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The type VI secretion system of *Stenotrophomonas rhizophila* CFBP13503 limits the transmission of *Xanthomonas campestris* pv. *campestris* 8004 from radish seeds to seedlings

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Abstract

Stenotrophomonas rhizophila CFBP13503 is a seedborne commensal bacterial strain, which is efficiently transmitted to seedlings and can outcompete the phytopathogenic bacterium *Xanthomonas campestris* pv. *campestris* (Xcc8004). The type VI secretion system (T6SS), an interference contact-dependent mechanism, is a critical component of interbacterial competition. The involvement of the T6SS of *S. rhizophila* CFBP13503 in the inhibition of Xcc8004 growth and seed-to-seedling transmission was assessed. The T6SS cluster of *S. rhizophila* CFBP13503 and nine putative effectors were identified. Deletion of two T6SS structural genes, *hcp* and *tssB*, abolished the competitive advantage of *S. rhizophila* against Xcc8004 in vitro. The population sizes of these two bacterial species were monitored in seedlings after inoculation of radish seeds with mixtures of Xcc8004 and either *S. rhizophila* wild-type (wt) strain or isogenic *hcp* mutant. A significant decrease in the population size of Xcc8004 was observed during confrontation with the *S. rhizophila* wt in comparison with T6SS-deletion mutants in germinated seeds and seedlings. We found that the T6SS distribution among 835 genomes of the *Stenotrophomonas* genus is scarce. In contrast, in all available *S. rhizophila* genomes, T6SS clusters are widespread and mainly belong to the T6SS group i4. In conclusion, the T6SS of S. *rhizophila* CFBP13503 is involved in the antibiosis against Xcc8004 and reduces seedling transmission of Xcc8004 in radish. The distribution of this T6SS cluster in the *S. rhizophila* complex could make it possible to exploit these strains as biocontrol agents against *X. campestris* pv. *campestris*.

KEYWORDS
interbacterial competition, seed, seedling transmission, *Stenotrophomas rhizophila*, type VI secretion system, *Xanthomonas campestris* pv. *campestris*

1 | INTRODUCTION

Disease emergence of plant pathogens is the result of changes in host range and/or pathogen dispersion into a new geographic area (Engering et al., 2013). Regarding this second point, seed transmission represents an important means of pathogen dispersion and is therefore significant in the emergence of plant diseases (Baker & Smith, 1966). Indeed, the International Seed Testing Association Reference Pest List v9 identified 333 seedborne pests (viruses, bacteria, fungi, oomycetes and nematodes) in more than 50 plant species (Denancé & Grimault, 2022). Of these seedborne pests, 145 are directly transmitted to plants (Denancé & Grimault, 2022).

Pathogens are not the only microorganisms that can be carried by seeds. More than 1000 bacterial and fungal taxa were identified in the seed microbiota of 50 plant species (Simonin et al., 2022). This important microbial diversity observed on seed samples is, however, more restricted at the scale of an individual seed with one dominant taxon of variable identity (Chesneau et al., 2022; Newcombe et al., 2018). Because the seed is a limited habitat in terms of resources and space, microbial competition is likely to play an important role in seed microbiota assembly. Using these competition processes to promote seed transmission of nonpathogenic microorganisms at the expense of plant pathogens could be deployed as a biocontrol-based strategy (Barret et al., 2016). However, this approach requires a better understanding of the mechanisms involved in these microbial competition processes, notably the relative importance of exploitative competition (i.e., increase uptake and use of nutrients) versus interference competition (i.e., limiting the access of other cells to resources; Granato et al., 2019).

The *Lysobacteraceae* (earlier known as *Xanthomonadaceae*) family includes numerous species of plant pathogens such as *Xanthomonas* spp. (Jacques et al., 2016) and also ubiquitous *Stenotrophomonas* spp. such as commensal *S. rhizophila* (Wolf et al., 2002) and opportunistic human pathogens such as *S. maltophilia* (Gröschel et al., 2020). *Xanthomonas campestris* pv. *campestris* (Xcc), the causal agent of black rot disease of *Brassicaceae* (Vicente & Holub, 2013), is not only seed-transmitted in a range of *Brassicaceae* (Randhawa, 1984; Rezki et al., 2016; van der Wolf et al., 2019) but also in nonhost plants such as common bean (Darrasse et al., 2010). Diversity surveys of the radish seed microbiota have highlighted that Xcc shares the same habitat as numerous bacterial strains related to the *S. rhizophila* species (Rezki et al., 2016, 2018). Strains of *S. rhizophila* are efficient seedling colonizers of cotton, tomato, sweet pepper (Schmidt et al., 2012) and radish (Simonin et al., 2023) as well as commonly isolated in the rhizosphere of different plant species including rapeseed (Berg et al., 1996) and potato (Lottmann et al., 1999). The type strain of *S. rhizophila*, DSM14405^T, can protect plants against osmotic stress (Alavi et al., 2013; Egamberdieva et al., 2011) and limits the growth of fungal pathogens (Minkwitz & Berg, 2001). Other strains of *S. rhizophila* possess antibacterial activities (Lottmann et al., 1999). For instance, the strain *S. rhizophila* CFBP13503 decreases the population size of Xcc during in vitro confrontation assays (Torres-Cortés et al., 2019). This decrease in Xcc population size was attributed to exploitative competition because these strains share significant overlap in resource utilization (Torres-Cortés et al., 2019). However, the role of interference competition was only partially assessed through the production of diffusible molecules, while contact-dependent mechanisms were not tested.

Among the contact-dependent mechanisms involved in interbacterial competition, the type VI secretion system (T6SS) is probably the most widely distributed with more than 17,000 T6SS gene clusters distributed in more than 8000 genomes sequences (source SecReT6 v3; Zhang et al., 2022). The T6SS is a multiprotein complex composed of several core components, including the membrane complex TssJLM, the baseplate TssEFGK, the tail tube Hcp (TssD), the spike composed of VgrG (TssI) trimers topped by a protein containing a Pro-Ala-Ala-Arg Repeat (PAAR) motif, the contractile sheath TssBC, and the coordinating protein TssA, as well as the sheath disassembly ATPase ClpV (also known as TssH) (Cherrak et al., 2019; Cianfanelli et al., 2016; Ho et al., 2014). The T6SS allows bacteria to compete and survive in their environments by injecting toxins/effectors into target cells. Effectors are either fused (specialized effectors) to or interact (cargo effectors) with Hcp tube or VgrG/PAAR spike proteins (Cherrak et al., 2019; Cianfanelli et al., 2016; Jurėnas & Journet, 2021). The contraction of the sheath leads to the injection of Hcp and VgrG/PAAR proteins together with the effectors. Effector-immunity encoding gene pairs are often associated with genes encoding the elements involved in their delivery. These include Hcp, VgrG or PAAR proteins, and also accessory proteins named chaperones/adaptors, which facilitate the loading of effectors onto the T6SS elements (Unterweger et al., 2017). Adaptors identified so far are DUF4123-, DUF1795-, DUF2169- and DUF2875-containing proteins encoded upstream of their cognate effector (Berni et al., 2019; Unterweger et al., 2017). If effector-immunity can be orphan genes, they are often encoded in T6SS clusters or associated with *hcp* or *vgrG* in orphan *hcp/vgrG*-islands. Conserved domains or motifs have also been described for some effectors and immunity proteins that facilitate their identification (Lien & Lai, 2017). For effector proteins, these conserved domains can reflect their biochemical toxic activity. Recruitment domains and motifs, such as MIX (Marker for type sIX effectors) or FIX (Found in type sIX effectors) motifs, DUF2345/TTR (Transthyretin-like domains) domains or Rhs (Rearrangement hot spot) domains, can be found in T6SS effectors and are related to their mode of delivery (Cherrak et al., 2019; Cianfanelli et al., 2016; Jurėnas & Journet, 2021).

The T6SS secretion system is widespread among plant-associated bacteria and divided into five taxonomic groups (Bernal et al., 2018). The T6SS has been implicated in a wide range of biological processes, including microbial competition with bacteria and fungi (Luo et al., 2023; Trunk et al., 2018), epiphytic colonization of bacterial pathogens (Liyanapathiranage et al., 2021), and pathogen virulence (Choi et al., 2020; Montenegro Benavides et al., 2021; Shyntum et al., 2015). *Pseudomonas putida* KT2440 K1-T6SS also provides biocontrol properties by killing *X. campestris* when injected into plant leaves (Bernal et al., 2017). Commensal bacteria from seed microbiota carrying a T6SS could be good candidates as biocontrol agents

and may be used to limit bacterial pathogen transmission from seed to seedling. In the course of this work, we explored the possibility of limiting Xcc transmission from seed to seedling through a contact-dependent T6SS mechanism mediated by *S. rhizophila*. We also ask to which extent strains from the *Stenotrophomonas* genus share similar or different T6SS clusters.

2 | RESULTS

2.1 | Genomic organization of *S. rhizophila* CFBP13503 T6SS

Fourteen genes encoding T6SS core protein components were identified in the genome sequence of *S. rhizophila* CFBP13503 (Figure 1). These genes, located on a single genomic cluster of 72 kb, include genes encoding proteins involved in the membrane complex (TssJ, L and M: HKJBHOBG_02310, 02312, 02279), the baseplate (TssE, F, G and K: HKJBHOBG_02304, 02303, 02302, 02311), the contractile sheath (TssB and C: HKJBHOBG_02307, 02306), the coordinating protein (TssA: HKJBHOBG_02276), the disassembly ATPase (TssH: HKJBHOBG_02301), the inner tube (Hcp: HKJBHOBG_02305) and the puncturing structure (VgrG and PAAR). Regarding the puncturing structure, multiple genes encoding VgrG ($n = 7$) and PAAR domain-containing proteins ($n = 5$) were detected in the genome sequence.

Based on the genetic architecture of the T6SS genomic cluster, the T6SS is related to group i4 (Bayer-Santos et al., 2019). The T6SS putative accessory genes were identified in the core structural cluster, including the group 4-specific: (a) the group 4-specific *tagX* (HKJBHOBG_02282), which encodes an L,D-endopeptidase first proposed to be involved in cell wall degradation for T6SS assembly (Weber et al., 2016), but essential for polymerization of the contractile sheath and not required for assembly of the membrane complex and the baseplate (Lin et al., 2022); (b) *tagF* (HKJBHOBG_02278), which encodes a negative post-translational regulator of the *Pseudomonas aeruginosa* H1-T6SS (Lin et al., 2018); (c) *tagN/L* (HKJBHOBG_02277), whose role in T6SS assembly or regulation remains unknown; and (d) *tslA* (HKJBHOBG_02308), conserved in i4b T6SS and involved in cell-contact T6SS assembly (Lin et al., 2022).

2.2 | The T6SS of *S. rhizophila* CFBP13503 encodes a wealth of putative effectors

To identify putative T6SS effectors of CFBP13503, we screened the T6SS main cluster and the *vgrG* and PAAR islands for the presence of VgrG, Hcp or PAAR proteins, as well as the presence of N-terminal effectors motifs such as FIX or MIX domains. We also looked for conserved domains encoded by the genes in the vicinity of *vgrG*, *hcp* or *PAAR* or adaptor/chaperones that could be cargo effectors associated with immunity proteins.

We identified only one Hcp protein, encoded in the main T6SS cluster in between *tssE* and *tssC* genes. Seven *vgrG* genes (*vgrG-1* to *vgrG-7*) were identified, with five of them located adjacent to the T6SS cluster and two others scattered throughout the genome (Figure 2a,b). All VgrG proteins, except VgrG-6, contain a C-terminal DUF2345 domain extending the VgrG needle that can be important for recruiting effectors or carrying toxic activity (Flaugnatti et al., 2016, 2020; Storey et al., 2020). In contrast, VgrG-6 contains a C-terminal domain extension with a weak ($p = 5.5e{-}03$) similarity to the FliC/FljB family flagellin (accession: cl35635). Five PAAR-containing proteins were detected in the genome of CFBP13503: one in the T6SS cluster, one in each *vgrG* island and two orphan PAAR proteins (Figure 2). The latter two PAAR-containing proteins possess a C-terminal Ntox15 domain

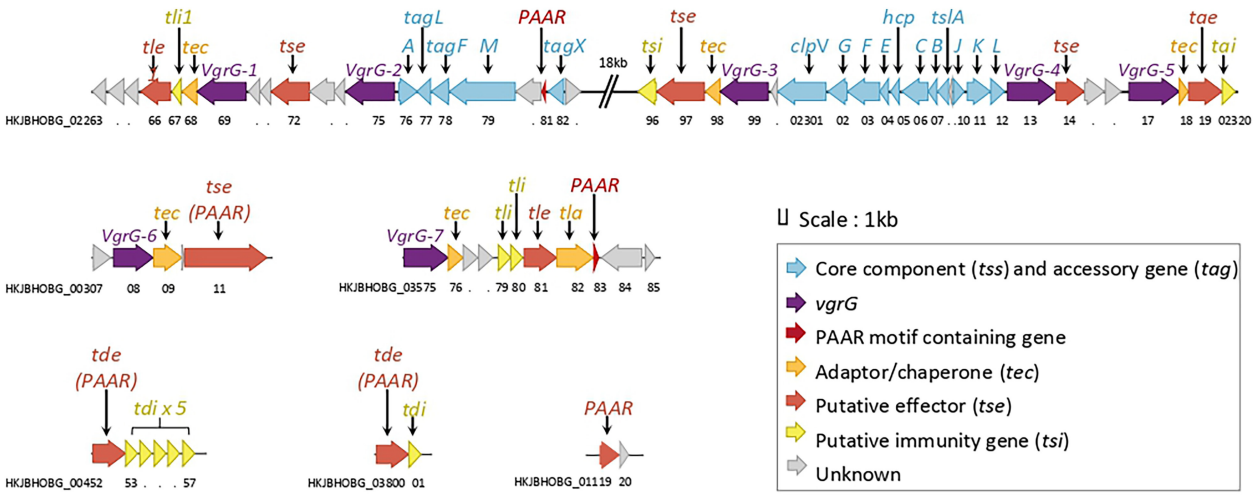

FIGURE 1 *Stenotrophomonas rhizophila* CFBP13503 type VI secretion system (T6SS) genomic architecture. Schematic representation of *S. rhizophila* CFBP13503 T6SS cluster along with orphan *vgrG* and PAAR clusters. Genes are coloured according to their functional roles: core component and accessory genes (blue), *vgrG* (violet), PAAR-motif containing genes (red), adaptor/chaperone (orange), putative effectors (orange-red), immunity genes (yellow), and genes with unknown function (grey).

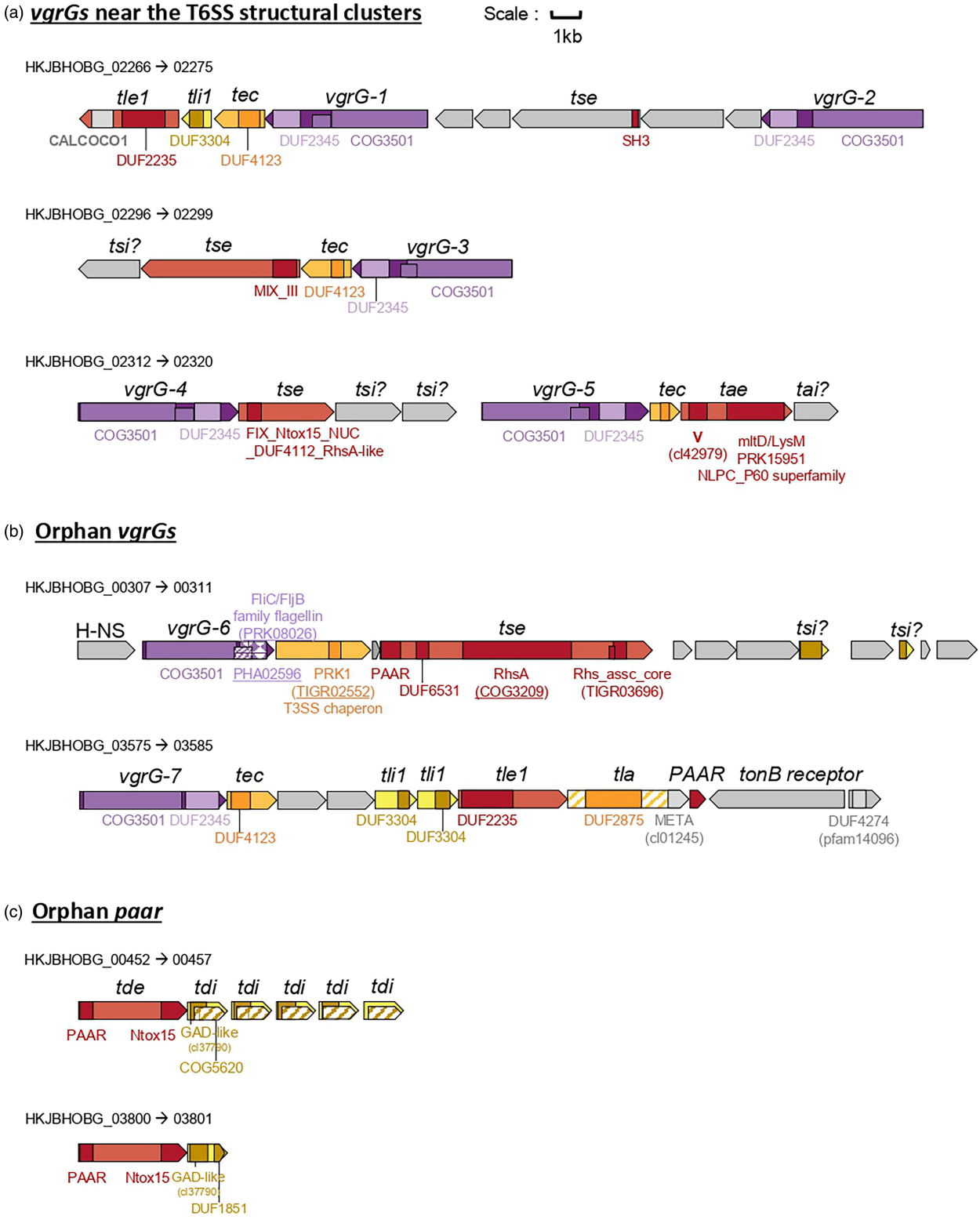

FIGURE 2 *Stenotrophomonas rhizophila* CFBP13503 type VI secretion system (T6SS) effectors. The conserved domain organization of genes encoding putative chaperone, effector and immunity proteins associated with (a) VgrG encoded in the main T6SS cluster, (b) orphan VgrG, and (c) orphan PAAR domain-containing effectors are represented. *vgrG* genes are indicated in violet, putative effectors with or without PAAR motif are shown in red, chaperone genes in orange, immunity protein genes in yellow and gene-encoded proteins with unknown functions are in grey.

(pfam15604) with a HxxD catalytic motif. Such domains were found associated with T6SS effectors with DNase activity called Tde (Type VI DNase effector) (Luo et al., 2023; Ma et al., 2014). These two predicted PAAR-fused Tde proteins are associated with genes encoding the DUF1851 domain, known to be associated with T6SS Tde immunity proteins (Tdi) (Luo et al., 2023; Ma et al., 2014) (Figure 2c).

In addition to specialized effectors, we detected several putative cargo effectors, immunity proteins and chaperone proteins. Regarding chaperones, three DUF4123 domain-containing proteins were identified in coding sequences located immediately downstream of *vgrG-1*, *vgrG-3* and *vgrG-7*. Another chaperone containing a DUF2875 domain was also encoded in the vicinity of *vgrG-7*. Concerning effector, two effector-immunity (E-I) encoding gene pairs *tle/tli* were associated with VgrG-1 and VgrG-7. Both *tle* encode proteins containing a GXSXG motif (GFSRG) and a DUF2235, characteristic of the T6SS phospholipase effector (Tle) of the Tle1 family. (Flaugnatti et al., 2016; Russell et al., 2013). Their corresponding Tli contained a DUF3304 domain found in several T6SS Tli1 immunity proteins (Russell et al., 2013). A putative amidase effector, *tae*, was associated with VgrG-5. This effector contained a murein transglycosylase D domain and a LysM motif involved in binding peptidoglycan, as well as an NlpC_P60 domain. Linked to the other *vgrG* genes, we also detected genes encoding T6SS effector-specific domains MIX and FIX. The MIX-containing effector located at the vicinity of *vgrG-3* and a tec protein-encoding gene may encode a pore-forming toxin. This toxin is predicted to encode four or five putative transmembrane domains at its C terminus. A predicted structure-based search using Alphafold2 predicted structure and Foldseek suggest that this protein shares structural homologies (over the 900 first residues) with VasX, a pore-forming toxin from *Vibrio cholerae* (Miyata et al., 2013). The downstream gene is a predicted inner membrane protein and could be the corresponding immunity protein. Unfortunately, we were unable to determine conserved domains or potential activities for the FIX-containing protein encoded downstream of *vgrG-4* so we referred to it as *tse*, which stands for 'type six effector'. Similarly, no function could be assigned to the proteins encoded by the genes downstream of *vgrG-4*. We assume that these genes could encode potential toxins and associated immunity proteins and potential chaperones. The 18 kb region between *tssM* and *tssA* and other structural genes contains a poly-immunity locus with a predicted formylglycine-generating enzyme family immunity protein encoding gene (Lopez et al., 2021) and eight duplications of the putative immunity gene HKJBHOBG_02263 containing a DUF6708 domain.

2.3 | *S. rhizophila* CFBP13503 outcompete Xcc8004 in vitro in a T6SS-dependent manner

S. rhizophila CFBP13503 is able to outcompete the phytopathogenic bacterial strain Xcc8004 in TSB10 (Torres-Cortés et al., 2019). After 6 h of confrontation on TSA10 medium between Xcc8004 and CFBP13503, a 10- to 100-fold decrease in Xcc8004 population was observed in comparison with Xcc8004 monoculture (Figure 3). Deletion of two genes encoding proteins involved in T6SS assembly (Δ*hcp* and Δ*tssB*) significantly increased the population size of Xcc8004 to a level comparable with Xcc8004 monoculture

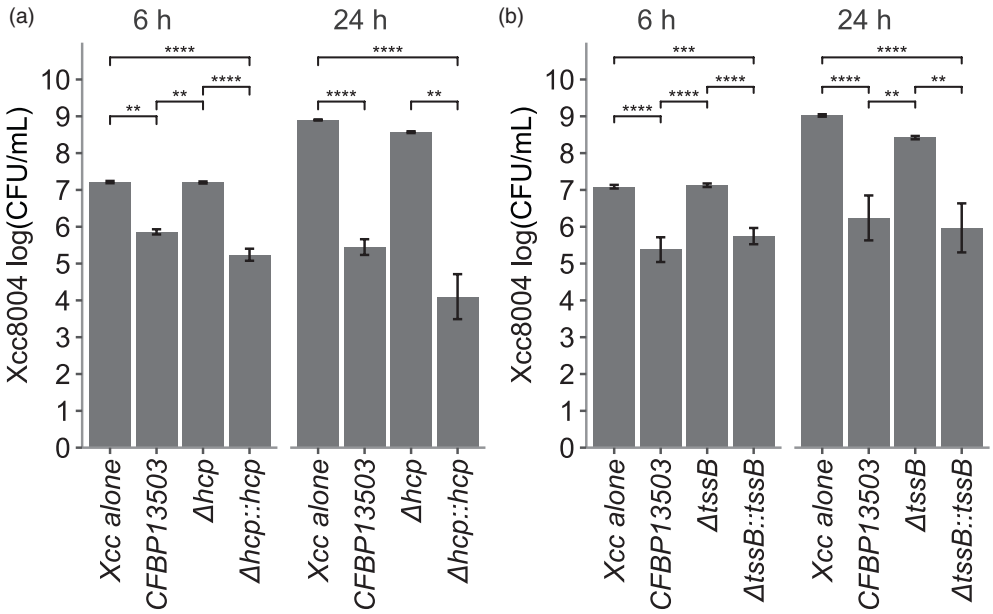

FIGURE 3 Bactericidal activity of *Stenotrophomonas rhizophila* CFBP13503 against *Xanthomonas campestris* pv. *campestris* 8004 (Xcc8004). Confrontation between Xcc8004 and CFBP13503 wild-type, type VI secretion system (T6SS)-deficient mutants Δ*hcp* (a) and Δ*tssB* (b) and the complemented mutants Δ*hcp::hcp* and Δ*tssB::tssB* in TSA10 medium for 6 and 24 h. Colony-forming units (CFU) were quantified on TSA10 supplemented with rifampicin. The averages ± *SD* of nine replicates are plotted. Statistical analyses were performed using Dunn's multiple comparison test (** $p < 0.005$, *** $p < 0.0005$, **** $p < 0.00005$).

(Figure 3). Complementation of these two mutants restored the decrease in CFU of Xcc8004. These results demonstrate that the T6SS of *S. rhizophila* CFBP13503 is involved in the antibiosis towards Xcc8004 from 6 h of confrontation. The T6SS effect size increased with time as 24 h after confrontation Xcc8004 population decreased from 1000 to 10,000 times in the wild-type strain and complemented mutants. At 48 h, the Xcc populations were reduced by the wild-type compared with the deletion mutants but increased by one $\log_{10}$ compared with the same wild-type treatment at 6 and 24 h (Figure S3). These results highlight the involvement of the T6SS of *S. rhizophila* CFBP13503 in the killing of Xcc8004 and thus its involvement in interbacterial competition.

2.4 | The T6SS of *S. rhizophila* CFBP13503 limits the seed-to-seedling transmission of Xcc8004 in radish

To investigate the bactericidal impact of CFBP13503 T6SS in planta, seedling transmission assays were carried out on radish seeds (Figure 4). Xcc8004 was co-inoculated with either the wild-type CFBP13503 strain or the Δ*hcp* mutant on sterilized seeds with inoculum ratios of 1:2.1 and 1:1.6, respectively. Hcp protein is a structural protein of T6SS syringe but can exert antibiosis against bacterial prey (Decoin et al., 2014; Fei et al., 2022). Thus, we chose the *hcp* mutant to prevent any toxicity. Bacterial population sizes were measured on seeds, germinated seeds (1 day post-inoculation [dpi]) and the aerial and root parts of seedlings (5 dpi) by quantification of CFU on selective media. The Xcc8004 population of inoculated seeds was variable (6.1 to 6.5 $\log_{10}$ CFU per sample) but presented no significant decrease when co-inoculated with wild-type CFBP13503 compared with the Δ*hcp* mutant. However, a significant decrease in the Xcc8004 population was observed from the germinated seed stage when co-inoculated with the wild-type strain. This decrease persisted over time, with a significant reduction in Xcc8004 population size in the aerial and root part of seedlings during the confrontation with the wild-type CFBP13503 (Figure 4). The population size of *S. rhizophila* was not impacted by the presence or absence of a functional T6SS (Figure 4). Altogether these findings show that the T6SS of *S. rhizophila* CFBP13503 restricted seedling transmission of Xcc8004 without providing a fitness advantage to *S. rhizophila* CFBP13503.

2.5 | Analysis of T6SS distribution within the *Stenotrophomonas* genus

Given the significant effect of *S. rhizophila* CFBP13503 T6SS on Xcc8004, it raises the question of T6SS distribution within the *Stenotrophomonas* genus. A total of 835 *Stenotrophomonas* genome sequences were then collected from the NCBI (experimental procedure). These genome sequences are divided into 95 groups (Figure S1) at a threshold of 50% shared 15-mers, an overall genome relatedness index employed as a proxy for species delineation (Briand et al., 2021). From this analysis, the strain CFBP13503 is grouped with *S. rhizophila* DSM14405^T in the same species complex (threshold 0.25) but differs from the DSM14405^T type strain of *S. rhizophila* (threshold 0.5). So, we describe here a new *S. rhizophila* complex.

Sixty-four strains (8.3% of the data set) of 22 groups contained at least one T6SS cluster (Figure 5). Based on the phylogenetic analysis of TssC (Figure 6), T6SS clusters were classified into three families i1 ($n=5$), i3 ($n=10$) and i4 ($n=57$). Just four species among the 28 groups of *S. maltophilia* species complex contain one T6SS except group 65, which contains two T6SS belonging to two different taxonomic groups (i3 and i4). All *S. rhizophila* strains ($n=5$) have a T6SS related to group i4.

3 | DISCUSSION

X. campestris pv. *campestris* is a frequent seed-colonizer of various host and nonhost plant species (Darrasse et al., 2010; Vicente & Holub, 2013). In the seed habitat, Xcc can co-occur with other bacterial species such as *S. rhizophila* CFBP13503 (Rezki et al., 2016), which can outcompete Xcc8004 in vitro (Torres-Cortés et al., 2019). Resource overlap was initially proposed as the mode of action involved in Xcc8004 growth reduction in the presence of *S. rhizophila* CFBP13503 (Torres-Cortés et al., 2019).

In this study, we showed that the growth inhibition of Xcc8004 by *S. rhizophila* CFBP13503 was T6SS-dependent. CFBP13503 decreased Xcc8004 population size from 10- to 1000-fold after 6 and 24 h of confrontation in solid medium, respectively. Deletion mutants of two genes encoding proteins (Δ*hcp* and Δ*tssB*) involved in T6SS assembly were no longer able to reduce Xcc8004 growth. After 48 h of confrontation in vitro, Xcc8004 strain partially escaped T6SS antibiosis due to the possible establishment of non-immune defences by Xcc such as the creation of dead cell barriers or the production of exopolysaccharides that limit cell-to-cell contact (Hersch et al., 2020). Antibacterial activities of T6SS can be contact-dependent with the translocation of effector proteins in bacterial cells (Jurėnas & Journet, 2021) or contact-independent with the secretion of metal-scavenging proteins in the surrounding media (Chen et al., 2016; Lin et al., 2017; Si et al., 2017). When the confrontation between Xcc8004 and CFBP13503 took place in a liquid medium with limited cell contacts, no difference in Xcc8004 growth was observed between the wild-type strain and the T6SS-deficient mutants (Figure S4). In conclusion, T6SS-mediated reduction in Xcc8004 growth is contact-dependent and therefore due to the injection of protein effectors in Xcc8004 cells.

Furthermore, *S. rhizophila* CFBP13503 is involved in reducing the transmission of Xcc8004 from seed to seedling. When comparing equivalent Xcc8004 populations on seeds, the presence of *S. rhizophila* CFBP13503 negatively impacted the population of Xcc8004 on germinated seeds compared with the mutant strain lacking the T6SS gene *hcp*. This highlights the potential role of T6SS during the

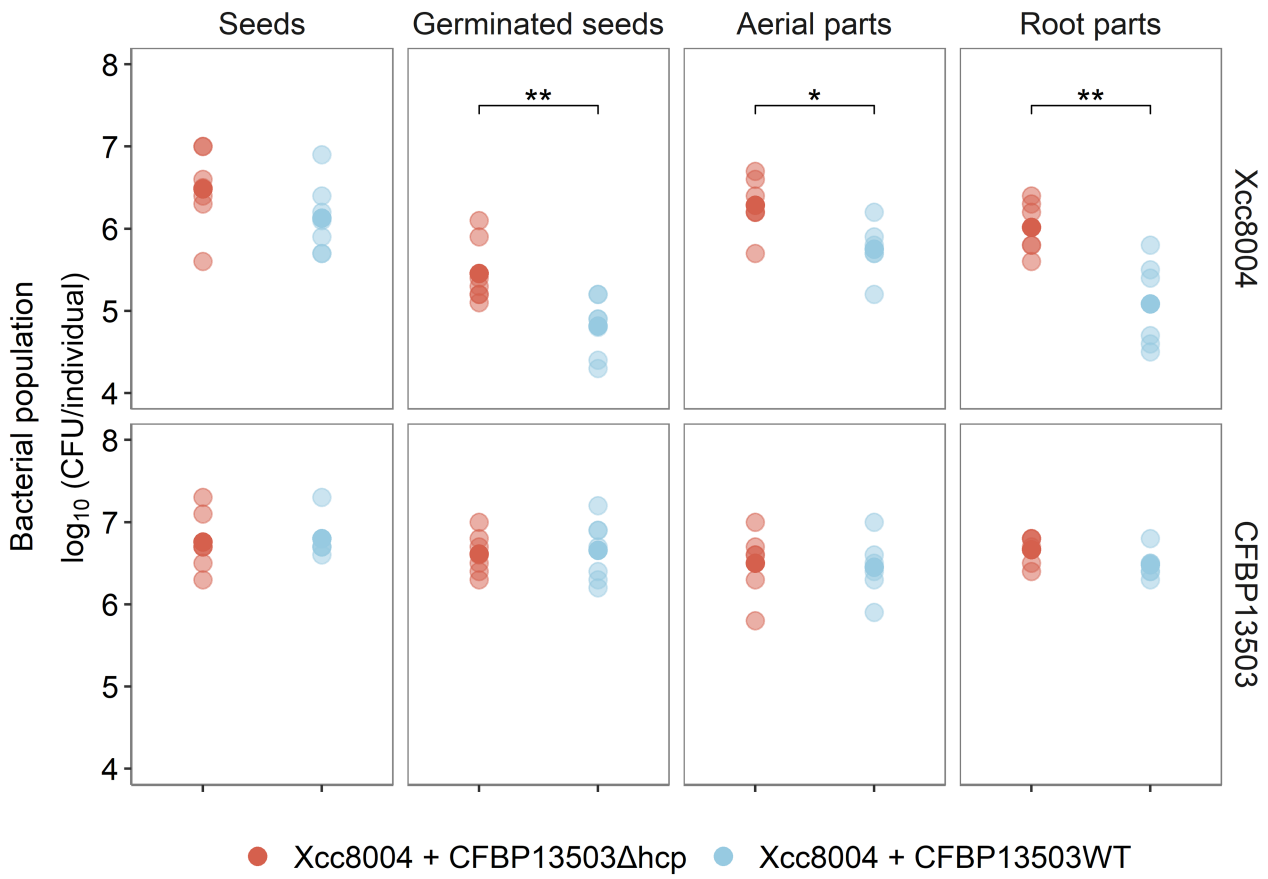

FIGURE 4 Bacterial population dynamics during seed-to-seedling transmission of *Stenotrophomonas rhizophila* CFBP13503 and *Xanthomonas campestris* pv. *campestris* (Xcc8004) in radish. Radish seeds were co-inoculated with Xcc8004 and CFBP13503 wild-type or type VI secretion system (T6SS)-deficient Δ*hcp*. Bacterial populations were assessed in radish seeds (0 days post-inoculation [dpi]), 24-h-old germinated seeds (1 dpi), 5-day-old seedling aerial parts, and 5-day-old seedling root parts (5 dpi). Colony-forming units (CFU) were quantified on selective media to differentiate Xcc8004 and CFBP13503 populations. The averages ± *SD* of two experiments ($n = 3$ and $n = 4$) are plotted. Statistical analyses were performed using Dunn's multiple comparison test (*$p < 0.05$, **$p < 0.005$).

early interactions between bacteria. The effects of *S. rhizophila* CFBP13503 T6SS persist overtime at the seedling stage, as a lower population of Xcc is observed in the presence of the wild-type strain. Because Xcc8004 is a seedborne pathogen, limiting its transmission to the seedling stage appears to be a promising strategy for managing this pathogen. However, further studies are needed on host plants to assess whether the T6SS of *S. rhizophila* CFBP13503 can limit the pathogenicity of Xcc8004 by reducing its population size.

It is also noteworthy that the presence or absence of T6SS, as well as its mutation, does not impact the transmission of *S. rhizophila* CFBP13503 when in competition with Xcc8004. Consequently, the T6SS of *S. rhizophila* CFBP13503 does not seem to be involved in its adhesion or colonization capacities of radish seed and seedling, unlike what has been observed in other bacterial species (Cassan et al., 2021; Mosquito et al., 2019).

S. rhizophila CFBP13503 possesses seven VgrG proteins, each of which is associated with a chaperone protein and a putative effector. This diversity of VgrG proteins may allow for various associations in the arrangement of VgrG trimers, enhancing the versatility of the T6SS. Additionally, *S. rhizophila* CFBP13503 has five PAAR-domains containing protein. The presence of PAAR proteins sharpens the tip of the VgrG trimer, creating opportunities for different toxic effector associations during each firing event. Two of these PAAR proteins possess a C-terminal toxic domain related to DNase activity. The extensive repertoire of effectors identified in *S. rhizophila* CFBP13503 includes Tle1-type phospholipases (Flaugnatti et al., 2016; Russell et al., 2013) capable of lysing the membranes of target bacteria, DNases (Tde) that exhibit antibacterial properties by targeting nucleic acids, amidases (Tae) that degrade peptidoglycan to lyse the target bacterium, and potentially a pore-forming effector that inhibits the growth of target cells by depolarizing the inner membrane. Furthermore, there are other effectors whose activities have yet to be discovered. These effectors are predicted to target different components of bacterial cells, contributing to the antibacterial phenotype against Xcc8004. Interestingly, some components and effectors in *S. rhizophila* CFBP13503 could also exhibit anti-eukaryotic activity. For example, the DUF2345 domain of VgrG has been shown to intoxicate yeast, as demonstrated by *Klebsiella pneumoniae* VgrG4 (Storey et al., 2020). Moreover, the two 'evolved' PAAR proteins, which contain a C-terminal Ntox15 domain, share a significant

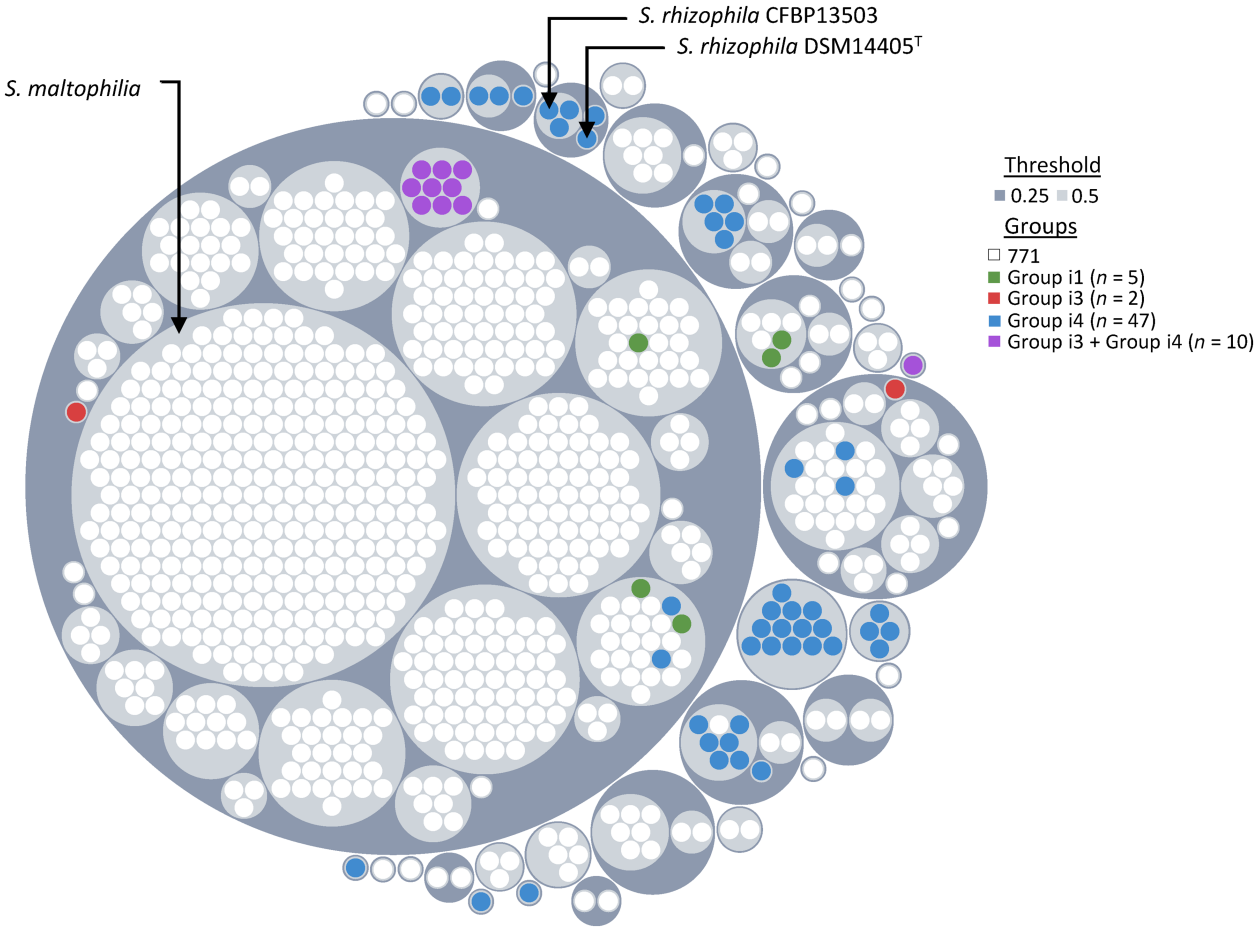

FIGURE 5 Type VI secretion system (T6SS) distribution among *Stenotrophomonas* sp. Circle packing representation of *Stenotrophomonas* sp. genomes ($n = 835$). Overall genome relatedness was assessed by comparing the percentage of shared 15-mers. Each dot represents a genome sequence, colour-coded based on the T6SS group. The genomes were grouped using two distinct thresholds to assess species-specific relationships (0.5) and interspecies relationships (0.25). Interactive circle packing representation is available in Figure S1. For the caption of species names when a reference strain exists see Figure S2.

identity (>30%) with the DNase effector TafE of *Acinetobacter baumannii* strain 17,978, known for its involvement in yeast killing (Luo et al., 2023). Some Tle effectors were also shown to target bacteria and eukaryotic cells (Jiang et al., 2014, 2016). The combination of these diverse effectors, either individually or in synergy (LaCourse et al., 2018), probably contributes to the competitive advantage of *S. rhizophila* CFBP13503 over Xcc in vitro. Despite possessing only one T6SS, the diverse repertoire of effectors enables *S. rhizophila* CFBP13503 to effectively combat bacterial competitors and potentially exert antibacterial effects against Xcc8004.

The T6SS is not frequently found in *Stenotrophomonas* genomes. Less than 10% of the genome sequences analysed possessed a T6SS genetic cluster, which is generally presented in a single copy. This frequency is relatively low compared with other bacterial genera of the *Lysobacterales* where T6SS is present in approximately 50% of sequenced strains (Bayer-Santos et al., 2019). A novel subgroup 3 within *Lysobacterales*, exclusively associated with *Stenotrophomonas* species, was revealed by TssC-based phylogeny analysis. Notably, this subgroup was not identified in the previous study conducted by Bayer-Santos et al. (2019) on T6SS classification within *Lysobacterales*. Consistent with their findings, our analysis also identified *Stenotrophomonas* T6SS classified into both group i1 and group i4. However, group i4 T6SS appears to be more prevalent within the *Stenotrophomonas* genus. This is the case for the T6SS of *S. rhizophila* CFBP13503 and more generally for strains affiliated with the *S. rhizophila* complex, including the type strain DSM14405^T (Wolf et al., 2002). *S. rhizophila* strains are not only known for their ability to colonize a wide range of plant species following seed inoculation (Schmidt et al., 2012; Simonin et al., 2023) but also to exhibit antifungal (Berg & Ballin, 1994) and antibacterial activities (Lottmann et al., 1999). For instance, the strain *S. rhizophila* DSM14405^T protects plants against *Fusarium solani* and displays antagonistic activity against various phytopathogenic fungi under high salt conditions (Egamberdieva et al., 2011). Interestingly, some T6SS genes of *S. rhizophila* DSM14405^T are strongly up-regulated in response to osmotic stress (Alavi et al., 2013; Liu et al., 2022). More available genomes from the *S. rhizophila* complex will confirm later the T6SS uniformity in these species. Nevertheless, the large range of putative T6SS effectors in CFBP13503 reinforces the interest in *S. rhizophila* antimicrobial activities.

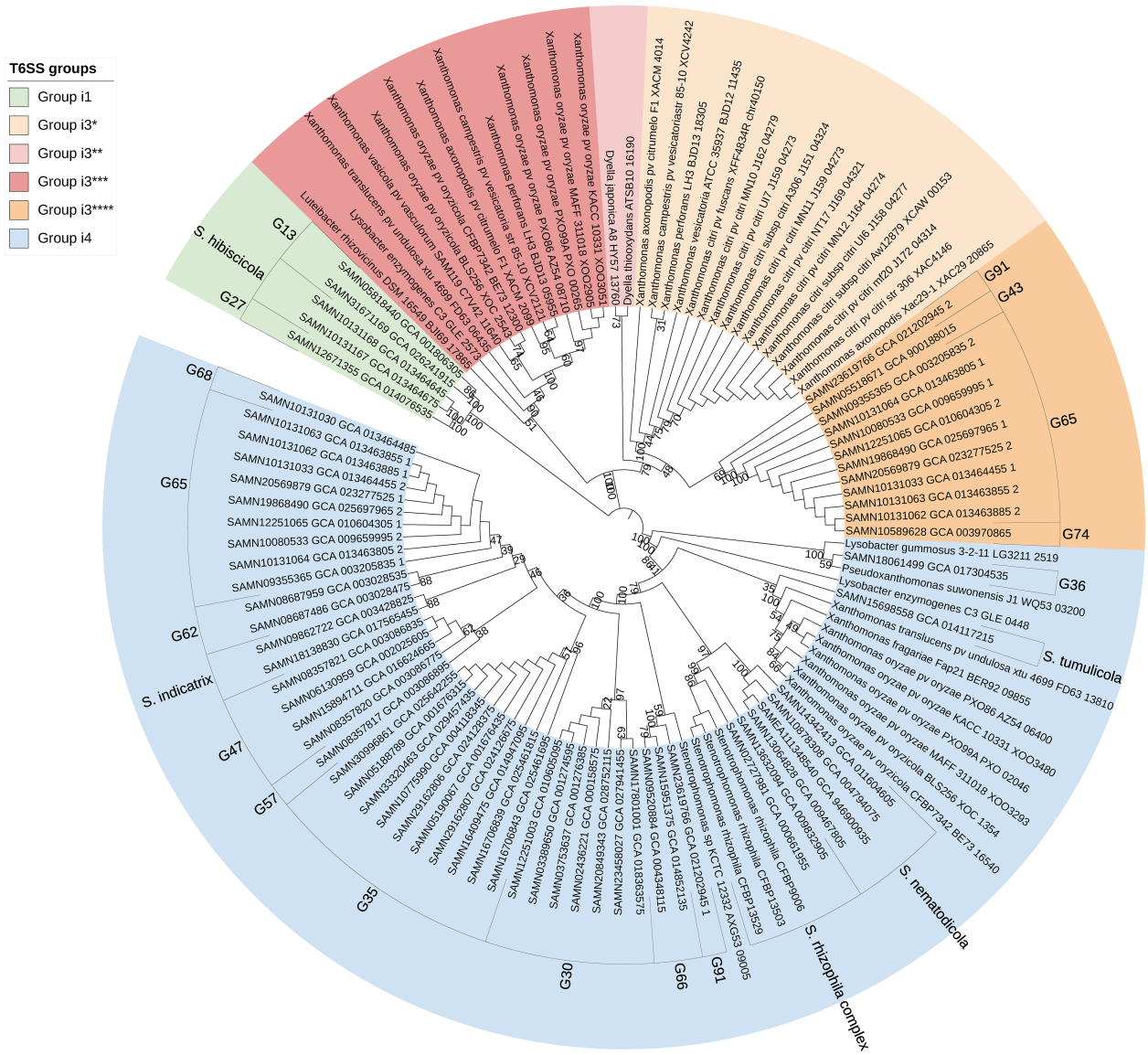

FIGURE 6 Type VI secretion system (T6SS) distribution among *Lysobacteraceae*. Phylogenetic tree based on TssC protein sequences, constructed using a Kimura two-parameter neighbour-joining method with 1000 bootstrap replicates. The tree includes *Stenotrophomonas* and other *Lysobacteraceae*, as studied by Bayer-Santos et al. (2019). Strain taxonomic affiliation is based on KI-S grouping (Figure S1).

The T6SS of *S. rhizophila* CFBP13503 plays a crucial role in its antibiosis against Xcc8004 and in limiting Xcc8004 transmission from radish seed to seedling, highlighting its potential in biocontrol of seedborne pathogenic bacteria. The T6SS has emerged as a powerful tool in biocontrol strategies, offering a novel approach to combat plant pathogens. However, further research is necessary to fully understand its impact within complex microbial ecosystems. By investigating the role of the T6SS in diverse bacterial communities, valuable insights can be gained regarding its functionality, interactions with other microorganisms and ecological consequences. Understanding the influence of the T6SS on complex bacterial communities is essential for unlocking its full potential and maximizing its contribution to biocontrol approaches.

4 | EXPERIMENTAL PROCEDURES

4.1 | Bacterial strains and growth conditions

Bacterial strains and plasmids used in this study are listed in Table S1. *S. rhizophila* CFBP13503 and Xcc8004::GUS-GFP (Cerutti et al., 2017) were grown at 28°C on tryptic soy agar 1/10× strength (TSA10; 17 g/L tryptone, 3 g/L soybean peptone, 2.5 g/L glucose, 5 g/L NaCl, 5 g/L K_2HPO_4, 15 g/L agar) or tryptic soy broth 1/10× strength (TSB10). *Escherichia coli* DH5α and *E. coli* MFD*pir* (Ferrières et al., 2010) were grown at 37°C on Luria-Bertani (LB; 10 g/L tryptone, 5 g/L yeast extract, 10 g/L NaCl) medium. LB medium was supplemented with 0.3 mM 2,5-diaminopimelic acid (Fisher Scientific) for auxotrophic *E. coli* MFD*pir*.

4.2 | Construction of *S. rhizophila* CFBP13503Δ*hcp* and CFBP13503Δ*tssB* and their complementation

Unmarked *hcp* (HKJBHOBG_02305) and *tssB* (HKJBHOBG_02307) deletions were performed by allelic exchange using the suicide vector pEX18Tc (Hoang et al., 1998). The deletion plasmids pEX18Tc-Δ*hcp* and pEX18Tc-Δ*tssB* were constructed using the TEDA cloning procedure (Xia et al., 2019). Briefly, pEX18Tc was digested with XbaI (New England Biolabs) followed by a dephosphorylation step using the shrimp alkaline phosphatase (Phusion High-Fidelity DNA polymerase; New England Biolabs). *hcp* and *tssB* flanking regions were PCR-amplified from CFBP13503 with the Phusion High-Fidelity DNA polymerase, and the primer pairs listed in Table S2. The dephosphorylated pEX18Tc vector and PCR products were purified using the NucleoSpin Gel and PCR Clean-up kit (Macherey-Nagel). TEDA reaction was then carried out by mixing 150 ng of pEX18Tc with the corresponding PCR products at a molar ratio of 1:4. One hundred microlitres of *E. coli* DH5α were transformed with 5 μL of TEDA reaction using the Inoue transformation procedure (Sambrook & Russell, 2006) modified by Xia et al. (2019). Amplicon insertions were validated by colony PCR with the primer pair M13F/M13R. Plasmids (pEX18Tc-Δ*hcp*) were extracted with the NucleoSpin plasmid kit (Macherey-Nagel), and insertion regions were verified by sequencing (Azenta Life Sciences). *E. coli* MFD*pir* was transformed with pEX18Tc-Δ*hcp* and pEX18Tc-Δ*tssB* using the modified Inoue method. Plasmids were transferred to *S. rhizophila* CFBP13503 by conjugation. *S. rhizophila* CFBP13503 transconjugants were selected on TSA10 supplemented with tetracycline (20 μg/mL). The resulting colonies were grown in TSB10 (28°C, 120 rpm, 3 h) and bacterial suspensions were spread on TSA10 supplemented with 5% saccharose. Allelic exchanges were validated by PCR and sequencing.

Deletion mutants were complemented by allele exchange. Briefly, *hcp* and *tssB* were PCR-amplified with the primer pairs Hcp-pEX18-UpF/Hcp-pEX18-DnR and TssB-pEX18-UcpF/TssB-pEX18-DnR (Table S2). TEDA reactions were performed at a vector:insert molar ratio of 1:1. pEX18Tc-*hcp* and pEX18Tc-*tssB* were transferred by electroporation to CFBP13503Δ*hcp* and CFBP13503Δ*tssB*, respectively. To carry out this electroporation step, bacteria were grown in TSA to OD_{600} of 0.5–0.7. Bacterial cultures were centrifuged (4100 *g*, 10 min, 2°C), and pellets were washed four times in cold sterile water, once in 10% glycerol and finally resuspended in 10% glucose before storage at −80°C. CFBP13503Δ*hcp* and CFBP13503Δ*tssB* were transformed with 150 ng of pEX18Tc-*hcp* and pEX18Tc-*tssB* (2 kV, 5 ms). Transformants were selected on TSA10 supplemented with tetracycline (20 μg/mL). The resulting colonies were grown in TSB10 (28°C, 120 rpm, 3 h), and bacterial suspensions were spread on TSA10 supplemented with 5% saccharose. Allelic exchanges were validated by PCR and sequencing.

4.3 | In vitro confrontation assays

S. rhizophila CFBP13503, the isogenic T6SS-deficient mutants, the complemented T6SS mutants and Xcc8004-Rif^R were cultured overnight in 10 mL of TSB10 (28°C, 150 rpm). Cultures were centrifuged (4000 *g*, 8 min, 20°C), and the resulting pellets were resuspended in sterile water. Bacterial suspensions were calibrated to OD_{600} of 0.5 (c. 10^9 cells/mL). For confrontation on a solid medium, calibrated suspensions were mixed at a ratio of 1:1 (i.e., 100 μL of each strain). Single suspensions were prepared as a control by mixing 100 μL of bacterial cultures with 100 μL of sterile water. Drops of 20 μL were deposited on TSA10, dried for 15 min under a laminar air flow and incubated at 28°C for 6 and 24 h. At each incubation time, cells were resuspended in 2.5 mL of sterile water, serially diluted and plated on TSA10 supplemented with 50 μg/mL rifampicin (selection of Xcc8004-Rif^R) or with 50 μg/mL spectinomycin and 100 μg/mL ampicillin (selection of *S. rhizophila* strains). For confrontation in liquid medium, calibrated suspensions were mixed at a ratio of 1:1 (i.e., 500 μL of each strain in 9 mL TSB10). As a control, single-strain suspensions were prepared by mixing 500 μL of bacterial cultures with 500 μL of TSB10. The confrontations were incubated at 28°C 150 rpm for 6 and 24 h. At each incubation time, confrontations were serially diluted and plated on TSA10 supplemented with 50 μg/mL rifampicin (selection of Xcc8004-Rif^R) or with 50 μg/mL spectinomycin and 100 μg/mL ampicillin (selection of *S. rhizophila* strains).

4.4 | In planta transmission assays

Three subsamples of 300 radish seeds (*Raphanus sativus* 'Flamboyant 5') were surface sterilized using the protocol described in Simonin et al. (2023). Sterilized seeds were dried 30 min before inoculation in a laminar flow cabinet. Bacterial suspensions were prepared at an OD_{600} of 0.5 from 24-h bacterial mats on TSA10. These suspensions corresponded to (i) Xcc8004, (ii) Xcc8004/CFBP13503 (1:1 ratio) and (iii) Xcc8004/CFBP13503Δ*hcp* (1:1 ratio). Seeds were either soaked into bacterial suspensions (15 min, 20°C, 70 rpm) or sterile water (noninoculated condition). Seeds were dried for 15 min on sterile paper under a laminar air flow. Inoculated and noninoculated seeds were placed on sterile folded moistened papers in sterile plastic boxes. Three repetitions (20 seeds per repetition) were carried out per condition. Boxes were incubated in a growth chamber (photoperiod: 16 h/8 h, temperature 20°C). Germinated seeds were collected 24-h post-inoculation ($n = 3$, 20 germinated seeds per repetition). Seedlings were harvested 5 days post-inoculation ($n = 3$, 20 seedlings per repetition). The same experiment was repeated with $n = 4$ repetitions. Bacterial population sizes were assessed by dilution and plating on TSA10 supplemented with appropriate antibiotics (see in vitro confrontation assays). Seed-associated bacteria were recovered 15 min after inoculation (initial time) by vortexing

20 seed pools in 2 mL of sterile water for 30 s. Germinated seeds (20 seedling pools) were ground in 4 mL of sterile water. The entire aerial and root parts of seedlings (20 seedling pools) including both endophytic and epiphytic bacteria were separated and ground in 4 mL of sterile water. No bacterial growth was observed on the selective media for the noninoculated seeds, germinated seeds and seedlings attesting the absence of culturable bacteria in the control.

4.5 | Genomic analysis of *S. rhizophila* CFBP13503 T6SS and effector prediction

The genomic sequence of *S. rhizophila* CFBP13503 (SAMN09062466) was initially obtained through paired-end Illumina sequencing (Torres-Cortés et al., 2019). To circularize the genomic sequence of CFBP13503, PacBio sequencing was performed on an RS2 machine (Genotoul). PacBio reads were filtered and demultiplexed using the ccs v. 6.3.0 and lima v. 2.5.1 tools of the PacBio SMRT Tools v. 11.0.0.146107 toolkit and then assembled and circularized using Flye v. 2.9 (Kolmogorov et al., 2019). The sequence start was fixed using the fixstart option of Circlator v. 1.5.1 (Hunt et al., 2015). Polishing with PacBio reads was performed using Flye v. 2.9 (Kolmogorov et al., 2019). Polishing with Illumina HiSeq3000 short reads was done using Pilon v. 1.24 (Walker et al., 2014) with the setting --mindepth 0. Genome annotation was performed with Prokka v. 1.14.6 (Seemann, 2014).

The T6SS components were identified by conducting NCBI BLASTP analysis on protein sequences. Effector-immunity encoding gene pairs and chaperones were identified by analysing genes downstream of *vgrG* and PAAR motif-containing genes. The conserved domain database of the NCBI was used to identify T6SS-related conserved domains. Structural homology-based searches were made using Alphafold2 (Jumper et al., 2021) structure prediction of putative effectors followed by a DALI (Holm et al., 2023) search analysis or using the Foldseek search server (van Kempen et al., 2023).

4.6 | Phylogenetic analysis of T6SS

A total of 991 genome sequences of *Stenotrophomonas* were downloaded from the NCBI. Genomes with fewer than 10 markers (Marker_lineage = f__Xanthomonadaceae) absent or in multicopy (CheckM v. 1.1.6; Parks et al., 2015) were conserved for further analysis. A multilocus species tree was created with Automlst (Alanjary et al., 2019). Non-*Stenotrophomonas*-affiliated genomes were excluded from further analyses, resulting in a final dataset comprising 835 *Stenotrophomonas* genomes. Sequence relatedness between the selected 835 genomes sequences was assessed with KI-S (Briand et al., 2021) using 50% of shared 15-mers, a proxy for delineating bacterial species. Genome sequences were annotated with Prokka v. 1.14.6 (Seemann, 2014). The presence of T6SS genomic clusters was predicted with MacSyFinder2 (Néron et al., 2023). TssC protein sequences were retrieved following BLASTp searches using TssC sequences of *S. rhizophila* CFBP13503 (iT6SS group 4b) and *Stenotrophomonas* sp. LM091 (iT6SS group 1). BLASTp hits with >25% identity over 75% of protein length were conserved. TssC sequences were aligned using MUSCLE. A Kimura two-parameter neighbour-joining tree was constructed with 1000 bootstraps with SeaView v. 4.7 (Gouy et al., 2010). The T6SS groups have been assigned according to the previously defined nomenclatures (Bayer-Santos et al., 2019; Bernal et al., 2017; Gallegos-Monterrosa & Coulthurst, 2021).

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CONFLICT OF INTEREST STATEMENT

The authors declare that they have no conflicts of interest.

DATA AVAILABILITY STATEMENT

Sequence data generated during this work can be found in the GenBank database. The coding sequence of CFBP13503 has been deposited in GenBank at www.ncbi.nlm.nih.gov with accession number CP128598.

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

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