv ΔhrpF were significantly lower than those in the TRV2 leaves inoculated with Xcv ΔhrpF (Figure 5). PTI5, WRKY28, and LRR22 mRNA levels were also significantly reduced in the Xcv-infected TRV2-TTF1 leaves relative to the Xcv-infected control leaves. Taken together, these data show that TTF1 expression is required for the mRNA accumulation of these PTI marker genes in susceptible tomato leaves challenged with Xcv or Xcv ΔhrpF.

The C-terminus of XopN is required for TTF1 binding

If TTF1 is a bona fide virulence target for XopN, then mutations that disrupt XopN/TTF1 binding should attenuate Xcv virulence in tomato. To test this, we roughly mapped the TTF1 binding site in XopN. A series of N- and C-terminal XopN deletion mutants were constructed and then assayed for interaction with TTF1 using the GAL4-based two-hybrid assay in yeast.

Wild type XopN and five XopN deletion mutants (Figure 4A) were cloned into pXDGATyc186 containing the GAL4 DNA-binding domain (DBD) to create DBD-XopN fusion proteins (i.e. XopN, N, C, M4, M5 and M6). TTF1 was cloned into pGADT7 containing the GAL4 activation domain (AD) to create AD-TTF1. The DBD-XopN fusion proteins (BAIT) were then tested for interaction with AD-TTF1 (PREY) in targeted yeast two-hybrid assays. Protein expression levels in yeast are shown in Figure S3. The XopN mutants M4, M5, and M6 were highly expressed. Derivative C expression was similar to XopN, whereas derivative N expression was less than XopN. TTF1 interacted with the C-terminal (C) but not the N-terminal (N) domain of XopN (Figure 4B). Selection on media containing 1 mM 3-amino-1,2,4-triazole, a competitive inhibitor of the HIS3 gene product, indicated that TTF1 binding to the C-terminal domain is stronger than binding to full-length XopN (Figure 4B). TTF1 also interacted with the M4 mutant lacking XopN amino acids 1–221 (Figure 4B) but failed to interact with the M5 and M6 mutants lacking the C-terminal 605–733 and 515–733 amino acids of XopN, respectively (Figure 4B). These data suggest that TTF1 binds preferentially to XopN’s C-terminal domain in yeast.

We next verified that TTF1 binds to the C-terminal domain of XopN in planta by performing a Ni-NTA pull-down assay using N. benthamiana protein extracts. N. benthamiana leaves were hand-infiltrated with a 6 × 10⁸ CFU/mL suspension of A. tumefaciens expressing TTF1-HA alone or coexpressing TTF1-HA and XopN-6His (full-length), XopN₁₋₃₄⁹-6His (N-terminal domain), or XopN₃₄⁵₋₇₃₃-6His (C-terminal domain). Leaf samples were collected at 48 HPI and total soluble protein extracts were isolated. Using Ni-NTA agarose beads, XopN-6His, XopN₁₋₃₄⁹-6His or XopN₃₄⁵₋₇₃₃-6His were purified by affinity chromatography from the protein extracts and then analyzed by protein gel blot analysis. As expected, TTF1-HA copurified with XopN-6His (Figure 4C). More TTF1-HA copurified with XopN₃₄⁵₋₇₃₃-6His than XopN-6His consistent with the finding that TTF1 exhibited stronger binding to the C-terminal domain of XopN than the full-length polypeptide in the yeast two-hybrid assay. Only a low level of TTF1-HA was detected in the pull-down with XopN₁₋₃₄⁹-6His (Figure 4C). Although XopN₁₋₃₄⁹-6His was less stable than XopN-6His and XopN₃₄⁵₋₇₃₃-6His in total protein extracts, the protein was highly enriched by affinity chromatography (Figure 4C) and able to copurify TARK1-HA in control experiments (Figure S4). TARK1 is an atypical receptor kinase that binds to the N-terminus of XopN [28]. These data suggest that the large C-terminal deletion of XopN did not grossly alter the structure of its N-terminal domain. The data also suggest that TTF1 binds preferentially to the C-terminus of XopN.

The importance of XopN’s C-terminal domain for binding to TTF1 was further supported by pull-down analysis using the M5 mutant (amino acids 1–604) (Figure 4A). TTF1-HA and XopN-6His or XopN₁₋₆₀⁴-6His were transiently co-expressed in N. benthamiana and affinity purified as described above. Weak binding of TTF1-HA to the Ni-NTA agarose beads was observed. TTF1-HA was enriched in the XopN-6His pull-down but not in the XopN₁₋₆₀⁴-6His pull-down (Figure 4D). This indicates that some
of the amino acid residues between 605–733 in XopN are required for TFT1 binding.

**XopN C-terminus is important for XopN-dependent virulence in tomato**

To determine the importance of the XopN’s C-terminal residues for XopN-dependent virulence in tomato, we examined growth and symptom development of the Xcv \(DxopN\) mutant expressing wild type XopN-HA, the C-terminal deletion mutant XopN1–604-HA, or the vector control. All of the XopN constructs contained the \(xopN\) promoter (690 bp 5’ of the \(xopN\) ATG start site) that was shown to be sufficient to express the wild type XopN protein and restore full virulence of the Xcv \(DxopN\) mutant strain [28]. Susceptible VF36 tomato leaflets of 4 week-old plants were hand-infiltrated with a \(1\times10^5\) CFU/mL suspension of bacteria. At 0, 6, and 8 DPI, the number of bacteria in each leaflet was quantified. As expected, the titer of the Xcv \(DxopN\) (vector) strain was approximately 5-fold lower than that of the complemented Xcv \(DxopN\) (XopN-HA) strain demonstrating that XopN is required for maximal Xcv growth in planta (Figure 5A). Reduced Xcv \(DxopN\) (vector) growth resulted in reduced leaf symptom development (Figure 5B). Xcv \(DxopN\) expressing XopN1–604-HA exhibited reduced bacterial growth and symptom development comparable to that of the Xcv \(DxopN\) (vector) null mutant (Figure 5A,B). Protein gel blot analysis of total protein extracted from the Xcv strains confirmed that XopN1–604-HA protein levels were similar to that of XopN-HA (Figure S5A). Thus, XopN amino acid residues 605–733, which are critical for TFT1 binding, are also required for XopN-dependent virulence in tomato.

**XopN is phosphorylated in plant extracts**

Examination of the C-terminal sequence of XopN revealed a putative Mode II recognition motif for 14-3-3 binding proteins [50] between amino acid residues 684–690, REXVSAP (Figure 6A). Mode II binding sites have the consensus sequence RXXXpS/TXP, where pS/pT represents phospho-serine or phospho-threonine and X can be any amino acids [50]. This suggested that serine residue 688 might be phosphorylated. To begin to address this, we first determined if XopN is phosphorylated in plant extracts using Phos-tag SDS-PAGE gels. His-tagged XopN \(xopN\) expression resulted in reduced leaf symptom development (Figure S5B). XopN express XopN1–604-HA exhibited reduced bacterial growth and symptom development comparable to that of the XopN-HA null mutant (Figure 5A,B). Protein gel blot analysis of total protein extracted from the Xcv strains confirmed that XopN1–604-HA protein levels were similar to that of XopN-HA (Figure S5A). Thus, XopN amino acid residues 605–733, which are critical for TFT1 binding, are also required for XopN-dependent virulence in tomato.

**Figure 3. Reduced TFT1 mRNA expression in VIGS tomato leaves correlates with reduced PTI marker mRNA abundance in response to Xcv infection.** Relative mRNA levels for four PTI marker genes (PTI5, GRAS4, WRKY28, and LRR22) in 4 control (TRV2) and 4 TFT1-silenced (TRV2-TFT1) tomato lines. Leaflets on the same branch were inoculated with \(1\times10^5\) CFU/mL of Xcv or Xcv \(DxopN\) mutant. Total RNA isolated from inoculated leaves at 6 HPI was used for Q-PCR. Actin mRNA expression was used to normalize the expression value in each sample. Error bars indicate SD for four plants. Asterisk indicates significant difference (t test, \(P<0.05\)) in the infected TRV2-TFT1 lines compared to the similarly infected TRV2 lines. doi:10.1371/journal.ppat.1002768.g003
proteins were transiently expressed in *N. benthamiana*, purified using Ni⁺ affinity chromatography and then incubated with and without calf intestinal alkaline phosphatase (CIAP). Proteins were then separated in an 8% SDS-PAGE gel containing 50 mM α-Phos-tag and then analyzed by immunoblot analysis. XopN-6His treated with CIAP migrated faster in the Phos-tag gel compared to untreated XopN-6His indicating that XopN is phosphorylated in *N. benthamiana* extracts (Figure 7A).

Next we examined the phosphorylation state of XopN when S688 was mutated to alanine, XopN(S688A)-6His. We also monitored the phosphorylation state of XopN(L64A,L65A)-6His, a mutant with reduced virulence activity [28]. Leucine 64 and 65 are required to bind to TARK1 in plant extracts and to suppress PTI [28], highlighting the importance of the N-terminal domain in XopN virulence. The migration patterns of XopN(L64A,L65A)-6His with and without CIAP treatment were similar to that of XopN-6His (Figure 7A). By contrast, untreated XopN(S688A)-6His migrated similarly to the dephosphorylated form of XopN-6His, XopN(L64A,L65A)-6His. The XopN(S688A)-6His mutant protein was generally less abundant than XopN-6His and XopN(L64A,L65A)-6His. We also examined the migration of a triple mutant, XopN(L64A,L65A,S688A)-6His. The triple mutant migrated similarly to XopN(S688A)-6His (Figure 7A). Phos-tag gel analysis indicates that mutation of S688 affects the extent to which the XopN polypeptide is phosphorylated in *N. benthamiana* leaf extracts.

Phosphopeptide enrichment followed by mass spectrometry (MS) was then performed with XopN-6His protein purified from *N. benthamiana* extracts to determine if S688 is phosphorylated. The
Figure 5. XopN residues 605–733 are important for TFT1 binding and contribute to XopN-dependent virulence in tomato. (A) Growth of Xcv ΔxopN (vector) (grey bars), Xcv ΔxopN (XopN1–604-HA) (blue bars), or Xcv ΔxopN (XopN-HA) (black bars) in susceptible tomato VF36 leaves. Leaves were inoculated with a 1 × 10^6 CFU/mL suspension of bacteria. Number of bacteria in each leaf was quantified at 0, 6 and 8 DPI. Data points represent mean CFU/cm^2 ± SD of three plants. Analysis was repeated at least three times. Vector = pVSP61. Different letters at day 8 indicate statistically significant (one-way analysis of variance and Tukey’s HSD test, P < 0.05) differences between the samples. (B) Phenotype of tomato leaves inoculated with strains described in (A). Leaves were photographed at 12 DPI. Similar phenotypes were observed in 3 independent experiments.

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phosphopeptide EHVpSAPSSPNR was identified (Figure 7B), confirming that XopN is phosphorylated in the putative 14-3-3 Mode II recognition motif at S688. Mutation of Serine 688 in XopN disrupts TFT1 binding in yeast but not in planta. To determine if phosphorylation of S688 in XopN is required for TFT1 binding, we performed a directed yeast two-hybrid analysis using DBD-XopN(S688A) as the BAIT and AD-TFT1 as the PREY. The XopN(S688A) mutant did not interact with TFT1 (Figure 6B) despite the fact that DBD-XopN(S688A) was expressed at the same level as DBD-XopN in yeast (Figure S6B). Second, we performed a N. benthamiana pull-down assay to determine if TFT1 can still bind the XopN(S688A) mutant in plant extracts. N. benthamiana leaves were infected with a suspension of two A. tumefaciens strains expressing TFT1-HA and vector, or XopN-6His or XopN(S688A)-6His or XopN(S688D)-6His or XopN(S688E)-6His. Pull-down analysis was then performed as described above. Unexpectedly, TFT1-HA was still detected in the pull-down with XopN(S688A)-6His, although TFT1 enrichment was less than that obtained with wild type XopN-6His (Figure 6C).

Figure 6. Serine 688 in XopN is required for TFT1 binding in yeast but not in planta. (A) Schematic of putative 14-3-3 motifs in XopN protein. Black boxes represent regions for putative Mode I and II 14-3-3 binding motifs. Mode II site contains S688. PEST domain is underlined. N-terminal leucines (L64, L65) required for TARK1-binding are labeled. (B) XopN(S688A) mutant does not interact with TFT1 in yeast. Serine 688 in XopN was mutated to alanine. Yeast strain AH109 carrying pDGATcy86(GAL4-DNA binding domain) containing XopN, and XopN(S688A) was transformed with the following PREY constructs: pGADT7(GAL4 activation domain) alone (Vector) or pGADT7 containing TFT1. Strains were spotted on nonselective (SD-LT) and selective (SD-LTH) medium and then incubated at 30°C for 3d. (C) XopN(S688A) and two phosphomimetic mutants, XopN(S688D) and XopN(S688E), interact with TFT1 in N. benthamiana. Leaves were hand-infiltrated with a suspension (8×10^6 CFU/mL total) of two A. tumefaciens strains expressing TFT1-HA and XopN-6His or XopN(S688A)-6His or XopN(S688D)-6His or XopN(S688E)-6His. After 48 h, protein was extracted, purified by Ni^2+ affinity chromatography, and analyzed by protein gel blot analysis using anti-His and anti-HA sera. Expected protein MW: XopN-6His, S688A-6xHis, S688D-6His, and S688E-6His = 78.7 kDa; TFT1-HA = 29.3 kDa; +, protein expressed; −, vector control. (D) Growth of Xcv ΔxopN (vector), Xcv ΔxopN (XopN-HA), Xcv ΔxopN (XopN(S688A)-HA), Xcv ΔxopN (XopN(S688D)-HA), or Xcv ΔxopN (XopN(S688E)-HA) in susceptible tomato VF36 leaves. Leaves were inoculated with a 1×10^5 CFU/mL suspension of bacteria. Number of bacteria in each leaf was quantified at 0 and 10 DPI. Data points represent mean CFU/cm^2 ± SD of four plants. Different letters at day 10 indicate statistically significant (one-way analysis of variance and Tukey’s HSD test, P<0.05) differences between the samples. Vector = pVSP61. (E) Phenotype of tomato leaves inoculated with the strains described in (D). Leaves were photographed at 12 DPI. Analysis was repeated two times.
We also tested the affect of phosphomimetic mutations at S688 on XopN's binding interaction with TFT1. S688 was mutated to aspartic acid (D) or glutamic acid (E) creating the XopN(S688D)-His and XopN(S688E)-His mutants, respectively. The phosphomimetic mutants interacted with TFT1; however, as observed for the S688A mutant, less TFT1 was enriched in the pull-down using N. benthamiana extracts (Figure 6C). Collectively, these data indicate that mutation of S688 is not alone sufficient to disrupt or stabilize the XopN/TFT1 interaction detected in this binding assay.

S688 is not required for XopN virulence

The discrepancy between the interaction data observed in the yeast and in plant extracts prompted us to determine the effect of the S688A, S688D, and S688E mutations on XopN-dependent virulence in susceptible VF36 tomato leaves. These mutants were independently introduced into Xcv ΔxopN and then separated in the pull-down using N. benthamiana extracts (Figure 6C). Collectively, these data indicate that mutation of S688 is not alone sufficient to disrupt or stabilize the XopN/TFT1 interaction detected in this binding assay.

S688 is not required for XopN virulence

The discrepancy between the interaction data observed in the yeast and in plant extracts prompted us to determine the effect of the S688A, S688D, and S688E mutations on XopN-dependent virulence in susceptible VF36 tomato leaves. These mutants were independently introduced into Xcv ΔxopN and then the phenotypes of the resulting strains were analyzed by growth curve analysis. The mutant proteins were stably expressed in Xcv to similar levels as wild type XopN-HA (Figure S5B). Growth of Xcv ΔxopN expressing XopN(S688A)-HA, XopN(S688D)-HA or XopN(S688E)-HA in susceptible VF36 tomato leaves was not significantly different from that of Xcv ΔxopN expressing wild type XopN-HA (Figure 6D). Furthermore, the onset and severity of symptom development was similar for Xcv ΔxopN (XopN(S688A)-HA), Xcv ΔxopN (XopN(S688D)-HA), or Xcv ΔxopN (XopN(S688E)-HA) compared to Xcv ΔxopN (XopN-HA) (Figure 6E). Taken together, these data show that mutation of S688 does not impair XopN stability in Xcv or its virulence function in planta.

XopN(ΔM1/M2) and PEST mutants bind TFT1

One explanation for the XopN(S688A)/TFT1 interaction in planta could be to the presence of additional 14-3-3 binding sites in the C-terminal region of XopN. Closer examination of this region revealed a putative Mode I 14-3-3 binding site (Figure 6A) between residues 665–670 (amino acids SSSQP) that partially conforms to the motif RXXpS/TXP [51]. We generated a XopN mutant lacking both the putative Mode I and Mode II motifs (XopN(DM1/M2)) and tested for its ability to bind TFT1 in planta. Additionally, we noted a putative PEST motif in XopN at amino acid residues 659–677 that overlaps with the Mode I motif. PEST motifs are generally hyperphosphorylated regions rich in proline, glutamic acid, serine, and threonine residues that are found in proteins with short half-lives [52]. We deleted the PEST sequence to determine if it affected XopN stability and/or interaction with TFT1. Both XopN(ΔM1/M2) and XopN(APEST) interacted with TFT1 in the N. benthamiana pull-down assay (Figure S7). Moreover, deletion of the PEST motif did not significantly alter the abundance of the XopN(APEST) protein nor impair its ability to rescue the virulence defect of the Xcv ΔxopN mutant in tomato leaves (data not shown).
The XopN(L64A,L65A,S688A) triple mutant is impaired for TFT1 binding

Our mutation analysis suggests that the putative 14-3-3 motifs in XopN's C-terminal domain and/or phosphorylation of S688 are not the only structural determinants required for TFT1 binding specificity inside plant cells. Alternatively, the N-terminus of XopN may stabilize the XopN(S688A)/TFT1 complex in plant extracts. The N-terminus of XopN, specifically leucine 64 and 65, is required to bind TARK1 in plant extracts and to suppress PTI [28], highlighting the importance of the N-terminal domain in XopN virulence. Because we found that TARK1 can still bind XopN(S688A) in yeast (Figure S6A) and in plant extracts (Figure S8), we speculated that a TARK1 ortholog in N. benthamiana or another plant factor that binds to the N-terminus of XopN might strengthen the XopN(S688A)/TFT1 interaction in a protein complex.

To begin to test this hypothesis, we determined the role of XopN residues L64 and L65 on the XopN/TFT1 interaction. A triple point mutant XopN(L64A,L65A,S688A) was generated and its ability to bind TFT1 was assessed using the N. benthamiana pull-down assay. N. benthamiana leaves were hand-infiltrated with 6x10^8 CFU/mL suspension of Agrobacteria expressing TFT1-CHOP alone or coexpressing TFB1-CHOP and XopN(L64A,L65A-6His, XopN(L64A,L65A,S688A)-6His, or XopN-6His. Using Ni-NTA agarose beads, the respective His-tagged XopN proteins were purified by Ni-affinity chromatography and analyzed by protein gel blot analysis. TFT1-CHA was detected in the pull-downs with XopN-6His and XopN(L64A,L65A)-6His but not XopN(L64A,L65A,S688A)-6His (Figure S8A). These data indicate that L64, L65 and S688 are required to detect XopN/TFT1 binding in plant extracts.

To monitor the extent to which the XopN(L64A,L65A,S688A) mutant interacts with TFT1 in live plants cells, we utilized the transient bifluorescence complementation (BiFC) assay in N. benthamiana (Figure 8B). The non-fluorescent N-terminal domain of YFP was fused to the C-terminal domain of wild type and three mutant versions of XopN creating XopN-nYFP fusions. The non-fluorescent C-terminal domain of CFP was fused to the C-terminal domain of TFT1 creating TFT1-cCFP. For the BiFC assay, two Agrobacteria strains, each containing a different protein fusion construct, were mixed equally (final concentration 6x10^8 CFU/mL) and then the mixture was hand-infiltrated into N. benthamiana leaves. At 48 HPI, leaf epidermal cells were imaged by confocal microscopy. As expected, co-expression of XopN-nYFP and TFT1-cCFP resulted in the emission of bright fluorescence in the cytoplasm (Figure 8B). Co-expression of XopN(L64A,L65A)nYFP and TFT1-cCFP resulted in slightly less fluorescence relative to that observed for XopN-nYFP+TFT1-cCFP (Figure 8B). By contrast, co-expression of XopN(S688A)nYFP+TFT1-cCFP or XopN(L64A,L65A,S688A)-nYFP+TFT1-cCFP resulted in very, weak fluorescence (Figure 8B). This weak fluorescence was greater than the negative control (i.e. GUS-nYFP+TFT1-cCFP) or detectable background fluorescence. All proteins were expressed in N. benthamiana (Figure S9A). The BiFC data thus indicates that the triple mutant and the S688A mutant are still able to bind to TFT1 at some level in planta, however the interactions appear to be very weak. Reduced interaction between XopN(S688A)/TFT1 was detected in the pull-down assay (Figure 6C).

We also monitored interactions between TARK1 and the XopN mutants in the BiFC assay (Figure S9B,C). As expected, co-expression of TARK1-cCFP and XopN-nYFP resulted in bright fluorescence at the PM (Figure S9B). Co-expression of TARK1-cCFP and XopN(S688A)nYFP resulted in reduced fluorescence whereas co-expression of XopN(L64A,L65A)-nYFP or XopN(L64A,L65A,S688A)-nYFP with TARK1-cCFP only resulted in background fluorescence similar to the negative control (i.e. GUS-nYFP+TARK1-cCFP) (Figure S9B). These data are consistent with the pull-down assays showing the mutation of L64,L65 in XopN disrupts TARK1/XopN binding whereas the S688A mutation does not (Figure S8). The BiFC data suggest that the interaction between XopN(S688A)/TARK1 may be weaker than that of XopN/TARK1; however, this was not observed in the pull-down assay.

The XopN(L64A,L65A,S688A) triple mutant is impaired for virulence

We next assessed the impact of the triple mutant (L64A,L65A,S688A) on XopN-dependent virulence by monitoring Xcv growth and symptom development in tomato leaves as described above. Growth of Xcv ΔxopN expressing XopN(L64A,L65A,S688A)-HA was similar to that of the Xcv ΔxopN null mutant, and significantly less than that of Xcv ΔxopN expressing XopN-CHA (Figure 8C). Growth of Xcv ΔxopN expressing the double mutant XopN(L64A,L65A)-HA was greater than the triple mutant but less than Xcv ΔxopN expressing wild type XopN-CHA (Figure 8C). Leaf symptom development at 12 DPI correlated with bacterial titer. Leaves infected with Xcv ΔxopN(XopN-CHA) exhibited severe chlorosis and tissue necrosis whereas leaves infected with Xcv ΔxopN(XopN(L64A,L65A,S688A)-HA) or Xcv ΔxopN (vector) were only slightly chlorotic (Figure 8D). Leaves infected with Xcv ΔxopN(XopN(L64A,L65A)-HA) exhibited an intermediate phenotype – mild chlorosis but no tissue collapse (Figure 8D). All proteins were equally expressed in Xcv ΔxopN (Figure S5C). These data demonstrate that residues L64, L65 and S688 in XopN are important for XopN-dependent pathogen growth and symptom development in tomato.

XopN promotes TARK1 and TFT1 interaction in planta

Analysis of the XopN triple mutant (Figure 8) suggests that the N-terminus of XopN plays an important role in XopN/TFT1 binding in planta. It is possible that the N-terminal domain simply affects the conformation of the C-terminal domain in the context of the whole XopN polypeptide. Alternatively, but not mutually exclusive, it is possible that the N-terminus of XopN may bind a host factor, resulting in the formation of a protein complex that coordinates and/or stabilizes TFT1 binding at the C-terminus of XopN. We postulated that TARK1 might be one such host factor considering that it binds to the N-terminus of XopN [28] and binding to full-length XopN requires residues L64 and L65 (Figure S8). If TARK1 is required for XopN to bind TFT1, we reasoned that TARK1 may bind TFT1 and/or a complex comprising TARK1/XopN/TFT1 may exist in planta.

To begin to address this, we used the transient BiFC assay in N. benthamiana to directly monitor TARK1 and TFT1 protein-protein interactions inside plant cells in the presence and absence of wild type or mutant versions of XopN. For the BiFC assay, three Agrobacteria strains, each containing a different protein fusion construct, were mixed equally (final concentration 6x10^8 CFU/mL) and then the mixture was hand-infiltrated into N. benthamiana leaves. At 48 HPI, leaf epidermal cells were imaged by confocal microscopy. The three protein fusions tested were: (1) = TARK1-Venus; the non-fluorescent N-terminal domain of Venus fused to the C-terminal domain of TFT1; (2) TARK1-SCFP3A; the non-fluorescent C-terminal domain of SCFP3A fused to the C-terminal domain of TARK1; and (3) wild type or mutant XopN-6His or GUS-6His, a negative control. All of the fusion proteins analyzed were expressed in N. benthamiana (Figure S10).
Co-expression of TFT1-VenusN and TARK1-SCFP3A in the presence of GUS-6His did not result in fluorescence above background levels (Figure 9A), indicating that these two proteins do not interact in this assay. By contrast, co-expression of TFT1-VenusN and TARK1-SCFP3A in the presence of wild type XopN-6His resulted in bright fluorescence near the plasma membrane (PM) (Figure 9B). Interestingly, the fluorescence pattern at the PM resembles that observed for TARK1/XopN interaction in the BiFC assay [28] (Figure S9B). The fluorescence intensity for TFT1-VenusN + TARK1-SCFP3A in the presence of XopN(L64A, L65A, S688A)-6His (Figure 9C) or XopN(S688A)-6His (Figure 9D) was much weaker than that of wild type XopN-6His (Figure 9B), whereas in the presence of the triple mutant, no detectable fluorescence above background was observed (Figure 9E). The BiFC data suggest that XopN promotes TARK1/TFT1 interactions within the cell.

To confirm these findings, we developed an in vitro GST pull-down assay to monitor TARK1/XopN/TFT1 interactions. Recombinant GST and GST-TFT1 were expressed in E. coli and then purified using glutathione sepharose. TARK1-HA was coexpressed with vector, XopN-6His, XopN(L64A, L65A)-6His, XopN(L64A, L65A, S688A)-6His, or XopN(L64A, L65A, S688A)-6His in N. benthamiana leaves using Agrobacteria. Soluble protein extracts were isolated from leaves and then incubated with purified GST or

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Figure 8. XopN L64, L65 motif and S688 are required for TFT1 binding and XopN-dependent virulence. (A) Pull-down analysis of TFT1-HA and XopN(L64A, L65A, S688A)-6His, XopN(L64A, L65A)-6His, or XopN-6His in N. benthamiana. Leaves were infiltrated with a mixed suspension of A. tumefaciens expressing TFT1-HA (4 × 10^6 CFU/mL) and A. tumefaciens expressing XopN(L64A, L65A)-6His, XopN(L64A, L65A, S688A)-6His or XopN-6His (4 × 10^6 CFU/mL). After 48 h, protein was extracted, purified by Ni⁺ affinity chromatography, and then analyzed by protein gel blot analysis using anti-His and anti-HA sera. Expected protein MW: TFT1-HA = 29.3 kDa; XopN(L64A, L65A)-6His, XopN(L64A, L65A, S688A)-6His and XopN-6His = 78.7 kDa. +, protein expressed; −, vector control. STD, molecular weight standard. (B) BiFC analysis of XopN/TFT1 interactions in N. benthamiana. Leaves were hand-infiltrated with a suspension (8 × 10^6 CFU/mL total) of two A. tumefaciens strains expressing different fusion proteins (XopN-nYFP+TFT1-cCFP; L64A, L65A-nYFP+TFT1-cCFP; S688A-nYFP+TFT1-cCFP; L64A, L65A, S688A-nYFP+TFT1-cCFP; or GUS-nYFP+TFT1-cCFP) and then visualized by confocal microscopy at 48 hpi at 63X. White bar = 25 μm. (C) Growth of Xcv ΔxopN (vector), Xcv ΔxopN (L64A, L65A, S688A-HA), Xcv ΔxopN (L64A, L65A-HA), or Xcv ΔxopN (XopN-HA) strains in susceptible VF36 tomato leaves. Leaves were hand-infiltrated with a 1 × 10^5 CFU/mL suspension of bacteria. Number of bacteria in each leaf was quantified at 0 and 8 DPI. Data points represent mean CFU/cm² ± SD of three plants. Different letters at day 8 indicate statistically significant (one-way analysis of variance and Tukey’s HSD test, P < 0.05) differences between the samples. Vector = pVS61. Analysis was repeated at least three times. (D) Phenotype of tomato leaves inoculated with the strains described in (C). Leaves were photographed at 12 DPI. Similar phenotypes were observed in 3 independent experiments.

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GST-TFT1 in a standard GST pull-down assay. In the absence of wild type XopN, TARK1 was not purified by GST or GST-TFT1 (Figure 9F). This indicates that TARK1-HA does not physically interact with GST or GST-TFT1 under these assay conditions. By contrast, GST-TFT1 (but not GST alone) affinity purified TARK1-HA and XopN-6His when both proteins were present in the *N. benthamiana* extracts (Figure 9F). TARK1-HA was not enriched by GST-TFT1 when the plant extracts contained TARK1-HA and mutant versions of XopN-6His (i.e. XopN(L64A,L65A)-6His, XopN(S688A)-6His, or XopN(L64A,L65A,S688A)-6His). Proteins were purified using glutathione sepharose and analyzed by immunoblot analysis using anti-His, anti-HA, and anti-GST sera. Protein input levels are shown on the left. GST and GST-TFT1 pull-downs are shown on right. Expected protein MW: GST = 28 kDa; GST-TFT1 = 56.5 kDa; TARK1-HA = 67.9 KDa; XopN(L64A,L65A)-6His, XopN(L64A,L65A,S688A)-6His and XopN-6His = 78.7 KDa. +, protein expressed; −, vector control. STD, molecular weight standard.

**Figure 9.** XopN promotes TARK1 and TFT1 binding in *N. benthamiana*. (A-E) BiFC analysis of TARK1/TFT1 interactions in *N. benthamiana* leaves in the presence of wild type and mutant XopN protein. Leaves were hand-infiltrated with a suspension (6×10^8 CFU/mL total) of three *A. tumefaciens* strains expressing different fusion proteins: (A) GUS-6His+TARK1-SCFP3Ac+TFT1-VenusN; (B) XopN-6His+TARK1-SCFP3Ac+TFT1-VenusN; (C) XopN(L64A,L65A)-6His+TARK1-SCFP3Ac+TFT1-VenusN; (D) XopN(S688A)-6His+TARK1-SCFP3Ac+TFT1-VenusN; (E) XopN(L64A,L65A,S688A)-6His+TARK1-SCFP3Ac+TFT1-VenusN. Cells were visualized by confocal microscopy at 48 HPI at 63X. White bar = 40 μm. (F) GST-TFT1 affinity purification of TARK1 and XopN in vitro. GST or GST-TFT1 was incubated with *N. benthamiana* leaf extracts containing TARK1-HA = vector, XopN-6His or mutant XopN-6His (i.e. XopN(L64A,L65A)-6His, XopN(S688A)-6His, or XopN(L64A,L65A,S688A)-6His). Proteins were purified using glutathione sepharose and analyzed by immunoblot analysis using anti-His, anti-HA, and anti-GST sera. Protein input levels are shown on the left. GST and GST-TFT1 pull-downs are shown on right. Expected protein MW: GST = 28 kDa; GST-TFT1 = 56.5 kDa; TARK1-HA = 67.9 KDa; XopN(L64A,L65A)-6His, XopN(L64A,L65A,S688A)-6His and XopN-6His = 78.7 KDa. +, protein expressed; −, vector control. STD, molecular weight standard.

**Discussion**

In this study, we characterized the role of the tomato 14-3-3 TFT1 in plant defense and the relevance of a putative XopN/TFT1 complex in planta. Given that XopN suppresses PTI during infection, we hypothesized that TFT1 might function as: (1) a positive regulator of defense enzyme activity and/or defense signal transduction, in which case XopN may suppress TFT1 activity to promote virulence; (2) a negative regulator of defense whose activity and/or stability is positively regulated by XopN binding; or (3) a “clamp” to increase and/or facilitate XopN’s virulence activity within the plant cell. Our data show that *TFT1* is a PTI-induced gene (Figure 1) that is required for the expression of some
PTI marker genes (Figure 3) and to inhibit Xcv growth during infection in tomato (Figure 2). Moreover, mutations that prevent XopN from binding to TET1 in plant extracts attenuate XopN-dependent virulence in tomato (Figure 5 and 6). These findings are consistent with hypothesis 1, indicating that TET1 is a component of the PTI machinery that is targeted by XopN during Xcv infection.

How TET1 or any other 14-3-3 isoforms function as positive regulators of PTI is not yet clear. More is known about the role of 14-3-3s in ETI. The tomato 14-3-3 isoform 7 (TFT7) interacts with the C-terminal domain of tomato MAPKKKα and regulates PCD mediated by multiple R proteins [41,53]. Coexpression of TFT7 and MAPKKKα results in an increase in MAPKKKα protein abundance and kinase activity [53]. TFT7 was subsequently found to interact with tomato MKK2, a MAP kinase which functions downstream of MAPKKKα, revealing that TFT7 recruits multiple signaling components to mediate PCD associated with immunity [41]. In addition, plant 14-3-3s have been shown to influence R-protein function. In Arabidopsis, the 14-3-3 isoform λ (designated GF14λ) binds to the C-terminal domain RPW8.2 [40], an atypical R-protein that confers broad-spectrum resistance to powdery mildew disease in Arabidopsis [54]. Overexpression of GF14λ triggers localized PCD and enhanced resistance to powdery mildew, whereas reduced GF14λ expression compromises both basal and RPW8.2-mediated resistance [40]. In tobacco, several 14-3-3 isoforms were shown to interact with the viral resistance protein N [55]. It is speculated that the 14-3-3 acts as a scaffold between the N protein and the tobacco mosaic virus replicase in a receptor-ligand complex [55]. These studies indicate that plant 14-3-3s are functioning as clamps and scaffolds to regulate the kinetics of ETI signaling.

14-3-3s have also been implicated in the suppression of plant defense responses. Arabidopsis GF14λ interacts with the ankyrin repeat protein (AKR2) and ascorbate peroxidase 3 (AKR3) suggesting that GF14λ may regulate antioxidant metabolism [56]. In rice, silencing of GF14α led to the accumulation of reactive oxygen species, a lesion mimic phenotype and enhanced resistance to the bacterial pathogen Xanthomonas oryzae and fungal pathogen Rhizoctonia solani [57]. The client for GF14ε is not known. Thus, the extent to which 14-3-3s negatively regulate plant defense signal transduction remains to be determined.

The physical association of T3S effectors with host 14-3-3s has also been implicated in the suppression of plant defense responses. Arabidopsis GF14α interacts with the ankyrin repeat protein (AKR2) and ascorbate peroxidase 3 (AKR3) suggesting that GF14α may regulate antioxidant metabolism [56]. In rice, silencing of GF14α led to the accumulation of reactive oxygen species, a lesion mimic phenotype and enhanced resistance to the bacterial pathogen Xanthomonas oryzae and fungal pathogen Rhizoctonia solani [57]. The client for GF14ε is not known. Thus, the extent to which 14-3-3s negatively regulate plant defense signal transduction remains to be determined.

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14-3-3 proteins are known to form rigid dimers with many of their clients [37]. If XopN does interact with a 14-3-3 dimer, our data would be consistent with the existence of a low affinity 14-3-3 binding site in XopN’s N-terminus and a high affinity site in XopN’s C-terminus. (3) The N-terminus may be required for protein-protein interactions that result in the post-translational modification (e.g., phosphorylation) of XopN inside the plant cell. Such modifications may influence the strength of the interactions between XopN and TFT1. These roles are not necessarily mutually exclusive and we can’t yet rule out that the N-terminal domain simply affects the conformation of the C-terminal domain in the context of the whole polypeptide.

We tested the model that a TARK1/XopN/TFT1 complex exists in plant cells considering that both TARK1 and TFT1 play positive roles in PTI and XopN engages in binary interactions with both TARK1 and TFT1. BiFC analysis shows that co-expression of XopN with TARK1 and TFT1 in N. benthamiana results in the formation of a TARK1/TFT1 complex (Figure 9B). Importantly, mutations in XopN that impaired the formation of TARK1/XopN or XopN/TFT1 complexes in pull-down studies also impaired the formation of TARK1/TFT1 complexes in the BiFC analysis (Figure 9C–E). The existence of a TARK1/XopN/TFT1 complex was confirmed independently using an in vitro GST-TFT1 affinity pull-down assay (Figure 9F). Taken together, these data suggest that XopN may act as a protein bridge or scaffold to promote and/or stabilize TARK1/TFT1 complexes.

Why then does XopN promote the formation of a TARK1/TFT1 complex? We have shown that both TARK1 [28] and TFT1 are required to inhibit Xcv multiplication in tomato. Their precise roles in immunity however remain to be determined. Given that XopN suppresses PTI within the plant cell, it is likely that TARK1 and TFT1 function in PTI signaling downstream of Xcv recognition. TARK1 encodes a putative leucine-rich-repetitive receptor-like kinase (LRR-RLK) with a short extracellular domain (5 LRRs) and an inactive cytoplasmic kinase domain that is localized to the plant PM [28]. Based on TARK1’s protein features, we speculate that TARK1 might interact with a primary pathogen recognition receptor or a membrane-associated defense complex to regulate PTI signaling. XopN binding to TARK1’s kinase domain in the host cytoplasm could interfere with TARK1 protein-protein interactions, stability and/or signal transduction.

Currently, we do not know if TARK1 and TFT1 operate in the same or different immune pathways. In the absence of XopN, TARK1 and TFT1 do not appear to physically interact (Figure 9). This suggests that TARK1 is not likely a TFT1 client in uninfected plant cells. Interestingly, in the presence of XopN, TARK1/TFT1 complexes are detected at the cytoplasmic-PM interface. Moreover, XopN/TFT1 complexes appear to be restricted to the plant cytoplasm (Figure 6B) reflecting the subcellular distribution of XopN, not TFT1 [28]. It is thus tempting to speculate that XopN binding to TFT1 and/or TARK1 in binary or tertiary complexes (i.e. XopN/TFT1, XopN/TARK1, and TARK1/XopN/TFT1) may lead to the sequestration of inactive immune complexes at or near the cytoplasmic-PM interface. This could impact immune signaling in several ways: 1) Formation of XopN/TFT1 complexes could interfere with the assembly and regulation of bona fide TFT1-client interactions during infection. 2) Formation of XopN/TARK1 complexes could interfere with the association, dissociation, and/or post-translational modification of immune complexes at the PM. 3) Formation of TARK1/XopN/TFT1 complexes could trap TARK1 and TFT1 in incompetent signaling complexes preventing TARK1 and TFT1 from functioning in their respective immune signaling pathways. Future work will investigate the formation, dynamics, and relevance of TARK1/XopN/TFT1 interactions to provide insight into how PTI signaling restricts Xcv growth in tomato and the biochemical mechanism(s) by which XopN suppresses PTI.

In summary, we provide evidence that TFT1 plays a positive role in PTI in tomato and is required for the inhibition of Xcv growth. We also provide evidence that XopN directly binds to TFT1 to promote Xcv growth, indicating that TFT1 is a direct host target. Based on our mutation data, we speculate that protein interactions that occur at XopN’s N-terminus with other host factors directly affect the binding affinity of the XopN/TFT1 complex. These data support a model where XopN binds to TFT1 to interfere with TFT1-client interactions that are required to limit Xcv growth in tomato.

Materials and Methods

Accession numbers for genes used in study

xopN = AM039952; TFT1 = SGN-U580865; TFT3 = SGN-U580900; TFT6 = SGN-U581259; TARK1 = SGN-U574507; PR1b = SGN-U579545; LRR22 = SGN-U44576; GRAS4 = SGN-U575365; WRKY28 = SGN-U586086; PIT5 = SGN-U571539.

Bacterial strains, growth, and matings

Strains used in this study were as follows: Escherichia coli DH5α and TOP10; Agrobacterium tumefaciens C58C1 pCH32; Xanthomonas campestris pv. vesicatoria (Xcv) strain 85-10; and Xcv ΔxopN. E. coli and A. tumefaciens were grown on Luria agar medium [58] at 37°C and 28°C, respectively. Xcv strains were grown on nutrient yeast glycerol agar (NYGA) [59] at 28°C. Xcv antibiotic selection was rifampicin (Rif) 100 μg/mL, tetracycline (Tc) 10 μg/mL, and/or kanamycin (Km) 50 μg/mL. A. tumefaciens antibiotic selection was Tc 5 μg/mL, Km 50 μg/mL, and/or spectinomycin (Sp) 50 μg/mL. E. coli antibiotic selection was carbenicillin 50 μg/mL and/or Km 50 μg/mL.

PCR and DNA constructions

Polymerase chain reaction (PCR) was used to engineer restriction sites for construct gene fusions. PCR-generated DNA fragments were cloned into pCR-BluntII-TOPO or pENTR/D-TOPO (Invitrogen). Primer sequences used for PCR are listed in Table S1. Conditions used for PCR and cloning details will be available on request. The sequence of all DNA constructs was verified by cycle sequencing.

Bacterial growth curves

To monitor Xcv growth in planta, Solanum lycopersicum cultivar VF36 leaves were hand-inoculated by complete infiltration of the leaf tissue with a 1×10⁶ CFU/mL suspension of bacteria in 10 mM MgCl₂ using a needless syringe. Leaflets of the same age and position within each plant were used for each experimental test. Plants were kept under 16 h light/day at 28°C. Four leaf discs (0.5 cm²) per treatment per time point were ground in 10 mM MgCl₂ using a needleless syringe. Leaflets of the same age on the same branch were used for each experimental test. Plants were kept under 16 h light/day at 28°C. Four leaf discs (0.5 cm²) per treatment per time point were ground in 10 mM MgCl₂ and diluted and spotted onto NYGA plates in triplicate to determine bacterial load. Three or four biological replicates (i.e., three or four plants) were used, and the experiment was repeated at least three times. The average bacterial titer ± SD is reported.

Construction of XopN point mutants

The XopN(S688A, S688D, or S688E) mutants were generated with a QuikChange site-directed mutagenesis kit (Stratagene) using pCR-BluntII-TOPO as template and primer set BS32/BS33, JG684/JG685, or JG686/JG687. The XopNL64A/L65A/S688A mutant was generated by restriction enzyme digest of pCR-Blunt-
II (xopN(L64A,L65A)) and pCR-Blunt-II(xopN/S688A)) mutants with XbaI. The 639 bp fragment from pCR-BluntII(xopN/S688A)) and 5,721 bp fragment from pCR-BluntII(xopN(L64A,L65A)) were gel purified (QIAGEN), ligated, and sequenced to create pCR-BluntII(xopN(L64A,L65A,S688A)).

Yeast constructs, two-hybrid analysis, and protein extraction

Wild type XopN and five XopN deletion mutants (i.e., N, C, M4, M5, and M6) were generated by PCR using the primer sets BS1/BS2, BS1/BS4, BS3/BS2, BS6/BS2, BS1/BS7, and BS1/BS8, respectively. XopN(S688A), XopN(L64A,L65A), and XopN(L64A,L65A,S688A) were generated by PCR using the primer set BS1/BS2 on pCR-Blunt-II(xopN/S688A)), pCR-Blunt-II(xopN(L64A,L65A)), and pCR-Blunt-II(xopN(L64A,L65A,S688A)), respectively. The respective PCR products were cloned into pENTR/D-TOPO, and then recombined into the pXDGATcy86 destination vector [60] via a Gateway LR reaction to create pXDGATcy86(xopN), pXDGATcy86(xopN(L64A,L65A)), pXDGATcy86(xopN(L64A,L65A,S688A)).

Construction of XopN mutants in binary vectors

Wild-type and three deletions mutants (xopN(L64A,L65A,S688A)-6His) were then subcloned into the XopN345–733-6His, and XopN1–604-6His were generated by PCR using the primer sets JG282/JG283, JG284/JG285, and TOPO cloned into pCR-Blunt-II(xopN(L64A,L65A,S688A)). Yeast constructs, two-hybrid analysis, and protein extraction

Protein gel blot analysis

Proteins were separated by SDS-PAGE and analyzed by immunoblot analysis as described [61]. Proteins were visualized by chemiluminescence analysis using anti-HA (Covance), anti-cc-myc (Covance), anti-GFP (BD Biosciences), anti-foxHis (Qiagen), and anti-XopN antibodies [28], peroxidase-conjugated secondary antibodies (Bio-Rad) and ECL reagent (GE Biosciences).

Construction of XopN mutants in binary vectors

Wild-type and three deletion mutants (xopN1–349-6His, xopN1345–735-6His, and XopN1–604-6His) were generated by PCR using the primer sets JG282/JG285, JG282/JG283, JG284/JG285, JG282/JG656, respectively, and pCR-Blunt-II(xopN) as template. The genes were TOPO cloned into pCR-Blunt-II. XopN(S688A, S688D, or S688E)-6His, XopN(L64A,L65A)-6His, and XopN(L64A,L65A,S688A)-6His were generated by PCR amplification of pCR-Blunt-II(xopN/S688A, S688D, or S688E)), pCR-Blunt-II(xopN(L64A,L65A)), and pCR-Blunt-II(xopN(L64A,L65A,S688A)) templates, respectively, using the primer sets JG282/JG283 and TOPO cloned into pCR-Blunt-II. XopN1–604-6His, XopN1–349-6His, XopN345–735-6His, XopN1–604-6His, XopN(S688A, S688D, or S688E)-6His, XopN(L64A,L65A)-6His, and XopN(L64A,L65A,S688A)-6His were then subcloned into the HindIII and XbaI sites of pZEKR-IC-LCY creating pZEKR(xopN1–604-6His), pZEKR(xopN1–349-6His), pZEKR(xopN345–735-6His), pZEKR(xopN1–604-6His), pZEKR(xopN1–349-6His), pZEKR(xopN345–735-6His), pZEKR(xopN1–604-6His), pZEKR(xopN1–349-6His), pZEKR(xopN345–735-6His), and pZEKR(xopN1–604-6His), respectively. To construct binary plasmids containing one gene, TARK1-HA and TFT1-HA were independently cloned into the XbaI and SacI sites of the pAUTC940 vector (a gift from Stanton B. Gelvin) containing the super-promoter [62]. To construct binary plasmids containing two genes, TARK1-HA and TFT1-HA were each sub-cloned into the XbaI and SacI sites of pBSH[SP-T] [29], a vector containing the (α5)3μas super-promoter (SP) and NOS terminator (T) sequences. SP-TARK1-HA-NOS and SP-TFT1-HA-NOS fragments were then sub-cloned into the SacI site of the pEZRK-derived vectors creating pEZRK(xopN1–604-6His+TARK1-HA), pEZRK(xopN(S688A)-6His+TFT1-HA), pEZRK(xopN1–604-6His+TFT1-HA), pEZRK(xopN(L64A,L65A,S688A)-6His+TFT1-HA), pEZRK(xopN(L64A,L65A)-6His+TFT1-HA), pEZRK(xopN(S688A)-6His+TFT1-HA), pEZRK(xopN(L64A,L65A,S688A)-6His+TFT1-HA), and pEZRK(xopN(S688A)-6His+TFT1-HA). All constructs were transformed into A. tumefaciens strain C58C1 pCH32 for transient protein expression in N. benthamiana.

Agrobacterium-mediated transient protein expression in N. benthamiana

All binary plasmids were transformed into Agrobacterium tumefaciens strain C58C1 pCH32 for transient protein expression in N. benthamiana. Strains were grown overnight at 28°C on Luria agar medium containing the appropriate antibiotics. Bacteria were collected and inoculated in media (10 mM MES, pH 5.6, 10 mM MgCl2, and 150 μM acetylsyringone; Acros Organics) 2 h before inoculation. Leaves were hand-inoculated with a suspension of either one (6×105 cells/mL) or two (3×105 cells/mL) strains in induction media. Plants were incubated at room temperature under continuous low light for 2 to 4 days.

N. benthamiana pull-down assays

Proteins were coexpressed in N. benthamiana leaves via the Agrobacterium-mediated transient expression assay. After 48 hours, leaves were frozen in liquid N2 and then pulverized in extraction buffer (1.5M NaOH and 7% 2-mercaptoethanol) and then proteins were precipitated in 10% trichloroacetic acid. Protein pellets were washed in 1M Tris, pH 6.8 and then resuspended in 8M urea sample buffer.

Protein gel blot analysis

Proteins were separated by SDS-PAGE and analyzed by immunoblot analysis as described [61]. Proteins were visualized by chemiluminescence analysis using anti-HA (Covance), anti-cc-myc (Covance), anti-GFP (BD Biosciences), anti-foxHis (Qiagen), and anti-XopN antibodies [28], peroxidase-conjugated secondary antibodies (Bio-Rad) and ECL reagent (GE Biosciences).
(L64A,L55A,S688A)-HA). The EcoRI fragment was then subcloned into pVSP61 to create pVSP61(pPspTFT1NcoI(5668A, S688D, or S688E)-HA) and pVSP61(pPspTFT1NcoI(564A,L55A,S688A)-HA). To create pVSP61-BHI, pVSP61 was digested with BamHI, treated with Klenow fragment and ligated. The EcoRI fragment of pCR-Blunt-II(pPspTFT1NcoI(5668A-64)-HA) was subcloned into pVSP61-BHI to create a vector pVSP61-BHI(pPspTFT1NcoI(5668A-64)-HA). The ORF encoding XopNΔ6 His was amplified from pCR-Blunt-II(pPspTFT1NcoI(5668A-64)-HA) using the primer set BS1/KT34 to generate pCR-Blunt-II(pPspTFT1NcoI(5668A-64)-HA). pCR-Blunt-II (pPspTFT1NcoI(5668A-64)-HA) and pVSP61-BHI(pPspTFT1NcoI(5668A-64)-HA) were digested with Xhol and BamHI. The 660 bp fragment from pCR-Blunt-II (pPspTFT1NcoI(5668A-64)-HA) was ligated into the pVSP61-BHI(pPspTFT1NcoI(5668A-64)-HA) digested with Xhol and BamHI to create pVSP61-BHI(pPspTFT1NcoI(5668A-64)-HA). All vectors were introduced into N. benthamiana by triparental mating.

**Virus-induced gene silencing in tomato**

A 457 bp fragment of the ~34 to 423 region of TFT1 was amplified using primer set JR207/JR208, cloned into pCR8/GW, and moved into the Gateway destination binary vector pTRV2 [63] using an LR clonase reaction (Invitrogen). Similarly, a 494 bp fragment of the phytoene desaturase (PDS) gene was amplified and moved into pTRV2 to serve as a silencing control [63]. Binary vectors were mobilized into A. tumefaciens C5801 pCH32 by triparental mating. A modified protocol [63] was used for VIGS. Vf36 tomato leaflets with fully expanded cotyledons but no true leaves (approximately 10 days old) were inoculated with a mixed inoculum containing a 1.5×10^6 CFU/mL suspension of Agrobacteria containing pTRV1 (contains the DNA polymerase of tobacco rattle virus) and a 1.5×10^6 CFU/mL suspension of Agrobacteria containing pTRV2 (contains the viral coat protein and fragments of genes for silencing), pTRV2(TFT1) or pTRV2(PDS). Seedlings were put into a growth chamber at 20°C, 80% humidity, and 16 hr of light for three weeks until PDS silencing symptoms (chlorosis) were observed in the control plants. Standard bacterial growth curves were performed with 4–5-week old vector and TFT1-silenced plants. Prior to infection (0 DPI), total RNA was isolated from two leaflets on the same branch for each plant line to measure TFT1, TFT3, and TFT6 mRNA levels by Q-PCR. The same leaflets were then inoculated with a 1×10^5 CFU/mL suspension of wild type Xcv or the Xcv ΔhrpF mutant. The number of bacteria in each leaflet was quantified at 0, 6, and 9 DPI. At 6 DPI, total RNA was isolated from the infected leaflets to measure PR-b1b, PTI5, GRAS, WRKY28, and LRR22 mRNA levels by Q-PCR.

**RNA isolation and quantitative RT-PCR**

Total RNA was isolated from leaves using Trizol reagent (Invitrogen) according to manufacturer’s instructions. Five μg of RNA were used for cDNA synthesis. Quantitative real-time RT-PCR was performed using the cDNA and gene-specific primers (Table S1). Each cDNA was amplified by Q-PCR using Maxima SYBR Green qPCR Master Mix (Fermentas) and the MJ Opticon 2 (Bio-Rad). ACTIN expression was used to normalize the expression value in each sample and relative expression values were determined against the vector control using the comparative Ct method (2^(-ΔΔCt)).

**Phos-tag gel analysis**

Phosphate affinity SDS-PAGE, using acrylamide-pendant Phos-tag (Wako Pure Chemicals) was performed as described by manufacturer to detect phosphorylated XopN mobility shifts in plant extracts. Wild type and mutant XopN-6His proteins were transiently expressed and purified using Ni-NTA chromatography as described above for the pull-down assays using modified extraction buffer (50 mM NaH2PO4, pH 8.0, 150 mM NaCl, 10 mM imidazole, 2% glycerol, 1% Triton X-100, 1 mM EDTA, 1X protease inhibitor cocktail, 5 mM NaF, and 2 mM Na3VO4) and wash buffer (50 mM NaH2PO4, pH 8.0, 150 mM NaCl, 10 mM imidazole, 2% glycerol, 1% Triton X-100). Purified proteins were incubated with buffer (50 mM Tris-HCl, pH 7.9, 100 mM NaCl, 10 mM MgCl2, 1 mM DTT) or buffer and 20 units of calf intestinal alkaline phosphatase for 60 min. Proteins were separated by 8% SDS-PAGE with 50 μM Mn2⁺-Phos-tag and then analyzed by protein gel blot analysis using anti-His sera.

**Phosphopeptide enrichment and mass spectrometry**

XopN-6His was transiently expressed in N. benthamiana leaves using Agrobacteria-mediated transformation. Protein was solubilized from 10 g of leaves using buffer containing 100 mM sodium phosphate (pH 8), 10 mM Tris (pH 8), 8 mM urea, 1% CHAPS, 5 mM NaF, 2 mM Na3VO4, and protease inhibitor cocktail (Sigma). XopN-6His protein (~5 μg) purified using Ni-nitrilotriacetic acid Superflow agarose (Qiagen) was excised from a Coomassie-stained SDS-PAGE gel and then digested with trypsin [64]. Phosphopeptides were enriched using TiO2 followed by HPLC and MS. The enrichment protocol was performed using titanium phosphate tips (GL Sciences) and methodology as reported [65]. Peptides were separated on a Proxeon nano HPLC (Thermo Fisher) using a self packed fused silica column with a ID of 75 μm, packed with a 3 μm C18 material (Peeke Scientific). Solvent A consisted of 99.4% water/0.6% acetic acid and solvent B was 98.4% acetonitrile/1% water/0.6% acetic acid. Flow rate was 300 nL/min infused into the MS using a Proxeon source with a potential of 2.2 kV. The MS was a LTQ Orbitrap Velos, set in data dependent acquisition mode to perform both HCD and ETD on the top 3 most intense precursor ions. MS/MS on charge states 2+ and higher were acquired. The data was analyzed using Sequest on a Sorcerer platform. Xcalibur software (Thermo Fisher) was used to manually inspect the data and produce ion chromatograms. A custom database was used to mitigate search time.

**Bifluorescence complementation assay**

To study XopN/TARK1 or XopN/TFT1 interactions, binary BiFC-Gateway destination vectors pXNGW, pXCGW, and pXCGW were used as previously described [28]. To study TARK1/TFT1 interactions, binary BiFC-Gateway destination vectors were obtained from Dr. Jorg Kudla [66]. Gateway LR reactions were performed with pENTR(TFT1) and pDEST(GW). VYNE to create pDEST(TFT1-VenusN) and pENTR(TARK1) and pMAS-DEST(WT)-SCFP244. Each BiFC binary vector was transformed into A. tumefaciens C581G1 pCH32. The resulting two vectors were mixed equally with a third C581G1 pCH32 strain containing pEZKR (GUS-6His), pEZKR(xopN-6His), pEZKR(xopN(x64A,L65A)-HA), pEZKR(xopN/L64A,L65A,S688A)-HA), or pEZKR(xopN/S688A)-HA) (final concentration 6×10^6 CFU/mL) and then infiltrated into N. benthamiana leaves. At ~48 HPI, leaf discs were placed on a slide and visualized using a 20× and 63× water immersion objective lens on a Leica TCS SP5 confocal microscope with Leica LAS AF software. Proteins were excited at 488 nm by an argon laser and emitted light was captured at 510 nm.

**GST-TFT1 affinity purification assay**

Plasmids pDEST15(GST) or pDEST15(GST-TFT1) were transformed into E. coli BL21(DE3) pLYS S for GST or GST-TFT1 protein expression. GST and GST-TFT1 were purified by Glutathione Sepharose 4B (GE healthcare) as described [14]. GST
or GST-TFT1 bound beads were washed three times with plant extraction buffer (50 mM Tris (pH 8), 150 mM NaCl, 2% glycerol, 1% Triton X-100), and protease inhibitor cocktail (Sigma) to eliminate background in the pull-down assay. TARK1-HA and vector, XopN-6His, XopN (L64A,L65A)-6His, XopN(S688A)-6His, or XopN(L64A,L65A,S688A)-6His were co-expressed in N. benthamiana leaves using Agrobacteria-mediated transformation. After 48 hours, proteins were solubilized in plant extraction buffer and then incubated with GST or GST-TFT1 bound beads for 2 hours at 4°C. Beads were washed three times with extraction buffer. Purified proteins were analyzed by gel blot analysis using anti-HA sera, anti-GST sera, and anti-His sera.

Supporting Information

Figure S1 Relative TFT1, TFT3 and TFT6 mRNA levels in the control (TRV2) and TFT1 silenced (TRV2-TFT1) tomato lines used in Figure 2. Total RNA isolated from leaves prior to growth curve analysis was used for Q-PCR to monitor (A) TFT1, (B) TFT3, and (C) TFT6 mRNA levels in TRV2 or TRV2-TFT1 tomato lines inoculated with Xcv, Xcv ΔxopN, or Xcv ΔhphF at day 0. Actin mRNA expression was used to normalize the expression value in each sample. Error bars indicate SD for four plants. (TIF)

Figure S2 Relative TFT1 mRNA levels in the control (TRV2) and TFT1 silenced (TRV2-TFT1) tomato lines used in Figure 3. Total RNA isolated from infected leaves at 6 HPI was used for Q-PCR. Actin mRNA expression was used to normalize the expression value in each sample. Error bars indicate SD for four plants. (TIF)

Figure S3 Protein gel blot analysis of proteins isolated from the yeast strains described in Figure 4B. Total protein was extracted from yeast cells and then examined by protein gel blot analysis using GAL4-DBD or HA antiserum. Yeast strains analyzed were AH109 carrying pXDGATcy86 (vector), XopN(L64A,L65A), XopN(S688A), or XopN(L64A,L65A,S688A) and pGADT7 (vector or TARK1CD). The expected molecular weights for each GAL4-DBD fused to XopN, XopN(N), XopN(C), XopN(M4), XopN(M5), and XopN(M6) are approximately 97, 56, 60, 74, 83, and 74 kDa, respectively. The expected molecular weight for GAL4-AD-HA fused to TFT1 is 52 kDa. Red arrowheads label the corresponding proteins. STD, molecular weight standard shown in kDa. (TIF)

Figure S4 XopN(1–349)-6xHis associates with TARK1-HA. Pull-down analysis of TARK1-HA and XopN-6His, XopN(1–349)-6His, or XopN(345–733)-6His transiently over-expressed in N. benthamiana leaves using Agrobacteria. Leaves were hand-infiltrated with a 6×10⁶ CFU/mL suspension of A. tumefaciens co-expressing TARK1-HA, and XopN-6His, XopN(1–349)-6His, or XopN(345–733)-6His and TARK1-HA. After 40 hours, protein was extracted, purified by Ni²⁺ affinity chromatography, and then analyzed by protein gel blot analysis using anti-His and anti-HA sera. Expected protein MW: TARK1-HA = 67.9 kDa; XopN-6xHis = 78.7 kDa; XopN(1–349)-6His = 38.0 kDa; XopN(345–733)-6His = 42.0 kDa. +, vector control. STD, molecular weight standard shown in kDa. (TIF)

Figure S5 Protein gel blot analysis of wild-type XopN-HA or XopN mutants in Xcv ΔxopN cell extracts. (A) Protein expression levels of XopN-HA or XopN(1–604)-HA in Xcv ΔxopN cell extracts for data shown in Figure 5. (B) Protein expression levels of XopN-HA, XopN(S688A)-HA, XopN(S688D)-HA, or XopN(S688E)-HA in Xcv ΔxopN cell extracts for data shown in Figure 6D,E. (C) Protein expression levels of XopN-HA or a series of XopN mutant proteins in Xcv ΔxopN cell extracts for data shown in Figure 8C,D. Xcv strains were grown overnight at 28°C on nutrient yeast glycerol agar (NYGA) medium containing the appropriate antibiotics. Bacteria were collected and incubated in Minimal Media (7.5 mM (NH₄)₂SO₄, 0.1 M KH₂PO₄ (pH 7.0), 2 mM Na-Citrate, 0.3% casein amino acid hydrolysate, 10 mM sucrose, 1 mM MgSO₄, 5×10⁻⁷% thiamine) 12 h at 28°C with shaking. Cells were collected and washed once with 10 mM MgCl₂. A 4 ml bacterial culture (4×10⁸ CFU/mL) MA media pH 5.4 was grown 4.5 h with shaking at 28°C. Cells were collected, resuspended in 100 μL urea sample buffer, and then analyzed by gel blot analysis using anti-HA sera. Expected protein MW: XopN-HA, L64A,L65A-HA, S688A-HA, S688D-HA and S688E-HA = 78.7 kDa; XopN(1–604)-HA = 63.2 kDa; N-term-HA = 33.8 kDa; C-term-HA = 48.0 kDa. Vector = pVSP61. STD, molecular weight standard shown in kDa. (TIF)

Figure S6 TARK1 and TFT1 interaction with XopN(L64A,-L65A,S688A) triple mutant in yeast. (A) Yeast strain AH109, pXDGATcy86(GAL4-DNA binding domain) containing XopN, XopN(L64A,L65A), XopN(S688A), or XopN(L64A,L65A,S688A) were independently transformed with the following PREY constructs: pGADT7(GAL4 activation domain) alone (Vector) or pGADT7 containing TARK1CD or TFT1. Strains were spotted on nonselective (SD-LT) and selective (SD-LTH) media and then incubated at 30°C for 3d. (B) Protein gel blot analysis of proteins isolated from the yeast strains described (A). Total protein was extracted from yeast cells and then examined by protein gel blot analysis using GAL4-DBD or HA antiserum. Yeast strains analyzed were AH109 carrying pXDGATcy86 (vector, XopN, XopN(L64A,L65A), XopN(S688A), or XopN(L64A,L65A,S688A)) and pGADT7 (vector or TARK1CD). The expected molecular weight for each GAL4-DBD fused to XopN and point mutants is ~97 kDa, and GAL4-AD-HA fused to TARK1CD is ~62 kDa. Red arrowheads label the corresponding proteins. STD, molecular weight standard shown in kDa. (TIF)

Figure S7 The putative 14-3-3 binding sites and PEST motif are not required for TFT1 binding in planta. (A) XopN-AM1/M2-6His and (B) XopN-AP6-6His interact with TFT1 in N. benthamiana. Leaves were hand-infiltrated with a 6×10⁶ CFU/mL suspension of A. tumefaciens co-expressing TFK1-HA and XopN-6His, XopN-AM1/M2-6His, and XopN-AP6-6His. After 48 h, protein was extracted, purified by Ni²⁺ affinity chromatography, and then analyzed by protein gel blot analysis using anti-His and anti-HA sera. Expected protein MW: XopN-6His = 78.7 kDa; XopN-AP6-6His = 76.1 kDa; XopN-AM1/M2-6His = 76.6 kDa; TFK1-HA = 29.3 kDa. (TIF)

Figure S8 XopN(S688A)-6His interacts with TARK1-HA in pull-down assay. Pull-down analysis of TARK1-HA and XopN-6His, XopN(L64A,L65A)-6His, or XopN(S688A)-6His transiently over-expressed in N. benthamiana leaves using Agrobacteria. Leaves were hand-infiltrated with a 6×10⁶ CFU/mL suspension of A. tumefaciens expressing TARK1-HA or co-expressing TARK1-HA and XopN-6His, XopN(L64A,L65A)-6His, or XopN(S688A)-6His. After 48 hours, protein was extracted, purified by Ni²⁺ affinity chromatography, and then analyzed by protein gel blot analysis using anti-His and anti-HA sera. Expected protein MW: TARK1-HA = 67.9 kDa; XopN-6His, XopN(L64A,L65A)-6His,
XopN(S688A)-6His = 78.7 kDa. +, protein expressed; −, vector control. STD, molecular weight standard shown in kDa. (TIF)

**Figure 59** Protein gel blot analysis and confocal microscopy for BiFC analyses. (A) Protein gel blot analysis of the BiFC assay monitoring XopN/TFT1 interactions shown in **Figure 8B**. Anti-XopN, anti-His and anti-GFP sera were used. (B) BiFC assay of XopN/TARK1 interactions in *N. benthamiana* leaves. Leaves were hand-infiltrated with a 8×10^8 CFU/mL total suspension of two *A. tumefaciens* strains expressing different fusion proteins (i.e., XopN-nYFP+TARK1-cCFP; L64A,L65A-s6His+TART1-cCFP; S688A-nYFP+TARK1-cCFP; L64A,L65A,S688A-TARK1-cCFP; or negative control GUS-nYFP+TARK1-cCFP) and then visualized by confocal microscopy at 48 HPI at 63X. White bar = 25 μm. (C) Protein gel blot analysis of the BiFC assay in (B) above. Anti-XopN, anti-His and anti-GFP sera were used. (TIF)

**Figure 10** Protein gel blot analysis for TARK1/TFT1 BiFC assays shown in **Figure 9A-E**. Proteins were isolated from infected *N. benthamiana* leaves at 48 HPI and then analyzed by gel blot analysis using anti-His, anti-HA, and anti-c-Myc sera. Lane 1: XopN-6His+TARK1-SCFP3A+TFT1-VenusN; Lane 2: XopN-(L64A,L65A)-6His+TART1-SCFP3A+TFT1-VenusN; Lane 3: XopN-S688A-6His+TARK1-SCFP3A+TFT1-VenusN; Lane 4: XopN-(L64A,L65A,S688A)-6His+TART1-SCFP3A+TFT1-VenusN; Lane 5: GUS-6His+TARK1-SCFP3A+TFT1-VenusN. VenusN domain has the c-Myc epitope. SCFP3A domain has the HA epitope. (TIF)

**Table 8** List of primers used in this study. (DOC)

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**Author Contributions**

Conceived and designed the experiments: KWT, JGK, MBM. Performed the experiments: KWT, JGK, XBS, CDA, JAR, CMA. Analyzed the data: KWT, JGK, XBS, CDA, JAR, CMA, MBM. Contributed reagents/materials/analysis tools: KWT, JGK, XBS, CDA, JAR, CMA, MBM. Wrote the paper: KWT, JGK, CMA. Authors contributed equally to this work: KWT, JGK.

### References