Cyclic di-GMP inactivates T6SS and T4SS activity in Agrobacterium tumefaciens

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Summary

The Type VI secretion system (T6SS) is a bacterial nanomachine that delivers effector proteins into prokaryotic and eukaryotic preys. This secretion system has emerged as a key player in regulating the microbial diversity in a population. In the plant pathogen Agrobacterium tumefaciens, the signaling cascades regulating the activity of this secretion system are poorly understood. Here, we outline how the universal eubacterial second messenger cyclic di-GMP impacts the production of T6SS toxins and T6SS structural components. We demonstrate that this has a significant impact on the ability of the phytopathogen to compete with other bacterial species in vitro and in planta. Our results suggest that, as opposed to other bacteria, c-di-GMP turns down the T6SS in A. tumefaciens thus impacting its ability to compete with other bacterial species within the rhizosphere. We also demonstrate that elevated levels of c-di-GMP within the cell decrease the activity of the Type IV secretion system (T4SS) and subsequently the capacity of A. tumefaciens to transform plant cells. We propose that such peculiar control reflects on c-di-GMP being a key second messenger that silences energy-costing systems during early colonization phase and biofilm formation, while low c-di-GMP levels unleash T6SS and T4SS to advance plant colonization.

Introduction

Interspecies bacterial competition plays a key role in shaping microbial populations and determining what bacterial species are dominant in a given niche (Kapitein and Mogk, 2014; Bernai et al., 2017a; McNally et al., 2017; Chassaing and Cascales, 2018). It is indeed increasingly clear that any specific environmental niche, including within various parts of the human body (Rojo et al., 2017), will profile the establishment of specific microbial populations. How bacteria respond to environmental variations or intrusion of ‘foreign organisms’ by triggering an attack/defence war game with other bacteria is not clearly understood. Yet, despite the numerous protein secretion systems encoded within bacterial genomes, one has emerged as being the ‘weapon’ of choice through which bacteria mediate interspecies competition, for example, in the human gut (Russell et al., 2014b; Chatzidaki-Livanis et al., 2016; Sana et al., 2016; Anderson et al., 2017) or in planta (Ma et al., 2014; Bernai et al., 2017a; 2017b). This system, termed the Type VI Secretion System (T6SS), is found on the genome of a wide variety of Gram-negative bacteria and can deliver a remarkable array of toxins such as nucleases, amidases and phospholipases (Russell et al., 2011; Russell et al., 2012; Ma et al., 2014; Russell et al., 2014a; Alcoforado Diniz et al., 2015). It is noticeable that in Gram-positive bacteria the type VII secretion system (T7SS) is now emerging as the antibacterial nanoweapon (Cao et al., 2016). Whereas many of these toxins are antibacterial (Russell et al., 2014a), some are also designed to target eukaryotic host cells (Hachani et al., 2016) and fungi (Trunk et al., 2018) or have a dual function like phospholipases (Jiang et al., 2014; Alcoforado Diniz et al., 2015). These toxins can be encoded as part of a large T6SS cluster and thus genetically linked with genes encoding core T6SS components, or be found independently in so-called vgrG/hcp islands (Hachani et al., 2014; Whitney et al., 2014). It has recently emerged that T6SS toxins can specifically interact with VgrG proteins (Bondage et al., 2016; Cianfanelli et al., 2016a; Flaugnatti et al., 2016), the puncturing...
device of the T6SS nanomachine, or can be found fused to VgrG thus forming what is referred to as an evolved VgrG (Pukatzki et al., 2007; Durand et al., 2012) or fused to a PAAR domain which loads the toxin onto a cognate VgrG (Whitney et al., 2015; Quentin et al., 2018). Some bacterial species have been shown to encode numerous T6SSs, with experimental evidence highlighting specific target or prey such as the H1-T6SS in Pseudomonas aeruginosa being associated with interbacterial competition while the H2-T6SS was proposed to preferentially target eukaryotic cells (Sana et al., 2012; Hachani et al., 2014; Jones et al., 2014). Now, it seems that a clear-cut system specificity is unlikely to be the case as the H2-T6SS was recently shown to also be antibacterial (Allsopp et al., 2017).

Agrobacterium tumefaciens is a soil bacterium that causes crown gall disease in a wide range of plants as a result of the delivery of T-DNA to plant cells via the Type IV Secretion System (T4SS) (Pitzschke and Hirt, 2010; Christie et al., 2014; Hwang et al., 2017). Agrobacterium tumefaciens strain C58 has also been shown to carry a single T6SS cluster composed of two divergently transcribed operons and featuring three toxins, Tae, a putative peptidoglycan amidase, and two DNases, Tde1 and Tde2 (Fig. 1A) (Ma et al., 2014). The Tde effectors have been shown to play a role in interbacterial competition and plant colonization. While ample information is now available consistently describing the structural components of the T6SS nanomachine (Cianfanelli et al., 2016b; Joshi et al., 2017; Nguyen et al., 2018) and its associated arsenal of toxins (Durand et al., 2014; Hachani et al., 2016; Lien and Lai, 2017), the type of regulatory elements that control expression of the system is variable from one species to another and has not always been conclusively determined. Well characterized signalling cascades have been shown to play a role in activating the T6SS such as the Gac/Rsm cascade (Moscoso et al., 2011; Allsopp et al., 2017) and the LasR/MvfR (PqsR) quorum sensing systems in P. aeruginosa (Lesic et al., 2009; Majerczyk et al., 2016; Sana et al., 2012), or, for example, the autoinducer-2 quorum sensing system and QstR in Vibrio cholerae (Ishikawa et al., 2009; Jaskolska et al., 2018). The environmental stimuli that may trigger T6SS expression are also poorly understood but some modulators have been proposed to be bile salts (Reen et al., 2012; Bachmann et al., 2015), contact dependent

![Fig. 1. Impact of c-di-GMP on Tde1, Tae and Hcp levels.](image-url)

A. The T6SS cluster composed of the divergently transcribed imp (Green) and hcp (Red) operons encoding 14 and 9 genes, respectively, and the remote island starting from atu3642 (vgrG-2) encoded by A. tumefaciens strain C58.

B. Expression of wild-type SadC and a catalytically inactive SadC (psadC*) in wild-type A. tumefaciens grown to early exponential phase in 523 medium.

C. Western blots using Tde1, Tae, Hcp and RpoA (Loading Control) antibodies on whole lysates of ΔtssL cells (No secretion control) or wild-type cells transformed with either pBBRMCS4 (vector control), psadC, psadC*, psadC†, psadC‡, pWSPR and pPA2133 grown to early exponential phase in 523 medium.

D. C-di-GMP levels were quantified via LC-MS/MS. Transformed cells were grown for 16 h in 523 medium and cells equivalent to an OD600 5 were collected. Samples of interest were compared to a standard curve derived from measurements of known concentrations of pure c-di-GMP to determine the concentration (in nM) of c-di-GMP in the samples. All experiments are the mean of two independent biological experiments with standard deviation error bars. Statistical significance was determined using students t-test with p < 0.05*, p < 0.01 **, p < 0.001***.
and counter-attack based induction (Russell et al., 2011; Basler et al., 2013), part of the competence regulon in *V. cholerae* (Borgeaud et al., 2015), or danger signal released from lysing cells in a *P. aeruginosa* population (LeRoux et al., 2015). To date in *A. tumefaciens* C58, only the ExoR/ChvG/ChvI signalling cascade has been shown to be capable of regulating the T6SS, with induction of this system at low environmental pH leading to activation of the T6SS (Wu et al., 2012). This is believed to play a key role in allowing *A. tumefaciens* to transform plant cells as determined by a transient transformation assay. This duality is quite remarkable and suggests that at a specific stage during the *A. tumefaciens* colonization process interaction with the rhizosphere and with the plant cells should both be kept silent.

**Results**

The *P. aeruginosa* diguanylate cyclase SadC suppresses T6SS activity in *A. tumefaciens* C58

The universal second messenger c-di-GMP regulates a wide variety of bacterial phenotypes including motility, protein secretion, exopolysaccharide production, virulence, or biofilm formation (Romling and Balsalobre, 2012; Romling et al., 2013; Jenal et al., 2017). Across almost all eubacteria, paradigms have emerged that correlate high intracellular levels of c-di-GMP with loss of motility, increased polysaccharide production and biofilm formation (Valentini and Filloux, 2016; Conner et al., 2017). The T6SS has also emerged as being subject to c-di-GMP control, with high levels of c-di-GMP associated with activation and low levels associated with suppression of this secretion system (Moscoso et al., 2011; Romling et al., 2013) as shown clearly with *P. aeruginosa* and to a lesser extent with *Vibrio alginolyticus*. In the latter case, it was proposed that the PppA phosphatase has a negative impact on both the activity of the T6SS and the levels of c-di-GMP (Sheng et al., 2013). In the case of *Pseudomonas fluorescens* it was also proposed that c-di-GMP could directly bind to the ClpB2 ATPase one of the core component in the T6SS (Tripari et al., 2015). In *A. tumefaciens* C58, it has been shown that high levels of c-di-GMP are associated with increased extracellular polysaccharide (EPS) production and biofilm formation (Heindl et al., 2014; Feirer et al., 2015), but the impact of c-di-GMP on T6SS has not been explored. *Agrobacterium tumefaciens* has one T6SS cluster which is composed of two divergently transcribed operons, the *imp* operon which primarily encodes the structural components of the secretion system and the *hcp* operon that encodes two of the known *A. tumefaciens* T6SS toxins, i.e. Tae and Tde1 (Wu et al., 2008; Lin et al., 2014). There is also an orphan cluster that encodes Tde2, the only known T6SS toxin not directly encoded in the *A. tumefaciens* primary cluster (Fig. 1A) (Ma et al., 2014). Here, we investigate the impact of c-di-GMP on the functionality of this system, and introduced plasmids encoding the well characterized *P. aeruginosa* diguanylate cyclases (DGC) SadC and WspR (Guvener and Harwood, 2007; Merritt et al., 2007a; Dahlstrom and O’Toole, 2017; McCarthy et al., 2017a), a mutated version of SadC that has the canonical catalytic site GGEEF domain changed to AAAEF (psadC) and a
known functional phosphodiesterase PA2133 (Ueda and Wood, 2010), into a wild-type strain of A. tumefaciens. The recombinant strains were grown to early exponential phase and the levels of the T6SS DNase effector Tde1, amidase effector Tae and T6SS nanotube building block Hcp were assessed by western blotting (Ma et al., 2014). Firstly, it was striking to observe that the clumping/hyperbiofilm phenotype resulting from SadC overexpression and usually associated with high levels of c-di-GMP (Moscoso et al., 2014) was no longer seen when the catalytically inactive sadC* mutant was expressed indicating as expected that this enzyme was no longer capable of generating c-di-GMP (Fig. 1B). The reduction in activity of this mutated version of SadC was confirmed by LC-MS/MS and was shown to be comparable to another mutated version of SadC that had the GGEEF domain changed to GGAAF (Supporting Information Fig. S1). Furthermore, it was readily observed that expression of the sadc-encoded membrane bound DGC dramatically abrogated Tde1, Tae and Hcp production. Levels seen in the strains containing plasmids encoding the SadC catalytic site mutant were comparable to strains carrying the empty vector (pBBRMC54) (Fig. 1C) suggesting that the intracellular levels of c-di-GMP were effectively responsible for the reduction in the level of these T6SS components and toxins. The expression of the wspR-encoded cytoplasmic DGC did not alter the levels of Tde1, Tae or Hcp (Fig. 1C). This suggests that the intracellular activity of WspR in A. tumefaciens might not be strong enough to impact the levels of Tde1/Hcp or that membrane association of the DGC is instrumental to the phenotype. Note that the overexpression of the cytoplasmic phosphodiesterase (PDE) PA2133 also did not significantly impact the levels of Tde1, Tae or Hcp (Fig. 1C). The proposed reduced activity of WspR in A. tumefaciens was confirmed by quantifying the levels of c-di-GMP using LC-MS/MS. This analysis confirmed that SadC produced significantly more c-di-GMP than WspR when expressed in A. tumefaciens (Fig. 1D). Overall, these findings are opposite to the established P. aeruginosa paradigm of positive regulation of the T6SS by c-di-GMP. Such variation in control is likely depending on how and where c-di-GMP is acting and this may dramatically differ from one bacterial species to the other. For example, in P. aeruginosa, the control exerted by master regulators such as RetS/LadS is observable on all H1-T6SS genes (Allsopp et al., 2017) whereas in Pseudomonas syringae it can only be seen on a subset of T6SS genes (e.g. icmF) but not on others (e.g. hcp) (Records and Gross, 2010).

SadC has a significant impact on T6SS-dependent interbacterial competition in vitro and in planta

The T6SS is known to play a key role in shaping the microbiota and this is particularly true in the plant rhizosphere (Bernal et al., 2017a; Bernal et al., 2017b). To investigate if the impact of c-di-GMP on T6SS was biologically significant and capable of influencing the structure of a bacterial population, bacterial competition assays were performed as described in experimental procedures and using as an attacker strain A. tumefaciens which constitutively expresses wild-type (psadc) or mutant version of sadc (psadc*). The bacterial prey Escherichia coli carries the pRL662 plasmid conferring gentamicin resistance and survivors after A. tumefaciens contact could be recovered as colony forming units (CFU) on gentamicin-containing plates. Expression of wild-type sadc in A. tumefaciens significantly reduced the ability of A. tumefaciens to kill the prey bacterium E. coli (Fig. 2A) when compared to a strain harbouring the vector control or expressing the non-functional version of sadc, sadc*. The low levels of SadC-dependent killing were comparable to those seen with an A. tumefaciens mutant strain lacking a core gene for the T6SS machinery, tssL, thus resulting in T6SS inactivation and confirming the T6SS downregulation through SadC activity. To fully rule out that the observed reduction in killing was not a consequence of the increased cell to cell aggregation seen when overexpressing psadc, the assay was repeated in P. aeruginosa, where increased expression of sadc is also known to impact cell to cell aggregation (Moscoso et al., 2014). Competition assays between P. aeruginosa PAO1 expressing sadc and E. coli demonstrated increased levels of killing, contrary to what was observed in the A. tumefaciens competition assays (Supporting Information Fig. S2). A similar increase in killing was seen when using a P. aeruginosa ΔrsmA mutant, which is known to have elevated levels of sadc expression (Moscoso et al., 2014). This suggests that the impact seen on cell-to-cell aggregation by the expression of sadc does not impact the activity of the T6SS.

Endogenous A. tumefaciens DGCs suppress the T6SS activity

The use of a well-characterized P. aeruginosa DGC to increase the intracellular levels of c-di-GMP in A.
c-di-GMP and secretion in Agrobacterium tumefaciens
tumefaciens does not guarantee that DGCs encoded within the A. tumefaciens genome can have a similar impact on T6SS. To investigate this, we focused on endogenous A. tumefaciens DGCs, 16 of which are encoded within the genome (Romling et al., 2013), of these we selected 6 that encoded transmembrane domains and carry the canonical GGDEF domain, namely Atu2091, Atu2691, Atu1207 and Atu5372 as well as the two previously described DGCs DgcA (Atu1257) and DgcC (Atu2179) both of which have been shown to impact EPS production (Xu et al., 2013) (Supporting Information Fig. S3). The rationale here was that both SadC and WspR have been shown to be active DGCs, but only the membrane bound SadC was capable of impacting c-di-GMP associated phenotypes (Fig. 1C). This could suggest that the localization of the the DGC may have a critical impact on phenotypic outcomes. The genes encoding these DGCs were amplified and cloned under the control of the IPTG-inducible lac promoter in the pTrc200 vector. Using agar plates-containing Congo red, it is possible to reveal exopolysaccharide (EPS) production in response of increased intracellular levels of c-di-GMP (Howie and Brewer, 2009; Heckel et al., 2014; Heindl et al., 2014; Feirer et al., 2015; Feirer et al., 2017). It was clear that some of the A. tumefaciens transformed with the above recombinant plasmids yielded colonies displaying a wrinkly phenotype (Fig. 3A). This confirmed that as previously described DgcA and DgcC could impact EPS production (Xu et al., 2013) but also that Atu2091 and Atu5372 were increasing the levels of exopolysaccharide production, suggesting they are active cyclases, while Atu1207 and Atu2691 had little or no effect (Fig. 3A).

To assess if anyone of these DGCs was capable of shutting down the T6SS, as SadC did, a secretion assay was performed using a Hcp and a Tde1 specific antibody as described above. This assay revealed that Atu2091, Atu5372 and DgcA were all capable of down-regulating the secretion of Hcp and Tde1 to non-detectable levels, and these levels were comparable to those observed with the non-functional T6SS mutant A. tumefaciens ΔtssL (Fig. 3B). DgcC also had a negative impact on Hcp levels but to a lesser extent. The cellular levels of Hcp, TssB (subunit of the T6SS sheath) and ClpV (T6SS AAA+ ATPase), revealed a similar profile to what was seen with Hcp secretion, with expression of Atu2091, Atu5372 and DgcA leading to reduced levels of these proteins and DgcC having a lesser effect (Fig. 3C). As for the EPS assay, Atu1207 and Atu2691, did not shut off T6SS activity, thus suggesting that they may not be active or are generating levels of c-di-GMP too low to trigger observable phenotypic changes.

We then performed in vitro killing assays with each of the recombinant strains. Significant reductions in killing, comparable with what is observed with the tssL mutant, were seen upon expression of dgcA and atu5372 while a reduced but not statistically significant killing was observed for strains expressing atu2091 and dgcC (Fig. 4A). No
A reduction in killing was observed with strains expressing \textit{atu1207} and \textit{atu2691}. To confirm that the observed phenotypes were a direct result of altered levels of c-di-GMP, the levels of c-di-GMP were quantified in strains expressing either \textit{atu5372} or \textit{atu2691}. As expected, the strain expressing \textit{atu2691} did not display elevated levels of c-di-GMP compared to the vector control, while a strain expressing \textit{atu5372} had levels of c-di-GMP higher...
A. tumefaciens strains with either an empty vector control, pdgcA, patu2091, pdgcC, patu2691, patu1207 and patu5372 were incubated for 14 h on a 1 M medium (pH5.5) with E. coli containing pRL662 which harbours a gentamicin cassette. Bacteria were then resuspended in PBS and plated on LB agar-containing gentamicin. All experiments are the mean of three independent biological experiments with standard deviation error bars. Statistical significance was determined using students t-test comparing each strain with the vector control, p < 0.05 *, p < 0.01 **.

B. C-di-GMP levels were quantified via LC-MS/MS in strains expressing either an empty vector control or patu5372 or patu2691. Native DGSc were induced with 0.5 mM IPTG for 16 h in 523 medium, but also in minimal media (AB-MES pH7), a condition where ExoR-mediated repression of T6SS has previously been demonstrated (Wu et al., 2012). Remarkably, it was observed that in the exoR mutant, expression of sadC and thus high levels of c-di-GMP are still capable of down-regulating the T6SS, as seen by monitoring Hcp, ClpV and TssB production (Fig. 5A) suggesting that the elevated pool of c-di-GMP is acting independently of the ExoR network. Since all data presented thus far of c-di-GMP impact on T6SS were at the protein level, we also wanted to establish if this regulation was originally exerted at the transcriptional level independently of the ExoR cascade. To assess if the impact on T6SS through c-di-GMP signalling involves this cascade, psadC was introduced into an A. tumefaciens exoR mutant which is known to have elevated activity of T6SS. If the elevated pool of c-di-GMP is acting through the ExoR cascade, then c-di-GMP transmission should be interrupted in the exoR mutant and no longer be able to impact on the T6SS. This was assessed in standard 523 medium, but also in minimal media (AB-MES pH7), a condition where ExoR-mediated repression of T6SS has previously been demonstrated (Wu et al., 2012). Remarkably, it was observed that in the exoR mutant, expression of sadC and thus high levels of c-di-GMP are still capable of down-regulating the T6SS, as seen by monitoring Hcp, ClpV and TssB production (Fig. 5A) suggesting that the elevated pool of c-di-GMP is acting independently of the ExoR network. Since all data presented thus far of c-di-GMP impacting the T6SS were at the protein level, we also wanted to establish if this regulation was originally exerted at the transcriptional level. To address this, RNA was isolated from A. tumefaciens transformed with either the cloning vector, a vector expressing a nonspecific protein GFP, psadC, psadC*, patu2691, a proposed inactive DGC or patu5372, a native A. tumefaciens DGC that was shown to have a significant impact on clumping, interspecies killing and Hcp secretion. qRT-PCR was performed on cDNA synthesized using RNA extracted from these strains and primers specific to genes belonging to both divergent operons of the A. tumefaciens T6SS cluster, namely tssB, tha, hcp and clpV (Figs 1A and 5B,C). Remarkably, all others might need a higher threshold. This observation might also be in line with the established concept for the need of spatial pools of c-di-GMP (Christen et al., 2010), and specific subcellular localization of some DGs such as within the cytoplasmic membrane, or their direct interaction with the effector generating the output (McCarthy et al., 2017a), would overcome the threshold issue.

**Fig. 4.** Impact of native DGC on interspecies killing and cdi-GMP levels. A. A. tumefaciens strains with either an empty vector control, pdgcA, patu2091, pdgcC, patu2691, patu1207 and patu5372 were incubated for 14 h on a 1 M medium (pH5.5) with E. coli containing pRL662 which harbours a gentamicin cassette. Bacteria were then resuspended in PBS and plated on LB agar-containing gentamicin. All experiments are the mean of three independent biological experiments with standard deviation error bars. Statistical significance was determined using students t-test comparing each strain with the vector control, p < 0.05 *, p < 0.01 **. B. C-di-GMP levels were quantified via LC-MS/MS in strains expressing either an empty vector control or patu5372 or patu2691. Native DGSc were induced with 0.5 mM IPTG for 16 h in 523 rich medium and cells equivalent to an OD_{600} 5 were collected. Samples of interest were compared to a standard curve derived from measurements of known concentrations of pure cdi-GMP to determine the concentration (in nM) of c-di-GMP in the samples. All experiments are the mean of two independent biological experiments with standard deviation error bars.
of these genes were significantly down-regulated when \textit{atu5372} or \textit{sadC} was expressed, but not upon expression of an inactive \textit{sadC}*, a proposed inactive DGC \textit{atu2691} or a nonspecific protein GFP, confirming that the impact of c-di-GMP on T6SS also occurs at the transcriptional level and that all T6SS genes are impacted.

C-di-GMP negatively impacts expression of components of the T4SS and the ability of \textit{A. tumefaciens} to transform plant cells

The significant impact of c-di-GMP on the activity of the T6SS and biofilm formation led us to ask whether other determinants involved in infection progression, such as the T4SS, were also responsive to the intracellular levels of c-di-GMP. The rationale here was in line with previous reports where protein secretion systems, e.g. the T6SS and T3SS, are antagonistically controlled (Moscoso \textit{et al.}, 2011; McCarthy \textit{et al.}, 2017b). As described above for the control of EPS production, the regulation of the T4SS is dependent on activation of the VirA/VirG signalling by acidity or phenols such as acetosyringone (AS), in which the transcription of the gene encoding the VirG response regulator is activated via the ExoR/ChvI/ChvG signalling system (Heckel \textit{et al.}, 2014). Activation of this cascade subsequently confers the ability of \textit{A. tumefaciens} to transfer T-DNA into the host plant cell. We thus analysed the expression of a number of different T4SS genes (\textit{virB1}, \textit{virB2}) and T4SS effector gene \textit{virE2} in cells expressing the native DGCs (Fig. 6A). qRT-PCR was performed on cDNA synthesized using RNA isolated from cells transformed with either a vector control, \textit{pGFP}, \textit{patu2691} or \textit{patu5372} grown to early exponential phase. Similar results were seen when cells were expressing \textit{psadC}, although only partial but significant restoration of expression was seen when expressing \textit{psadC}* (Fig. 6C).

To further interrogate this and determine if this impact on transcription is biologically relevant, an AGROBEST assay was performed (Wu \textit{et al.}, 2014). This is an...
Agrobacterium-mediated Arabidopsis transformation assay (Agrobacterium-mediated enhanced seedling transformation) that utilizes β-glucuronidase (GUS) as a reporter carried on the T-DNA to determine the impact of native regulatory elements on Agrobacterium transformation activity (Wu et al., 2014). Four-day-old Arabidopsis seedlings were infected with A. tumefaciens strain C58C1 (pTiB6S3ΔT) carrying either an empty vector control, a vector expressing a nonspecific protein GFP, patu2691 or patu5372 and expressing a GUS reporter. The assay was allowed to proceed for 3 days before seedlings were stained with 5-bromo-4-chloro-3-indolyl glucuronide (X-Gluc) to visualize the GUS staining. Remarkably, only expression of patu5372 leads to a dramatic reduction in GUS staining (Fig. 7A) indicating that, in concordance with the qRT-PCR data, the activity of the T4SS is significantly impacted by the intracellular levels of c-di-GMP. Similar findings were...
observed when cells were expressing psadC, although expression of psadC* could not completely abrogate this (Fig. 7B).

Discussion

Agrobacterium tumefaciens is a phytopathogen capable of causing tumorigenesis in a wide variety of plant species through T-DNA transfer via the T4SS (Gelvin, 2010). The start of this transfer process is centered on A. tumefaciens sensing characteristic changes in the rhizosphere such as a drop in pH and phytochemical release, indicative of a plant wound. Intriguingly, a drop in pH has also been shown to induce not only the T4SS but also the T6SS. The latter is central to A. tumefaciens outcompeting other bacteria within this niche whereas the former allows the unimpeded transfer of T-DNA and eventual formation of a crown gall (Wu et al., 2012). Other than low pH, the understanding of what factors regulate the activity of the T6SS in A. tumefaciens is relatively limited. In this study, we investigate the role of c-di-GMP in regulating T6SS and T4SS in A. tumefaciens. Previously characterized DGCs and PDEs from P. aeruginosa were transformed into A. tumefaciens. The membrane bound DGC called SadC (Merritt et al., 2007a) was shown to significantly induce a clumping phenotype, characteristic of high levels of c-di-GMP (Heindl et al., 2014) (Fig. 1B), and down-regulate the expression of both the T6SS toxins and T6SS machinery components (Fig. 1C). This is contrary to the established paradigm in P. aeruginosa where high levels of c-di-GMP are associated with increased levels of T6SS (Supporting Information Fig. S2) (Moscoso et al., 2011). We demonstrated that the ability to impact T6SS was dependent on SadC being active as a version of SadC that features a mutated GGDEF domain had no impact on bacterial clumping or T6SS activity (Fig. 1B and C). The biological relevance of this down-regulation is validated by the inability of a strain of A. tumefaciens transformed with a plasmid expressing sadC to kill a prey bacterium in vitro or in the native environment of a plant (Fig. 2A and B).

The use of an active DGC from P. aeruginosa could create an artificial pseudo-circuit inhibiting the activation
of the T6SS. To rule this out and to explore the capacity of native A. tumefaciens DGCs to down-regulate T6SS, the genes of six different A. tumefaciens DGCs, that have similar features as SadC, e.g. predicted transmembrane domains, were cloned and expressed. Three of these DGCs, DgcA, Atu2091 and Atu5372, were capable of down regulating the secretion of Hcp to non detectable levels, comparable to those observed in an A. tumefaciens T6SS mutant, ΔtssL (Fig. 3B). When further assessed, these DGCs were all capable of inhibiting interbacterial killing by A. tumefaciens both in vitro and in planta to differing degrees. These findings confirm the hypothesis that in A. tumefaciens high levels of c-di-GMP down-regulate T6SS but they also offer an intriguing insight into the specificity exhibited by different DGCs. The differing levels of killing observed in strains expressing different DGCs (Fig. 4A) highlights the importance of c-di-GMP threshold levels to trigger specific output, and may also lend support to an emerging phenomenon whereby the spatial and temporal localization of a DGC can significantly influence the resulting phenotypic impact (Romling et al., 2013; Dahlstrom and O’Toole, 2017).

The regulation of the T6SS is shown to occur at the transcriptional level with both divergent transcriptional units in the T6SS cluster being significantly down-regulated (Fig. 5B and C). The only characterized signalling cascade involved in the regulation of T6SS in A. tumefaciens is the ExoR/ChvI/ChvG system (Wu et al., 2012; Heckel et al., 2014); however, we collected data suggesting that the impact of c-di-GMP acts independently of this regulatory network (Fig. 5A). This finding prompted us to explore the influence of intracellular c-di-GMP levels on the T4SS, another ExoR/ChvI/ChvG target. Intriguingly, we observed a significant transcriptional down-regulation in the expression of key components of the T4SS machinery when a DGC was expressed, sadC or atu5372, and this requires c-di-GMP synthesis since an inactive SadC, SadC*, displays only traces of inhibition of T-DNA transfer into Arabidopsis plant cells (Fig. 7AB). Intriguingly, it seems here that c-di-GMP signalling is independent of the master regulator for T4SS and T6SS expression, i.e. Chvl/ChvG/ExoR. This is slightly different from what is observed with P. aeruginosa, in which the master network controlling T6SS activity, Gac/Rsm, is entangled with c-di-GMP signalling. In this case, the gene encoding the DGC SadC, is directly controlled by the translational repressor RsmA (Moscoso et al., 2014), which in turn modulates c-di-GMP levels. Note that the absence of ExoR, relieves the kinase ChvG which can then phosphorylate the response regulator Chvl and therefore activate the T6SS and the T4SS genes. In this case if c-di-GMP was binding Chvl or ChvG to inhibit their activity, such inhibition should have been detected in an exoR mutant, which was not the case (Fig. 5A). Alternatively, a plausible explanation is that c-di-GMP could modulate the activity of another protein, e.g. a membrane protein interacting with ExoR. This protein could capture the periplasmic ExoR when it is not bound to c-di-GMP. Instead, when such an integral membrane protein is bound to c-di-GMP, interaction with ExoR does not occur and ExoR is free and available to inhibit the ChvI kinase (Fig. 8). This type of control at the interface cytoplasm/periplasm and across the cytoplasmic membrane was previously shown in the case of the P. fluorescens Lap system (Hinsa and O’Toole, 2006; Newell et al., 2009). In this case, the degenerated LapD cyclase/phosphodiesterase is an integral cytoplasmic protein, which can bind c-di-GMP and then interact with the periplasmic LapG protease. When LapD is c-di-GMP-bound, it prevents the LapG protease from cleaving and releasing the surface adhesin LapA, which contributes to biofilm formation only when it remains associated with the cell surface (Navarro et al., 2011; Dahlstrom and O’Toole, 2017). This is in agreement with the dogma-high c-di-GMP/high biofilm. Future work could focus on identifying possible missing links such as the one suggested above. Interestingly the active cyclases are membrane embedded, such as SadC in contrast to WspR, and that may reinforce the idea that the signalling could be a transmembrane inside-out signalling, where the membrane cyclase or an interacting partner therein plays a key role in the process (Navarro et al., 2011). In the inside-out signalling mechanism described by the O’Toole laboratory, the transmission of the signal involves HAMP domains so a directed approach could be used to assess known c-di-GMP-related proteins with a HAMP domain (Navarro et al., 2011). Alternatively a non-biased approach using random transposon mutagenesis in a strain overexpressing a DGC and carrying a reporter fusion for T6SS or T4SS expression could be used. Screens could be aimed at identifying mutants whose T4SS or T6SS activity goes high up even in the context of DGC expression, thus pinpointing any players in the circuitry. In any case, c-di-GMP signalling has shown that the combination and sequence of events that lead from synthesis to output is far from a simple and stereotyped trajectory. Examples from within A. tumefaciens have shown that a dual DGC-PDE, called DcpA, can see its activity balanced from DGC to PDE based on its interaction with another protein called PruA, a pterin reductase. In the presence of PruA, DcpA is a PDE while in its absence it is a DGC. This implies that when DcpA is expressed in a heterologous host, such as E. coli in which PruA is absent, the main activity is PDE, while in Agrobacterium it is mostly a DGC (Feierer et al., 2015). This has also lend support to our rationale to analyse the impact of native Agrobacterium DGC versus heterologous ones from P. aeruginosa to fully validate our phenotypic observations.

In P. aeruginosa, the switch in lifestyle from biofilm to motile is also tightly linked to a concomitant switch
from T6SS to T3SS respectively (Moscoso et al., 2011; Valentini and Filloux, 2016; McCarthy et al., 2017b). This makes sense if considering that the T6SS may help killing unwanted members of a biofilm population and instead preferring the T3SS cytotoxicity when adopting an acute infectious style. In the case of Agrobacterium, simultaneous down-regulation of the T6SS and T4SS when biofilm formation is induced gives an intriguing insight into the phases of A. tumefaciens infection. The upregulation of motility genes, the T6SS and the T4SS by low pH and phytochemical release associated with a plant wound is the first step in A. tumefaciens targeting the wound site and ensuring a mono-infection by killing competing species (Merritt et al., 2007b; Wu et al., 2012). Once at the site of the wound it is possible that intracellular levels of c-di-GMP are elevated stimulating the production of EPS, attachment and biofilm formation (Heindl et al., 2014). T6SS and T4SS are concurrently downregulated possibly as an economy measure allowing more efficient channelling of resources towards establishing infection at the site of the wound. Once initial sustainable colonization is established, variation in c-di-GMP levels can then allow further colonization and again competition with other bacteria and modification of the plant cell environment. The orchestration of c-di-GMP levels and its variation in different cells and at a different localization in each cell, would be in accordance with a model, where the spatio-temporal dynamics of c-di-GMP is key (Christen et al., 2010; Abel et al., 2013; Kulasekara et al., 2013; Skotnicka et al., 2016). It will be instrumental to the fate of the community at a population level but may of course be specific to some individuals, offsprings of which will constitute a new sub-population with distinct aims, such as, for example, dispersal from the biofilm. Changes in c-di-GMP within a cell have been demonstrated on numerous instances to significantly alter the behavior of that cell, examples of this include the temporally oscillating global pools of c-di-GMP in Caulobacter crescentus which play a key role in regulating the swarmer to stalked cell transition and in Myxococcus xanthus where fluctuations in c-di-GMP levels control the developmental cycle that results in fruiting body formation (Abel et al., 2013; Kulasekara et al., 2013; Ozaki et al., 2014; Lori et al., 2015; Rotem et al., 2015; Skotnicka et al., 2016).

The impact seen in A. tumefaciens is to down-regulate both T4SS and T6SS, so this duality may have significant impact on shaping future bio-control efforts in the agri-sector. Exploiting the knowledge that both the T4SS and the T6SS are down regulated in the presence of elevated levels of c-di-GMP (Fig. 8) may also prompt the development of exogenous soil treatments that could influence the accumulation of this signalling molecule within the cell and in turn influence its physiology/pathogenicity. Similar approaches have proven successful in disrupting

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Fig. 8. Regulation of T6SS and T4SS in A. tumefaciens. In acidic pH conditions such as those found around a plant wound site, the periplasmic regulator ExoR is degraded, this allows the activation of ChvG via autophosphorylation, ChvG can then activate its cognate response regulator ChvI, which then activates the T6SS. The activation of native DGCs by environmental stimuli leads to an increase in the local levels of cyclic di-GMP. These increased levels of c-di-GMP are capable of repressing the transcription of the T6SS and the T4SS via an as yet uncharacterized regulator(s).
P. aeruginosa biofilms in the cystic fibrosis lung, whereby exposure of the lung to nitric oxide induces biofilm dispersal through the modulation of the activity of phosphodiesterases, thus manipulating the intracellular levels of c-di-GMP (Barraud et al., 2006; Barraud et al., 2009; Howlin et al., 2017). In all, while the hypothesis that c-di-GMP is fine tuning the behaviour of A. tumefaciens as it transitions from the rhizosphere to the plant surface remains to be verified, here we have demonstrated that c-di-GMP is capable of significantly influencing the ability of A. tumefaciens to compete with other bacterial species and thus may shape the microbial diversity within the soil and also significantly impacts the capacity of A. tumefaciens to carry out one of its most defining features, the ability to transform the plant cell with interkingdom DNA transfer.

**Experimental procedures**

**Bacterial strains and plasmids**

Strains, plasmids and primer sequences used in this study are shown in Supporting Information Table S1 and S2. Escherichia coli was cultured in Lysogeny Broth, whereas 523 medium (Kado and Heskett, 1970) was routinely used for A. tumefaciens strains unless otherwise indicated. Growth conditions were previously described (Ma et al., 2009). When required, appropriate antibiotics were added to the medium as follows: for E. coli, 50 µg ml⁻¹ ampicillin, 50 µg ml⁻¹ gentamicin (Gm), 50 µg ml⁻¹ kanamycin (Km) and 100 µg ml⁻¹ spectinomycin (Sp); and for A. tumefaciens, 200 µg ml⁻¹ spectinomycin. About 1mM Isopropyl-β-D-thiogalactopyranoside (IPTG) was used when necessary. Site directed mutagenesis was performed on pBBRMCS4-sadC using primers (Supporting Information Table S1) targeted to the catalytic site GGDEF site with specific nucleotide changes corresponding to mutation of the target cells. All experiments are the mean of three independent biological experiments with standard deviation error bars. Statistical significance was determined using students t-test with p < 0.05 *, p < 0.01 **. Bacterial competitions with P. aeruginosa were carried out as described before (Pissaridou et al., 2018). Briefly, strains harbouring indicated plasmids were grown over night with appropriate antibiotics and competition assays were performed the next day on LB agar plates without antibiotics using a 1:1 ratio of attacker to prey and incubating at 37°C for 24 h. Attacker strains were P. aeruginosa PAO1 and PAO1 ΔrsmA and prey strain was E. coli Top10 pRL662-gfp. Competitions were recovered and serially diluted prior to spot plating on LB agar plates with antibiotics for selection and grown overnight at 37°C. Survival was assessed by quantitative colony counts on selective media (using gentamicin for selection of E. coli and ampicillin for P. aeruginosa).

**Measurement of c-di-GMP levels**

For c-di-GMP quantification, samples were prepared as described previously (Valentini et al., 2016) and analysed by liquid-chromatography mass spectrometry (LC-MS/MS). In brief, A. tumefaciens C58 strains harbouring pBBRMCS4 vectors constitutively expressing DGCs were grown overnight in 20 mL SM 523 medium and cells equivalent to an OD₆₀₀ 5 were collected by centrifugation. Strains harbouring pTrC200 vector or derivatives were grown overnight, adjusted to an OD₆₀₀ 0.1 and grown to an OD₆₀₀ 0.7. Native DGCs were induced with 0.5 mM IPTG for 16 h and cells equivalent to an OD₆₀₀ 5 were collected. Collected cells were resuspended in extraction solution (Acetonitrile/methanol/water, 2/2/1, v/v/v), incubated on ice for 15 min and heated for 10 min at 95–99°C. Cells were centrifuged for 10 min at 4°C, 20,800 x g and supernatant fluid was collected. Extraction was repeated twice and supernatant fluids of the 3 extraction steps were combined and incubated at −20°C overnight. Extraction fluids were centrifuged again and supernatant fluid was analysed at the BIOLOG Life Science Institute (Biolog, Bremen) via LC-MS/MS. Samples of interest were compared to a standard curve derived from measurements of known concentrations of pure c-di-GMP to determine the concentration (in nM) of c-di-GMP in the samples.

**Interbacterial competition assay in planta**

Interbacterial competition assays in planta were performed as previously described (Ma et al., 2014). The intra-species A. tumefaciens competition assay was performed with a 10:1 attacker-to-target ratio by leaf infiltration of N. benthamiana. Briefly, 523 overnight-cultured A. tumefaciens cells were sub-cultured at 28°C in the same medium for further growth to OD₆₀₀ 1.0–1.5. The harvested cells were resuspended in 1/2 Murashige and Skoog (MS) medium (pH 5.5) to an appropriate OD₆₀₀. The attacker (OD₆₀₀ 5) and target, E. coli DH10B containing pRL662 (OD₆₀₀ 0.5) were mixed equally before infiltration into 2-month-old leaves of N. benthamiana with use of a needleless syringe. After 24-h incubation at room temperature, the infiltrated spot was punched out, ground in 0.9% NaCl, serially diluted, and plated in triplicates on LB agar containing appropriate antibiotic to select for the target cells. All experiments are the mean of three independent biological experiments with standard deviation.
error bars. Statistical significance was determined using students t-test with p < 0.05 *, p < 0.01 **.

**Agrobacterium infection in Arabidopsis seedlings and GUS activity assay**

The procedures for the seedling transient transformation assay were adapted from (Kim et al., 2006; Wu et al., 2014) with modifications. Agrobacterium tumefaciens cells were pre-induced by addition of 200 μM of acetosyringone at 28°C for 16 h and resuspended in appropriate buffer with cell density OD_{600} 0.02. Four-day-old A. thaliana seedlings were then incubated in 1ml of the buffer in a well of a 6-well plate for another 3 days. The seedlings were then removed from the buffer for GUS staining or GUS activity assay. For GUS staining, seedlings were stained with 5-bromo-4-chloro-3-indolyl glucuronide (X-Gluc) at 37°C for 6 h as described. GUS activity assay was determined by the conversion of 4-methylumbelliferone to 4-methylumbelliferone (4-MU) with amount of protein in the reaction was determined by a Bradford assay. The relative GUS activity was expressed as OD_{455} μg^{-1} protein (Wu et al., 2014).

**RNA extraction and quantitative RT-PCR**

Strains were grown to early exponential phase before cells were pelleted. Total RNA was extracted from pellets by Total RNA Extraction Kit (Arrowtech). First-strand cDNA was synthesized from 4 μg of total RNA with SuperScript III Reverse Transcriptase (Invitrogen) and random primers. Quantitative PCR were performed in QuantStudio 12 K Flex Real-Time PCR machine (Applied Biosystems) with Power SYBR Green PCR Master Mix (Invitrogen).

**Production of T6SS components and T6SS-dependent secretion assay**

The T6SS components and effectors in whole cell and during secretion assays were performed as described previously (Lin et al., 2014). Strains were grown to early exponential phase in both AB-MES pH7 medium and 523 medium. Whole cell extract and secreted proteins were separated by SDS/PAGE and transferred onto a PVDF or nitrocellulose membrane using a transfer apparatus (Bio-Rad). The membrane was probing with primary antibody against Tde1 epitope (Ma et al., 2014), Hcp (Wu et al., 2008), Tae (Ma et al., 2014), ClpV (Wu et al., 2012) and RpoA (Lin et al., 2014) was used as an internal control then incubated with horseradish peroxidase-conjugated anti-rabbit secondary antibody (1:20,000) and visualized with the ECL system (Perkin-Elmer).

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**Author contributions**

RMC, AF, MY, EML designed research. RMC, MY, KG, YCW performed research. RMC, AF, MY, EML analysed data. RMC and AF wrote manuscript.

**Data availability statement**

The data that support the findings of this study are available from the corresponding author upon reasonable request.

**References**


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**Supporting Information**

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

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