Identification of Collimonas gene loci involved in the biosynthesis of a diffusible secondary metabolite with broad-spectrum antifungal activity and plant-protective properties

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Summary

In greenhouse and field trials, a bacterial mixture of Collimonas arenace Cal35 and Bacillus velezensis FZB42, but not Cal35 alone or FZB42 alone, was able to protect tomato plants from challenge with the soil-borne fungal pathogen Fusarium oxysporum f.sp. lycopersici (Fol). To identify genes and mechanisms underlying this property in Cal35, we screened a random transposon insertion library for loss of function and identified two mutants that were impaired completely or partially in their ability to halt the growth of a wide range of fungal species. In mutant 46A06, the transposon insertion was located in a biosynthetic gene cluster that was predicted to code for a hybrid polyketide synthase–non-ribosomal peptide synthetase, while mutant 60C09 was impacted in a gene cluster for the synthesis and secretion of sugar repeat units. Our data are consistent with a model in which both gene clusters are necessary for the production of an antifungal compound we refer to as carenaemins. We also show that the ability to produce carenaemins contributed significantly to the observed synergy between Cal35 and FZB42 in protecting tomato plants from Fol. We discuss the potential for supplementing Bacillus-based biocontrol products with Collimonas bacteria to boost efficacy of such products.

Introduction

The ability to suppress fungal growth is a common characteristic among members of the bacterial genus Collimonas (Leveau et al., 2010). For its best known and studied representative, Collimonas fungivorans Ter331 (CTer331), two sets of genes that contribute to antifungal activity have been described. One is the NLP gene that codes for a non-ribosomal peptide synthetase (NRPS) and directs the biosynthesis of a lipopeptide with a predicted Leu-Thr-X-Ser-Ile peptide core attached to a fatty acid side-chain and with in vitro efficacy against the plant pathogenic fungi Fusarium culmorum and Rhizoctonia solani (Song et al., 2015). The other is the colABC-DEFG gene cluster (Kai et al., 2018), which is located on a chromosomal locus called cluster K (Fritsche et al., 2014) and codes for the biosynthesis of polyacetylenic compounds referred to as collimomycins (Fritsche et al., 2014) or collimonsins (Kai et al., 2018). These compounds feature an ene–triyne moiety that is essential for antifungal activity (Kai et al., 2018) and is formed through the combined action of the polyketide synthase (PKS) ColA and the desaturases ColB, ColC and ColD (Fritsche et al., 2014; Kai et al., 2018). In confrontation with laboratory strains of the fungus Aspergillus niger, collimomycin-producing C/Ter331 induces the stunting, swelling, branching and pigmentation of hyphae (Fritsche et al., 2014; Kai et al., 2018) and interrupts the process of spore germination (Mosquera et al., 2020). Not all Collimonas strains for which fungal suppression has been demonstrated carry the NLP gene or gene cluster K (Mela et al., 2012; Fritsche et al., 2014; Song et al., 2015), suggesting the existence of much unexplored genetic potential for antifungal activity in the Collimonas pangenome.

The fungistatic properties of collimonads have sparked interest in their use as biocontrol agents for the management of fungal diseases of plants. C/Ter331 was shown to protect tomato plants from the soilborne fungal pathogen Fusarium oxysporum f.sp. radicis-lycopersici, which
causes tomato foot and root rot (Kamilova et al., 2007). Whether this protection is linked to the production of collimycin or the NLP-encoded lipopeptide remains unknown. Recently, another Collimonas isolate, C. aereae Cal35 (CaCal35), was shown to protect tomato plants from the root pathogen Fusarium oxysporum f. sp. lycopersici (Fol), the causal agent of Fusarium wilt (Doan et al., 2020). However, it did so only when mixed together with Serenade Soil, a commercially available biocontrol product that features Bacillus velezensis (formerly subtilis) strain QST713 (BvQST713) as its active ingredient. Neither CaCal35 by itself nor Serenade Soil by itself was able to mitigate the formation of symptoms that are typical of Fusarium wilt and include vascular discoloration and reduced shoot weight (Doan et al., 2020).

The mechanism underlying this emerging property of ‘biocombicontrol’ (Doan et al., 2020) by the CaCal35-BvQST713 mixture is not known. BvQST713 has been shown to synthesize and secrete a suite of lipopeptides, including iturin, agrastatin/plipastatin and surfactin, which cause inhibition of spores and germ tubes (Marrone, 2002; Manker, 2004). No such secondary metabolites have yet been ascribed to CaCal35, which in laboratory assays outperformed all other tested Collimonas strains, including Ter331, in terms of overall fungal target range and growth suppression (Doan et al., 2020). CaCal35 does not possess a gene cluster K (Wu et al., 2015), which rules out a role for collimycin.

The goal of the study reported here was to identify and characterize the genes that underlie the antifungal activity of CaCal35 and to determine if these genes contribute to biocombicontrol together with Bacillus bacteria. Instead of BvQST713-based Serenade Soil, we opted to use another well-studied biocontrol strain called B. velezensis FZB42 (BvFZB42) (Borriss, 2011). Formerly known as Bacillus amyloliquefaciens subsp. plantarum FZB42 (Borriss, 2011; Chowdhury et al., 2015a; Dunlap et al., 2016; Fan et al., 2018), this bacterium suppresses the growth of many plant pathogenic fungi in vitro and protects crop plants such as cotton, tomato and lettuce against various plant pathogens (Yao et al., 2006; Gül et al., 2008; Chowdhury et al., 2013; Chowdhury et al., 2015b). Much like BvQST713, BvFZB42 produces lipopeptides with antifungal properties, including bacillomycin D (an iturin), fengycin (related to plipastatin) and surfactin (Chen et al., 2007; Chowdhury et al., 2015a). The BvFZB42 double-mutant AK3, which is unable to produce bacillomycin D as well as fengycin, is severely impaired in its ability to inhibit fungal growth (Koumoutsi et al., 2004).

We show here that the ability of CaCal35 to suppress in vitro the hyphal growth of previously tested and untested fungi, including A. niger and Fol, is correlated with the production of a diffusible activity that we refer to as carenaemin. Screening of a CaCal35 transposon insertion library for loss-of-function mutants led us to two chromosomal loci with a purported role in carenaemin production. The genetic and molecular characterization of these loci allowed us to propose a model for the PKS/NRPS-dependent synthesis of carenaemin and for the way in which carenaemin contributes to the reduction of Fol-induced symptoms on tomato plants by a mixture of CaCal35 and BvFZB42.

Results

Broad-spectrum, diffusible antifungal activity produced by CaCal35

In no-contact confrontation assays on PDA plates, CaCal35 inhibited colony expansion of A. niger, Fusarium oxysporum f.sp. lycopersici (Fol), F. oxysporum f.sp. fragariae (Fof), Rhizoctonia solani, Sclerotium rolfsii, Sclerotinia sclerotiorum, Verticillium dahliae and Magnaporthe grisea (Fig. 1, panels A2-H2), compared to control plates (fungus only, Fig. 1, panels A1-H1). For A. niger, this antifungal activity of CaCal35 (Fig. 2B, compared to 2A, fungus only) was shown to be diffusible and expressed in the absence of fungus, as follows. After culturing CaCal35 in the presence (Fig. 2B) or absence (Fig. 2D) of A. niger on PDA agar plates for 3 days, the sections of agar containing bacteria and fungi were removed using a sterile surgical blade. The remaining sections of agar were inoculated with A. niger spores at different distances relative to where CaCal35 had been growing on the plate. Compared to the control (Fig. 2A), A. niger was unable to grow on agar on which CaCal35 had been previously and proximally grown in the presence of A. niger (Fig. 2C), suggesting that the antifungal activity of CaCal35 was water-soluble and diffusable through agar. We also observed that growth of A. niger was inhibited on agar on which CaCal35 had been previously and proximally grown in the absence of A. niger and that the degree of inhibition decreased as a function of the distance between A. niger and CaCal35 (Fig. 2E–G). This observation is consistent with diffusion and dilution of the antifungal activity away from its source, CaCal35. We postulate that this antifungal activity represents a secondary metabolite that will be referred to hereafter as carenaemin.

Biocontrol of tomato Fusarium wilt by CaCal35 in combination with BvFZB42

Notwithstanding the observed antifungal activity of CaCal35 against Fol on agar plates (Fig. 1, panel B2), greenhouse-grown tomato plants were not protected from Fol-induced loss of biomass (Fig. 3A) or vascular discoloration (Fig. 3B) by prior root inoculation with...
CaCal35. Under the same conditions, BvFZB42 did not protect tomato plants from Fol either (Fig. 3A and B). However, when mixed together, CaCal35 and BvFZB42 (referred to as ‘Colli42’) significantly reduced ($P < 0.05$) Fol-induced loss of biomass (Fig. 3A) as well as vascular discoloration (Fig. 3B). Fol-challenged plants that were Colli42-treated looked like unchallenged (i.e. no-Fol) plants (Fig. S1D and A, respectively), whereas Fol-challenged plants that were treated with CaCal35 or BvFZB42 looked like untreated Fol-challenged plants (Fig. S1C, E, and B respectively).

Protection by Colli42 was also observed in an experimental Fol-infested field of tomato plants: only the Colli42 treatment significantly ($P < 0.05$) reduced Fol-

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induced vascular discoloration, whereas CaCal35 by itself or BvFZB42 by itself did not (Fig. 4A). Colli42 also returned the highest marketable yield of all treatments (i.e. 37.46 US tons of red tomato fruit per acre), but the differences between treatments were not significant (Fig. 4B).

Isolation and characterization of CaCal35 transposon mutants with reduced antifungal activity

To identify the gene(s) underlying the observed antifungal and biocombicontrol activity of CaCal35, approximately 6,500 random EZ-Tn5 transposon insertion mutants of CaCal35 were generated and screened for reduced antifungal activity against A. niger in a bottomless 96-well microtitre plate set-up (see Experimental Procedures). Two such mutants, designated 46A06 and 60C09, were identified (Fig. S2). We confirmed in a standard confrontation assay that both mutants had lost the ability to inhibit hyphal growth of A. niger (Fig. 1, panels A2 and A3). Mixing the two mutants together did not result in restoration to wild-type levels of inhibition (Fig. 1, panel A5). Also, A. niger appeared unaffected after inoculation onto a PDA plate on which either 46A06 or 60C09 was previously grown prior. Three days later, plates were photographed (C, E, F, G, I and K). While asterisks indicate the spot where A. niger spores were inoculated. Photograph A shows growth of A. niger by itself on PDA.

Genetic characterization of mutant 46A06

Genomic flank sequencing of the transposon in mutant 46A06 revealed the insertion site as 5'-GTGTACGGA-3' inside locus LT85_RS01670 (Fig. S3A–C). This gene is part of a 76.95-kb region of the CaCal35 genome (NCBI coordinates 365,248-442,201 of NZ_CP009962.1). This region harbours at least 35 predicted genes (Table 1) and was tagged by antiSMASH as containing a hybrid PKS-NRPS gene cluster. No hybrid PKS-NRPS gene clusters like it were found on the published genomes of other Collimonas strains, including C. fungivorans Ter6 and Ter331, C. pratensis Ter91 and Ter291, C. arenae Ter10 and Ter282, and Collimonas sp. ES_A1-A1, PA-H2, OK607, OK242, OK412, OK307, and UBA1456. However, we were able to identify gene clusters with similar synteny and predicted function on the genomes of Chromobacterium violaceum ATCC 53434 (Parker et al., 1988; Singh et al., 1988), Chitinimonas koreensis...
DSM 17726 (Kim et al., 2006), Paraburkholderia megapolitana LMG 23650 (Vandamme et al., 2007) and Paraburkholderia acidophila ATCC 31363 (Horsman et al., 2017). The similarity appeared to be limited to a stretch of genes corresponding to LT85_RS01720 → LT85_RS01665 in CaCal35, which includes the gene carrying the transposon insertion in 46A06, i.e. LT85_RS01670 (Fig. S4).

LT85_RS01670 is the ninth in a predicted superoperon of 11 genes (LT85_RS01720 → LT85_RS01660; Fig. 6A, Table S1), which we refer to as cplABCDEFGHIJK (where cpl stands for carenaemin production locus). According to the ‘co-linearity rule’ (Fischbach and Walsh, 2006), the first five genes of this superoperon (cplABCDEFG) were predicted to code for the production of carenaemin biosynthesis by Collimonas bacteria

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a secondary metabolite featuring a core scaffold of three amino acid residues, with the first and second amino acids linked through a peptide bond and the second and third by a -CH2-CHOH- moiety (Fig. 6B and C). The middle amino acid is predicted to be a serine, based both on NRPSPredictor2 and on the Stachelhaus sequence (i.e. DVWHFSLVDK) of the corresponding adenylation domain in the cpiB gene product. The Stachelhaus sequences of the other two adenylation domains (DIWQFGLILK in cpiA and DALFMGAVMK in cpiC) were most similar (but not identical) to those reported for glutamine (DAWQFGLIDK) and leucine (DALVMGAVMK) respectively (Rausch et al., 2005). The presence of an epimerization domain in the predicted cpiC product suggested that the third amino acid exists in D-configuration in the structure. The presence of a ketosynthase/malonyltransferase domain and an aminotransferase domain at the N-terminal end of the cpiA gene product puts a predicted R1-CNHN2-CH2- group at one end of the secondary metabolite (which generates a glycine amino acid), with a CO-R2 group predicted at the other end, based on the ketosynthase/malonyltransferase domain in cpiD. The chemical formula of the predicted core structure shown in Fig. 6C, not including R1 and R2, is C21H35O8N5, with a predicted mass of 485.53 Da.

The LT85_RS01670 gene (i.e. cplI) which carried the transposon insertion in mutant 46A06 is annotated to code for a polysaccharide pyruvyl transferase family protein (accession number WP_081991923). Pyruvyl transferases catalyse the transfer of the pyruvate moiety to a saccharide target (Hager et al., 2019). Proteins belonging to this functional family include CsaB (Fujinami and Ito, 2018; Hager et al., 2018), WcaK (Stevenson et al., 1996), AmsJ (Wang et al., 2012) and PssM (Ivashina et al., 2010), which are all involved in the production of exopolysaccharides (EPS), including secondary cell wall polymers in Bacillus species, colanic acid in Escherichia coli, amylovoran in Erwinia and EPS in Rhizobium leguminosarum respectively. Immediately downstream of cplI and part of the same predicted operon as cplI (LT85_RS01665) and cplK (LT85_RS01660), annotated as a hypothetical protein and a deaminated glutathione amidase respectively.

Genetic characterization of 60C09. In mutant 60C09, the EZ-Tn5 transposon was found inserted into the sequence 5'-GTATAAGCA-3’, where TAA is the stop codon for gene LT85_RS04520 (Fig. S3D–F). Multiple genes in the immediate vicinity of LT85_RS04520 (Fig. 6B; Table 2) are predicted to contribute to the so-called Wzy-dependent pathway for synthesis and incorporation of oligosaccharide repeat units into cell
surface lipopolysaccharides (Kalynych et al., 2014). This pathway involves the initial transfer of a sugar moiety to a lipid carrier (probably catalysed by the product of LT85_RS04530), the addition of sugar groups by glycosyltransferases (LT85_RS25805, LT85_RS04525) to generate an oligosaccharide repeat unit. Individual units are transported into the periplasm by a Wzx flippase (LT85_RS04500), where they undergo polymerization by a Wzy polymerase (LT85_RS25800) to yield a polysaccharide that then may be transferred to the inner-core oligosaccharide of lipid A by WaaL ligase (LT85_RS04650) and transported to the cell surface.

One of the sugars in the oligosaccharide repeat unit probably is rhamnose, seeing that (i) LT85_04485, _04490 and _04495 resemble the rmlABCD genes for the conversion of D-glucose-1-P into deoxyxymidine diphosphate (dTDP)-L-rhamnose (King et al., 2009), and (ii) the LT85_RS25805 gene product is highly similar to RtfB, which is a dTDP-rhamnosyl transferase that in *Shigella flexneri* generates the N-acetylgalactosamine-Rha-Rha-Rha tetrasaccharide repeat (Morona et al., 1995). Another sugar in the oligosaccharide repeat unit may be 6-deoxytalose, given that the two genes flanking LT85_RS04520 are predicted to code for the conversion of dTDP-L-rhamnose into dTDP-L-6-deoxytalose (LT85_04515) and for adding dTDP-L-6-deoxytalose to the growing oligosaccharide repeat unit (LT85_04525), based on similarity to the tle and gtr29 gene products, respectively, from *Acinetobacter baumannii* (Kenyon et al., 2017). The LT85_RS04520 product itself is annotated as a serine acetyltransferase. It showed substantial homology to WcaB from *E. coli* which also carries the signature of a serine acetyltransferase, but has been shown to catalyse the acetylation of a galactosyl residue after its incorporation as the fourth sugar into the heptasaccharide repeat unit of colanic acid (Scott et al., 2019). This acetylation enables the next glycosyltransferase to add the fifth sugar onto the colanic acid repeating unit (Scott et al., 2019).

### Table 1. Genomic context of the transposon insertion in CaCal35 mutant 46A06.

| NCBI locus tag | Predicted protein | NCBI protein ID |
|----------------|-------------------|-----------------|
| LT85_RS01600   | Acetyl-CoA C-acyltransferase | WP_038484473.1 |
| LT85_RS01615   | SDR family oxidoreductase | WP_038484482.1 |
| LT85_RS01625   | Hypothetical protein | WP_038484490.1 |
| LT85_RS01630   | DGQHR domain-containing protein | WP_156117397.1 |
| LT85_RS01635   | LysE family translocator | WP_038484493.1 |
| LT85_RS01640   | Lrp/AsnC family transcriptional regulator | WP_038484496.1 |
| LT85_RS01645   | VOC family protein | WP_038484499.1 |
| LT85_RS01650   | MarR family transcriptional regulator | WP_038484502.1 |
| LT85_RS01655   | TCR/Tet family MFS transporter | WP_052135471.1 |
| LT85_RS01660   | Deaminated glutathione amidase | WP_172656931.1 |
| LT85_RS01665   | Hypothetical protein | WP_156117398.1 |
| **LT85_RS01670** | **Polysaccharide pyruvyl transferase family protein** | WP_038484508.1 |
| LT85_RS01675   | 4'-phosphopantechnethyne transferase superfamily protein | WP_052134537.1 |
| LT85_RS01680   | Thioesterase | WP_052134540.1 |
| LT85_RS01685   | Polyunsaturated fatty acid/polyketide biosynthesis protein | WP_052134542.1 |
| LT85_RS01690   | Hypothetical protein | WP_038484511.1 |
| LT85_RS01695   | Type I polyketide synthase | WP_038484514.1 |
| LT85_RS01700   | Non-ribosomal peptide synthetase | WP_052134544.1 |
| LT85_RS01715   | Hybrid non-ribosomal peptide synthetase/type I polyketide synthase | WP_081991927.1 |
| LT85_RS01720   | Hybrid non-ribosomal peptide synthetase/type I polyketide synthase | WP_038484528.1 |
| LT85_RS01725   | Helix-turn-helix transcriptional regulator | WP_038484531.1 |
| LT85_RS01730   | SDR family oxidoreductase | WP_081991930.1 |
| LT85_RS01735   | LysR family transcriptional regulator | WP_052134547.1 |
| LT85_RS01740   | alpha/beta hydrolase | WP_038484534.1 |
| LT85_RS25150   | PmrB family protein | WP_009049067.1 |
| LT85_RS01750   | NmrA/HSCARG family protein | WP_017604182.1 |
| LT85_RS01755   | Phosphoesterase | WP_052134552.1 |
| LT85_RS01760   | e-type cytochrome | WP_052135472.1 |
| LT85_RS01765   | Branched-chain amino acid transferase | WP_038484543.1 |
| LT85_RS01775   | NAD(P)-dependent alcohol dehydrogenase | WP_038484549.1 |
| LT85_RS01780   | AraC family transcriptional regulator | WP_038494762.1 |
| LT85_RS01785   | LysR family transcriptional regulator | WP_038484552.1 |
| LT85_RS01790   | SDR family oxidoreductase | WP_038484555.1 |
| LT85_RS01795   | SnoA-like domain-containing protein | WP_038484558.1 |
| LT85_RS01800   | DEAD/DEAH box helicase | WP_081991932.1 |

*a. Highlighted in bold is the gene (LT85_RS01670) that carried the transposon insertion in 46A06. This gene is part of the cplABCDEFGHIJK supraoperon (where cpl stands for carenaemin production locus, LT85_RS01720 → LT85_RS01660) which is highlighted in grey.*
Characterization of the antifungal activity produced by CaCal35

We were unsuccessful in our efforts to recover antifungal activity from culture supernatants of CaCal35 grown in broth. We therefore devised an agar diffusion assay to extract antifungal activity from CaCal35 grown on agar instead. This assay (Fig. S5) exploits the fact that such activity is produced by CaCal35 on agar in the absence of fungus and is diffusible through agar. The diffusates that were collected in this way from wild-type CaCal35 and from mutants 46A06 and 60C09 were tested in a modified confrontation assay with A. niger to reveal that hyphal growth of A. niger was reduced in the presence of diffusates extracted from CaCal35, but not with those extracted from mutants 46A06 and 60C09 (Fig. 7A). The diffusates were analysed by liquid chromatography–mass spectrometry, revealing two prominent peaks (labelled as a and b in Fig. 7B) that were present in the CaCal35 diffusate but absent in the diffusates collected from the mutants 46A06 (Fig. 7C) and 60C09 (Fig. 7D). These two peaks eluted with retention times of 13.3 and 13.7 min, and m/z values of 835.493 and 849.509 Da, respectively, in both negative and positive mode. The difference in m/z between peaks a and b equals 14.016 Da, which approximates (Patiny and Borel, 2013) the mass of a CH2 moiety. Furthermore, we observed two peaks that were unique to the diffusate from mutant 46A06 and absent from those of wild-type CaCal35 and mutant 60C09 (labelled as c and d in Fig. 7C). These peaks had retention times of 12.3 and 12.8 min, and m/z values were 765.488 and 779.503 Da in both negative and positive mode respectively. The difference in m/z between peaks c and d was 14.015, i.e. the same difference in m/z as between peaks a and b, and consistent with a CH2 moiety. In positive mode, the differences in m/z between peaks a and c and between peaks b and d were 70.006 and 70.005, respectively, which corresponds with a C3H2O2 moiety.
Discussion

Our data revealed that the ability of CaCal35 to inhibit the growth of a wide range of fungal species, including A. niger and Fusarium oxysporum f.sp. lycopersici (Fol), depends on the production and secretion of an antymycotic activity that we call carenaemin. We showed that this activity is water-soluble, diffusible, and produced in the absence of fungus. The activity was lost in two transposon insertion mutants (46A06 and 60C09) which led us to two gene loci of interest, on different parts of the CaCal35 chromosome.

Characterization of mutant 46A06 identified the cpl cluster as a major contender for involvement in the synthesis of carenaemin by CaCal35. This cluster codes for a hybrid PKS/NRPS that is predicted to produce a metabolite that has the amino acids Gln, Ser and Leu at its core (Fig. 6). Interestingly, the observation that the diffusate of wild-type Cal35 showed two major peaks (a and b) that differed in mass by a CH2 group may be explained by assuming promiscuity for one of the adenylation domains in the cpl gene cluster. Such promiscuity, more specifically as it relates to accepting two amino acids that differ by one CH2 group in their side-chain, is not uncommon (Qiao et al., 2011). For all three predicted amino acids in the carenaemin core (Gln, Ser, and Leu), there exists a corresponding amino acid that differs by only one CH2 group (Asn, Thr and Val, respectively), so it is unclear which one of the three adenylation domains in the cpl gene cluster might be the promiscuous one.

The same difference of one CH2 group was also observed between the two major peaks in the diffusate of the 46A06 mutant (peaks c and d). This suggests that the metabolites produced by this mutant, while lacking antifungal activity, likely contain the same peptide core as the active metabolites produced by wild-type Cal35. This is also consistent with the observation that the transposon insertion in 46A06 was not located inside of the cplABCDE genes that are presumed to be involved in the synthesis of the core.

Table 2. Genomic context of the transposon insertion in CaCal35 mutant 60C09.

| NCBI locus tag   | Predicted protein                        | NCBI protein ID          |
|-----------------|------------------------------------------|--------------------------|
| LT85_RS04480    | dTDP-glucose 4,6-dehydratase (RmlB)      | WP_038485799.1           |
| LT85_RS04485    | Glucose-1-phosphate thymidylyltransferase (RmlA) | WP_038485802.1           |
| LT85_RS04490    | dTDP-4-dehydrohammose 3,5-epimerase (RmlC) | WP_038485805.1           |
| LT85_RS04495    | dTDP-4-dehydrorhammose reductase (RmlD)   | WP_038485809.1           |
| LT85_RS04500    | flippase                                  | WP_081992030.1           |
| LT85_RS25800    | Oligosaccharide repeat unit polymerase    | WP_081992033.1           |
| LT85_RS25805    | dTDP-1-L-rhamnosyltransferase             | WP_081992035.1           |
| LT85_RS04515    | dTDP-L-rhamnose 4 epimerase (Tle)         | WP_038495031.1           |
| LT85_RS04520    | Serine acetyltransferase                  | WP_038485818.1           |
| LT85_RS04525    | dTDP-6-deoxy-L-talosyltransferase         | WP_038485820.1           |
| LT85_RS04530    | Lipid carrier: UDP-N-acetylgalactosamyltransferase | WP_038485823.1   |
| LT85_RS04535    | UDP-N-acetylglucosamine 4,6-dehydratase   | WP_052134643.1           |
| LT85_RS04540    | H-NS histone family protein               | WP_038485826.1           |
| LT85_RS04545    | Phosphomannomutase/phosphoglucomutase     | WP_038485829.1           |
| LT85_RS04550    | Lipopolysaccharide heptosyltransferase I  | WP_038485833.1           |
| LT85_RS25195    | Class I SAM-dependent methyltransferase   | WP_081992037.1           |
| LT85_RS04560    | Hypothetical protein                      | WP_038485836.1           |
| LT85_RS04565    | Class I SAM-dependent methyltransferase   | WP_172656939.1           |
| LT85_RS04570    | Glycosyltransferase                       | WP_052134650.1           |
| LT85_RS04575    | Glycosyltransferase                       | WP_038485842.1           |
| LT85_RS04580    | Hypothetical protein                      | WP_038485845.1           |
| LT85_RS04585    | DUF2142 domain-containing protein         | WP_172656940.1           |
| LT85_RS04595    | Selenocysteine-specific translation elongation factor | WP_038485851.1   |
| LT85_RS04600    | L-seryl-tRNA(Sec) selenium transferase    | WP_052134652.1           |
| LT85_RS04605    | Formate dehydrogenase accessory protein FdhE | WP_038485854.1          |
| LT85_RS04610    | Formate dehydrogenase subunit gamma       | WP_038485857.1           |
| LT85_RS04615    | Formate dehydrogenase subunit beta        | WP_038485861.1           |
| LT85_RS04620    | Formate dehydrogenase-N subunit alpha     | WP_156111742.1           |
| LT85_RS04625    | Sulfate ABC transporter substrate-binding protein | WP_038485868.1          |
| LT85_RS04630    | 3-deoxy-D-manno-5-ulose reductase (Kdo) hydroxylase | WP_038485871.1 |
| LT85_RS04635    | 3-deoxy-D-manno-octulosonic acid transferase | WP_038495045.1          |
| LT85_RS04640    | Ydcf family protein                       | WP_038485874.1           |
| LT85_RS04645    | Glycosyl transferase                      | WP_052134654.1           |
| LT85_RS04650    | O-antigen ligase domain-containing protein | WP_038485877.1           |
| LT85_RS04655    | UDP-glucose 4-epimerase GalE subunit       | WP_038485880.1           |

a. Highlighted in bold is the gene (LT85_RS04520) that carried the transposon insertion in 60C09. This gene is part of a predicted operon (highlighted in grey).
Instead, the transposon in mutant 46A06 was found inserted into a gene that lies downstream of cplABCDE and is predicted to code for a polysaccharide pyruvyl transferase. This annotation suggests a link between the production of the carenaemin peptide core and the polysaccharide synthesis gene cluster that was identified through mutant 60C09. Pyruvyl transferases add a pyruvyl group to monosaccharides and are typically mentioned in the context of cell surface polysaccharides (Hager et al., 2019). One typical outcome of pyruvyl transferase activity is the formation of a ketal structure which bridges two hydroxyl groups of a monosaccharide residue through pyruvate, thus forming a ring structure (Hager et al., 2019). In this process, two hydrogens (2H) are removed from the sugar moiety and a C3H4O2 group is added back, for a net addition of C3H2O2, which represents a monoisotopic mass of 70.005. Interestingly, this mass equals the difference that we found in positive and negative ion modes.

Fig. 7. Antifungal activity (or lack thereof) in diffusates from wild-type CaCal35 and mutants 46A06 and 60C09 (A) and LC-MS chromatograms of these same diffusates (B–D). In panel B, a and b represent two peaks that were present in diffusate from CaCal35, but absent in mutants 46A06 and 60C09. In panel C, c and d represent two peaks that were present in diffusate from 46A06, but absent from CaCal35 and 60C09. See text for more details on these peaks.
negative mode between the m/z values of peaks a and c and between the m/z values of peaks b and d in the diffusates of wild type and 46A06 respectively. Seeing that the diffusate of 46A06 lacked antifungal activity altogether, the simplest explanation for the difference in m/z between peaks a/b and c/d is that pyruvlation is required for antifungal activity. Because pyruvyl transferases act on monosaccharides, this conclusion also implies that carenaemin features at least one sugar moiety.

As for the nature of the purported sugar moiety in carenaemin, rhamnose and 6-deoxytalose are obvious candidates, given the proximity of the transposon insertion in mutant 60C09 to genes involved in the biosynthesis of dTDP-L-rhamnose and dTDP-L-6-deoxytalose. Metabolites that have antibacterial activity and feature rhamnose as a decoration include caprazamycin (Kaysser et al., 2010), spinosyn A (Chen et al., 2009), elloramycin (Blanco et al., 2001) and brabantamide (Schmidt et al., 2014), as well as the antifungals thailandin A (Greule et al., 2016) and hassallidin B (Neuhoft et al., 2006). Also, rhamnose, together with 6-deoxytalose, is a key component of the so-called non-specific glycopeptidolipids (GPLs) in the outer layer of the cell wall of non-tuberculous mycobacteria (Mullowney et al., 2018). It is known that rhamnose can be pyruvylated (Pan et al., 2015), and the differences between the m/z values of peaks a, b, c and d in the CaCal35 and 46A06 diffusates (835.5, 849.5, 765.5 and 779.5, respectively) and the calculated molecular mass of the predicted peptide core (485.5 Da) are sufficiently large (350 and 364 Da for CaCal35; 280 and 294 Da for 46A06, respectively) to be consistent with the presence of one pyruvylated rhamnosyl group (233.1 Da) or one non-pyruvylated rhamnosyl group (163.1 Da).

Worthwhile to note is that the transposon insertion in CaCal35 mutant 60C09 was not actually inside one of the sugar biosynthetic genes. This excludes the possibility that the failure to synthesize these sugars underlies the inability of mutant 60C09 to produce carenaemin. Also, we did not see in the diffusate of mutant 60C09 a unique compound (i.e. not found in the diffusates of CaCal35 or mutant 46A06) which could be interpreted as an aglyconic version of carenaemin. In other words, mutant 60C09 would appear to have the potential to produce the carenaemin core (it has an intact cpl gene cluster after all) and to synthesize the sugar(s) presumably needed to decorate the core, but its diffusate shows neither a sugar-bearing nor a sugar-free core. This observation is consistent with a scenario in which (i) the gene cluster knocked out in mutant 60C09 is responsible for attaching the sugar to the core and (ii) attachment of the sugar is necessary for secretion of the sugar-bearing core (seeing that secretion is a requirement for being detectable in the diffusate). Considering that we were able to detect what is assumed to be a sugar-decorated but non-pyruvylated core in the diffusate of mutant 46A06, pyruvlation seems to be unimportant for adding sugar to the core or for secretion of the sugar-bearing core.

The prediction that the gene cluster knocked out in 60C09 codes for the Wzy-dependent synthesis and export of oligosaccharide repeat units offers a possible mechanism for the observed coupling of glycosylation and secretion of carenaemin. The mechanism we propose here resembles steps involved in the synthesis and export of peptidoglycan units, where in the cytoplasm a pentapeptide is attached to a Lipid-II-bound disaccharide (N-acetylglucosamine-N-acetylmuramic acid) which then is transported across the membrane (Breukink and de Kruifff, 2006; de Kruifff et al., 2008). Similarly, the 46A06-produced peptide core may be attached to one of the sugars in the repeat unit of rhamnose and/or 6-deoxytalose that then gets flipped into the periplasm. Additional studies will be needed to test this hypothesis, to identify the enzyme responsible for attaching the 46A06-produced peptide core to the sugar repeat (pyruvylated or not) and to elucidate the steps that lead from the transport into the periplasm to the secretion of carenaemin.

An alternative scenario that is consistent with our observations is that the substrate that is loaded onto the KS domain encoded by cplA needs to be glycosylated before it can be accepted as a substrate for subsequent cplABCDE-encoded reactions leading to carenaemin. A similar scenario has been proposed for brabantamide, where the inability to detect an aglyconic (i.e. non-rhamnosylated) version of brabantamide was explained by assuming that the glycosylation reaction occurs early in the biosynthesis, not as a late-stage tailoring step (Schmidt et al., 2014). This alternative hypothesis for the synthesis and secretion of carenaemin will also require further experimental scrutiny, in order to identify the protein(s) responsible for the extracellular delivery of carenaemin and to explain the involvement of components of the Wzy-dependent pathway that are knocked out in 60C09.

Both of the scenarios described above are consistent with our observation that mutants 46A06 and 60C09 were unable to complement each other and restore antifungal activity to wild-type CaCal35 levels. In the first scenario, mutant 60C09 would be unable to secrete the peptide core and to make it available to 46A06 for glycosylation. In the second scenario, the 46A06-produced glycosylated substrate for CplABCDE would need to be secreted and taken up by 60C09 for production of functional carenaemin, which is unlikely.

The absence of a carenaemin biosynthesis gene cluster from other known Collimonas genomes suggests that
CaCal35 acquired the cpl genes horizontally from unrelated bacteria. We can assume that the cpl genes confer upon CaCal35, and upon the alleged donor, an advantage over other bacteria with which they shared the same environment. Collimonads are typically found in nutrient-poor conditions (Leveau et al., 2010) and a bacterium like CaCal35, which was isolated from the mineral horizon of a forest soil (Uroz et al., 2014) may benefit from carenaemin as a means to suppress fungal growth and exploitation of shared but limited resources. Of interest in this context is the reported origin of Paraburkholderia megapolitana LMG 23650, which is one of the strains we identified as carrying a cpl-like gene cluster in its genome (see Results section). This strain was originally isolated as Burkholderia phenazinum A3 from moss plants on the southern coast of the Baltic Sea in Germany (Vandamme et al., 2007). The site where A3 was found has been described as a nutrient-poor habitat, and A3 has been shown to possess antifungal activity (Opelt and Berg, 2004). Interestingly, from the same habitat, as part of the same expedition that unearthed A3, a Collimonas fungivorans isolate was recovered, labelled A23 (Opelt and Berg, 2004). This strain too was shown to have antifungal activity, specifically against V. dahliae (Opelt and Berg, 2004), Botrytis cinerea (Sylla et al., 2012), and Phytophthora cactorum and P. fragariae (Bisutti and Stephan, 2011). However, it remains unknown whether the A23 genome harbours a cpl gene cluster, and whether this gene cluster underlies the antifungal activities of A23 and A3 and contributes to their fitness in the nutrient-poor phytobiomes from which they were isolated.

In greenhouse and field experiments, CaCal35 suppressed the formation of symptoms by soilborne pathogen Fol on tomato plants, but only in combination with BvFZB42 (i.e. as a Cal442 mixture). Neither CaCal35 by itself, nor BvFZB42 by itself, had the ability to protect tomato plants. The same result was recently reported for a mixture of CaCal35 and the commercially available biofungicide Serenade Soil (active ingredient: BvOST713) (Doan et al., 2020). This emerging protective property of Collimonas-Bacillus mixtures has been dubbed ‘biocombicontrol’ (Doan et al., 2020). Seeing that mutant 46A06 did not show synergy with BvFZB42 under greenhouse conditions suggests that carenaemin contributes to the biocombicontrol phenomenon of Cal42. Similarly, the AK3 mutant of BvFZB42, unable to produce bacillomycin D and fengycin (Koumoutsi et al., 2004), did not show synergy with CaCal35 in our experiments. These observations lead us to hypothesize that the observed synergy between Collimonas and Bacillus is a result of the synergy between the antifungal metabolites that these bacteria produce. This hypothesis is practically relevant: seeing that Serenade Soil is one of the most popular Bacillus-based biofungicidal products on the market and that BvFZB42 is the active ingredient of the commercially available biocontrol product Rhizovital® 42 liquid (Borriss, 2011) and is a closely related ‘cousin’ of FZB24, which is the active ingredient in the commercially available formulation Taegro (Fan et al., 2018), the question can be asked whether all these and other Bacillus-based products might work even better by amending them with CaCal35.

**Experimental procedures**

**Microbial strains and growth conditions**

All bacterial strains used in this study were stored as glycerol stocks at −80°C, and grown in King’s medium B (KB; 20 g Bacto Proteose Peptone No.3, 1.15 g K2HPO4, 0.73 g MgSO4·7H2O, 10 ml glycerol per litre) or on KB agar (KB supplemented with 16 g agar per litre) or Potato Dextrose Agar (PDA) (39 g Difco Potato dextrose agar per litre). CaCal35 was originally isolated from forest soils (Uroz et al., 2014; Wu et al., 2015). BvFZB42 and its mutant AK3 were obtained from the Bacillus Genetic Stock Center (BGSC, Columbus, OH, USA). Aspergillus niger N402 (ATCC 64974; a derivative of CBS120.49, densely sporulating with short conidio- phores) (Bos et al., 1988) has been used previously in confrontation assays with collimonads (Mela et al., 2011; Fritsche et al., 2014; Doan et al., 2020; Mosquera et al., 2020). Fusarium oxysporum f.sp. lycopersici (Fol) race 3 strain D12 (Doan et al., 2020), F. oxysporum f.sp. fragariae (Fof) strain GL1080, Magnaporthe grisea strain GL787, Rhizoctonia solani, Sclerotinia rolfsii, Sclerotinia sclerotiorum and Verticillium dahliae strain T9 were gifted by Dr. Mike Davis (University of California, Davis, CA, USA). All fungal cultures were maintained as spore suspensions in glycerol stocks at −80°C or as mycelium on PDA.

**Confrontation assays**

Collimonas bacteria were streaked from −80°C glycerol stocks onto KB agar plates and incubated at 28°C for 3 days. To prepare fungal spore suspensions, two- to three-week-old PDA cultures (9 cm diameter petri dish) of A. niger, Fol or V. dahliae were flooded with 15 ml autoclaved water. Spores were suspended using a sterile glass slide and filtered through four layers of sterile cheese cloth (Doan and Davis, 2014). Spore concentrations were determined with a Neubauer Levy Ultra Plane Hemocytometer (Hauser Scientific, Horsham, PA, USA) and adjusted to 105 spores per ml with autoclaved water. For S. rolfsii, single mature sclerotia obtained from two- to three-week-old cultured PDA plates were used as a source of inoculum. For Fol, R. solani, S. sclerotiorum
and *M. grisea*, we used agar plugs excised from two-week-old PDA cultures.

Confrontation assays were performed as described (Fritsche et al., 2014) except that PDA was used instead of *N*-acetylglucosamine-supplemented water yeast agar. In a petri dish (9 cm diameter) containing 30 ml PDA, *Collimonas* bacteria were line-inoculated on one half of the plate. Five microlitres of a suspension of $10^5$ fungal spores per ml in water (*A. niger*, *Fol* or *V. dahliae*), single matured sclerotia (*S. rolfsii*) or agar plugs (*Fof*, *R. solani*, *S. sclerotiorum* and *M. grisea*) was inoculated on the other half of the plate, approximately 2 cm from the bacterial line. Control plates were inoculated with fungi only, i.e. no bacteria. The plates were sealed with parafilm and incubated at 28°C.

To test the diffusibility of the *Collimonas* antifungal activity, bacteria were line-inoculated in petri dishes containing 30 ml of PDA per plate. The plates were incubated at 28°C for 3 days, after which the section of agar covered with the bacteria was cut out and removed using a sterile surgical blade. Five microlitres of a suspension of $10^5$ *A. niger* spores per ml in water was then spot-inoculated on the remaining section of agar at increasing distances (approximately 1.5, 3 or 4.5 cm) from where the original bacterial line was. The plates were incubated for 3 days at 28°C, assessed for growth by *A. niger* and photographed.

Transposon mutagenesis of CaCal35

In a 500 ml flask, 100 ml of KB was inoculated with 1 ml of an overnight pre-culture of CaCal35 and incubated at 28°C with shaking until the optical density at 600 nm (OD$_{600}$) reached 0.5-0.7 (~6 h). Two 45 ml culture aliquots were transferred to 50 ml centrifuge tubes (Fisher Scientific, Pittsburgh, PA, USA) and incubated on ice for 30 min. The cells were then harvested by centrifugation at 2500 g for 15 min at 4°C. Supernatants were removed, and cells were resuspended in 2 x 25 ml of ice-cold Milli-Q water and centrifuged as before. After discarding the supernatant, cells were resuspended in 2 x 5 ml of ice-cold 10% glycerol in Milli-Q water. After another round of centrifugation, the cells were resuspended in 1 ml of ice-cold 10% glycerol. Fifty µl aliquots of this suspension were dispensed in microcentrifuge tubes and stored at ~80°C for future use, or mixed with no more than 1 µl of EZ-Tn5 transposome (Epicentre, Madison, WI, USA). After a few minutes on ice, the mixture was transferred to a sterile 0.1 cm electroporation cuvette (Bio-Rad, Hercules, CA, USA) and incubated on ice for 2-3 min. Electroporation was performed with a Bio-Rad Gene Pulser apparatus with the following settings: 25 µF, 200 ohms and 1.8 kV. Immediately after electroporation, 1 ml of SOC medium (Sambrook and Russel, 2001) was added to the cuvette and gently mixed by pipetting. The suspension was transferred to a 17 x 100 mm polypropylene tube (Fischer Scientific, Santa Clara, CA, USA) and incubated for 1 h at 28°C with gentle shaking. Part of the suspension was stored as a glycerol stock at ~80°C for future plating. Another part was immediately diluted and spread on KB agar plates with 50 µg of kanamycin per ml and incubated up to three days at 28°C for the selection of transposon insertion mutants. Mutant colonies were restreaked onto fresh KB agar supplemented with 50 mg kanamycin per litre with 48 mutants per plate and incubated for 3 days at 28°C. In total, 6,500 mutants were prepared in this way and screened for loss of antifungal activity, as described below.

Screening for CaCal35 mutants with reduced antifungal activity

Following the method described previously (Fritsche et al., 2014), the CaCal35 transposon library was screened for mutants with reduced or abolished antifungal activity towards A. niger in bottomless 96-well microtitre plates (Greiner Bio-One, Monroe, NC, USA). For this, the underside of the plates was sealed temporarily with sealing mats (Greiner Bio-One, Frickenhausen, Germany) and each well was filled with molten 250 µl PDA which was allowed to solidify. Afterwards, the sealing mat was removed and the agar in each well was inoculated on the bottom with one of the 6,500 *Collimonas* mutants (see above), while the top was inoculated with 3 µl of a $10^5$ ml$^{-1}$ spore suspension of *A. niger*. The plates were incubated at 28°C for 2 days and observed daily for hyphal growth of A. niger. Among the 6500 mutants screened, two mutants (46A06 and 60C09) showed reduced antifungal activity, which was confirmed by retesting the two mutants in a standard confrontation assay on PDA (described above).

Identification of transposon insertion sites in CaCal35 mutants 46A06 and 60C09

The transposon insertion site for mutants 46A06 and 60C09 was determined by genomic flank sequencing as described elsewhere (Tecon and Leveau, 2016). For this, genomic DNA was isolated from 2 ml of an overnight culture of each mutant using the DNeasy blood and tissue kit (Qiagen, Germantown, MA, USA) and resuspended in 50 µl of elution buffer. Three µl of DNA (~300-600 ng) in a total volume of 10 µl was further digested with 10 U of EcoRI or SacI (neither one of which cuts in the transposon) for 1 h at 37°C, followed by thermal inactivation at 65°C for 20 min. One µl of digested DNA was self-ligated in a final volume of 10 µl.
with 1000 U of T4 DNA ligase, for 2 h at room temperature. Two μl of ligation mixture was used as target DNA in a 25 μl PCR using primers KAN-2 FP1 (5’-ACCTACACAAAGCTCTCAGAAAACC-3’) and KAN-2 RP1 (5’-GCAATGTAACATCAGATTTTGAG-3’) at a concentration of 500 nM each. The reaction cycle was as follows: 95°C for 4 min; 30x [95°C for 30 sec, 55°C for 30 sec, 72°C for 90 sec]; 72°C for 5 min. Amplicons were separated and visualized on a 0.8% agarose gel, and purified from the gel using a QIAquick kit (Qiagen). PCR products were sequenced using primers KAN-2 FP1 and KAN-2 RP1. The flanking DNA sequences were mapped onto the genome sequence (NCBI accession number NZ_CP009962.1) of C. arenae Cal35 (Wu et al., 2015). The predicted function of the identified genes and gene clusters and the organization of genes into putative operons were assessed using the NCBI database, the biosynthetic gene cluster identification tool antiSMASH version 5.0.0 (https://www.antismash.com) (Medema et al., 2011) and the FGENESB online software at http://www.softberry.com (Solovyev and Salamov, 2011). Efforts to complement mutants 46A06 and 60C09 with full-length copies of the genes that carried a transposon insertion on their chromosomes were not successful.

Collection and characterization of CaCal35, 46A06 and 60C09 diffusates

In order to extract antifungal activity from PDA-grown wild type and mutant CaCal 35 strains, we used a sterile, 10 mm diameter cork borer to generate 10 wells in the agar of five PDA plates per strain. These wells were separated by about 2 mm and arranged in a U-shaped pattern (Fig. S5). CaCal35 or its mutant derivatives 46A06 and 60C09 were inoculated onto these PDA plates, with a distance of approximately 1 cm from the edge of the wells. The plates were sealed with parafilm and incubated at 28°C. After 3, 6, 24 and/or 48 h, aliquots were taken from the PDB in the wells and pooled for each plate. The plates were sealed with parafilm and incubated at 28°C. The plates were observed and photographed every 24 h for up to 4 days.

Liquid chromatography–mass spectrometry (LC-MS) analysis of Collimonas diffusates

Diffusates were diluted 10x in 100% LC-MS grade methanol, filtered over a 0.22 μm membrane and injected (5 μl) into a Thermo UltiMate 3000 UHPLC system equipped with a Thermo Q Exactive Hybrid Quadrupole-Orbitrap Mass Spectrometer (LC-HESI-HiRes MS). The column used for the separation was an Agilent ZORBAX RRHD Eclipse Plus C18 (2.1 X 150mm, 1.8 μM, 959759-902). The gradient elution involved a mobile phase consisting of (A) 0.1% formic acid in water and (B) 0.1% formic acid in acetonitrile. The initial condition was set at 5%-B for 1.0 min. A linear gradient to 95%-B was applied in 12 min followed by another 5 min of gradient to 100%-B. The gradient was then returned to starting conditions and held for 7 min. Flow rate was set at 0.3 ml/min. The electrospray ionization mass spectra were acquired in both positive and negative ion模式. Mass data were collected between m/z = 133 and 2,000. The ion spray voltage was set at 3.500 V; gas temperature and auxiliary gas temperature were maintained at 380°C and 425°C respectively. The sheath gas flow and auxiliary gas flow were set at 60 and 20 arbitrary units respectively. Sample analysis was performed using Progenesis with an intensity cut-off of 800. Compound identification was done with Chemspider, using BioCyc, KEGG, ChEBI, peptides, ChemBank, MassBank, Natural Products Updates, Nature Chemical Biology, Nature Chemistry, NIST, PlantCyc, PubMed and Wikidata as data sources.

Greenhouse experiments

To test the ability of CaCal35 and its mutant derivatives to protect tomato plants from Fol, we performed a greenhouse experiment as described before (Doan et al., 2020). Briefly, tomato seedlings (Early Pak 7) were grown from surface-sterilized seed in UC potting soil mix for 11–15 days (two true leaves), at which point whole plants were extracted from the soil and their roots dipped for five min in one of the following suspensions (in water): water only (control, no bacteria), CaCal35 (10⁶ cells/ml), BvFZB42 (10⁶ spores/ml), a 1:1 mixture of CaCal35 (10⁶ cells/ml) and BvFZB42 (10⁶ spores/ml) suspensions (we refer to this mixture as Calb42), a 1:1 mixture of CaCal35 (10⁶ cells/ml) and AK3 (10⁶ spores/ml), a 1:1 mixture of BvFZB42 (10⁶ spores/ml) and 46A06 (10⁶ cells/ml), or a 1:1 mixture of BvFZB42 (10⁶ spores/ml) and 60C09 (10⁶ cells/ml), before transfer to pots containing fresh UC potting soil mix. One week...
later, plants and their roots were again recovered from the soil, and roots were dipped for five min in either water (no-Fol control) or a Fol spore suspension in water (10^6 spores/ml), prepared as before (Doan et al., 2020) and transplanted to individual pots containing fresh UC potting soil mix. After three days, the soil around the crown of individual plants was drenched by pouring onto the soil surface 100 ml of water, or 100 ml of the same bacterial suspension that the roots of the plant had originally been dipped into. One week later, this drench was repeated. The plants received supplemental fertilization every day or every other day (all values in ppm: N 144.1, P 63.707, K 204.8, Ca 119.1, Mg 49.467, S 65.114, Fe 2.759, Cu 0.097, B 0.4, Mn 0.633, Mo 0.055 and Zn 0.097) through the irrigation system of the greenhouse.

Per treatment (of which there were eight: no-Fol, no bacteria; Fol-only, no bacteria; Fol plus Cal35 only; Fol plus BvFZB42 only; Fol plus Cal35 and BvFZB42 (i.e. Colli42); Fol plus Cal35 and AK3; Fol plus 46A06 and BvFZB42; Fol plus 46A06 and AK3), we used ten plants which were organized in a random block design in the greenhouse. Five weeks after Fol inoculation (i.e. at the onset of flowering), all ten tomato plants per treatment were assessed for vascular discoloration and shoot dry weight. Discoloration was measured as before (Doan et al., 2020) on a scale from 0 to 4 (0, no vascular discoloration; 1, <5% discoloration, typically light brown; 2, 5–20% discoloration, typically light brown; 3, 20–40% discoloration, typically dark brown; 4, >40% discoloration, typically dark brown). Shoots were dried at 65°C for 1 week before weighing.

The experiment was performed four independent times to compare the no-Fol, Fol-only, Cal35, Fol plus Cal35, Fol plus BvFZB42 and plus Colli42 treatments, and three independent times to compare the no-Fol, Fol-only, Fol plus Colli42, Fol plus Cal35 and AK3, Fol plus 46A06 and BvFZB42, and Fol plus 46A06 and AK3 treatments. For each one of the independent experiments, relative shoot biomass was calculated for each treatment as (a-b)/(c-b)×100%, where a is the shoot dry weight averaged for all ten plants of a particular treatment, b is the shoot dry weight averaged for all ten plants in the Fol-only treatment, and c is the dry weight averaged for all ten plants in the no-Fol treatment. Differences in relative biomass and in vascular discoloration between treatments across replicated experiments were statistically assessed using analysis of variance (ANOVA) with multiple comparisons using Tukey–Kramer test (P < 0.05).

Field trial

A field trial with Colli42 was carried out at the Armstrong Plant Pathology Field Station at UC Davis. This field was artificially infested with the tomato wilt pathogen Fol, race 3 in previous years (Doan et al., 2020). Tomato plants (Heinz 8504; VFFN, i.e. resistant to Fol race 1 and 2 but not race 3, and also resistant to V. dahliae race 1 and root knot nematode) were seeded in seedling trays with 3.5 x 3.5 x 6.5 cm cells and kept in the greenhouse for 3 weeks, at which time individual trays were dipped in one of the following bacterial suspensions (prepared and with cell densities as described in the section ‘Greenhouse experiments’): (i) no cells (i.e. water), (ii) Cal35, (iii) BvFZB42 or (iv) Colli42. Dipped trays were placed back in the greenhouse and after 1 week (on May 14, 2018), tomato seedlings were transplanted at 30 cm apart into a drip-irrigated plot with a randomized complete block design (single-row 92-cm beds with 60-cm between-row spacing beds, plus a pair of border rows; 30 plants per bed, four beds per treatment) featuring four blocks with four beds per block. After 1 week, 10 litres of water or a suspension of Cal35, BvFZB42 or Colli42 (prepared as before) was drip-delivered into each one of the corresponding blocks. One week later, this delivery was repeated. The field was drip-irrigated as needed. Fertilizer UN-32 (16.5% urea N, 7.75% nitrate N and 7.75% ammoniacal N) was applied through the drip once a week until flowering, at 75 ml per block and starting 12 days after transplanting. All plants also received a one-time application of Miracle-Gro Quick Start (Scotts Miracle-Gro, Marysville, OH) 5 days after transplanting, at 450 ml per block. Weeding was done manually, and no herbicides or pesticides were used. Fruits were harvested on 19 September 2018 (4 months after planting), at which time more than 90% of the fruit were ripe. Vascular discoloration (same scaling as for the greenhouse experiment) was determined and averaged for each one of 15 plants in the centre of each bed, as described above. Also determined for these 15 plants combined were the weights of red (marketable) tomato fruit. Marketable yield was calculated and expressed in tons per acre. Differences in yield and vascular discoloration between treatments were determined using analysis of variance (ANOVA) with multiple comparisons using Tukey–Kramer test (P < 0.05).

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Conflict of interest
None declared.

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Supporting information

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

**Fig. S1.** Photographs of tomato plants from a representative greenhouse experiment showing the protective effect of Coli42, i.e. a mixture of CaCal35 and BvFZB42, against Fol (panel D). Other panels: A, unchallenged plants (no-Fol); B, untreated, Fol-challenged plants (Fol-only); C, CaCal35-treated, Fol-challenged plants; and E, BvFZB42-treated, Fol-challenged plants. Note the inability of CaCal35 and BvFZB42 to protect plants from Fol.

**Fig. S2.** Identification of two transposon mutants of CaCal35, i.e. 46A06 and 60C09, with reduced antifungal activity. Shown are two 96-well, bottomless microtitre plates, where each well containing 250 µl PDA was inoculated from the top with 3 µl of a 10⁵ spores/ml A. niger spore suspension and from the bottom with one of 6,500 CaCal35 transposon insertion mutants. Plates were incubated at 28°C for 48 h and photographed from the top. Fungal growth was observed only on plate 46, row A, column 6 (left panel), which identified mutant 46A06 (left panel), while mutant 60C09 (right panel) was identified on plate 60, row C, column 9. The coloration in some of the other wells does not represent fungal growth on top of the PDA, but rather bacterial biomass on the bottom side.

**Fig. S3.** Transposon insertion sites for CaCal35 mutants 46A06 (panels A-C) and 60C09 (panels D-F). Shown for both mutants are the sequencing chromatograms generated by primer KAN-2FP1 (panels A and D) or KAN-2RP1 (panels B and E), and annotated (by underline) with the location of 19-bp mosaic ends and 9-bp insertion sites. Also shown (panels C and F) are the DNA sequences flanking the insertion sites (in red) for both mutants on the CaCal35 genome.

**Fig. S4.** Comparison of the CaCal35 genomic region identified through mutant 46A06 mutant to genomic regions *Chromobacterium violaceum* ATCC 53434, *Chitinimonas koreensis* DSM 17726, and *Paraburkholderia megapolitana* LMG 23650. Not shown is the corresponding genomic region of *Paraburkholderia acidophila* ATCC 31363, which is similar to that of *P. megapolitana* LMG 23650. Points of reference for the CaCal35 genomic region are genes LT85_RS01600 and LT85_RS01800 which are the first and last genes, respectively, listed in Table S1. Only the coloured genes in all of the other genomic regions represent genes with homologues in the CaCal35 genomic region; for the predicted products of those genes, amino acid sequence identity (in %) to that of the corresponding gene product in CaCal35 is shown. On the CaCal35 genomic region, starting with LT85_RS01720, eleven genes are labelled as belonging to the cpl (for carenaemin production locus) gene cluster. The black triangle indicates the location of the transposon insertion in 46A06 in LT85_RS01670 (i.e. cpl).

**Fig. S5.** Method for collection of diffusates from wild-type CaCal35 and mutants 46A06 and 60C09. Shown are representative PDA plates with wells in the agar (10 wells per plate) which were previously filled with PDB to allow recovery by diffusion of metabolites produced by the bacterial biomass growing on the agar surrounding the wells. See text for more details.

**Table S1.** BlastP analysis of predicted Cpl proteins encoded by the cpl gene cluster.