Cyclic-di-GMP signalling regulates motility and biofilm formation in *Bordetella bronchiseptica*

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The signalling molecule bis-(3′–5′)-cyclic-dimeric guanosine monophosphate (c-di-GMP) is a central regulator of diverse cellular functions, including motility, biofilm formation, cell cycle progression and virulence, in bacteria. Multiple diguanylate cyclase and phosphodiesterase-domain-containing proteins (GGDEF and EAL/HD-GYP, respectively) modulate the levels of the second messenger c-di-GMP to transmit signals and obtain such specific cellular responses. In the genus *Bordetella* this c-di-GMP network is poorly studied. In this work, we evaluated the expression of two phenotypes in *Bordetella bronchiseptica* regulated by c-di-GMP, biofilm formation and motility, under the influence of ectopic expression of *Pseudomonas aeruginosa* proteins with EAL or GGDEF domains that regulates the c-di-GMP level. In agreement with previous reports for other bacteria, we observed that *B. bronchiseptica* is able to form biofilm and reduce its motility only when GGDEF domain protein is expressed. Moreover we identify a GGDEF domain protein (BB3576) with diguanylate cyclase activity that participates in motility and biofilm regulation in *B. bronchiseptica*. These results demonstrate for the first time, to our knowledge, the presence of c-di-GMP regulatory signalling in *B. bronchiseptica*.

INTRODUCTION

Bis-(3′–5′)-cyclic-dimeric guanosine monophosphate (c-di-GMP) is a bacterial second messenger known to regulate a variety of cellular processes. c-di-GMP has been found to stimulate biofilm formation, inhibit motility and control the virulence of bacterial pathogens (Jenal & Malone, 2006; Kolter & Greenberg, 2006; Römling & Amikam, 2006). c-di-GMP is produced from two molecules of GTP by diguanylate cyclases (DGCs) and hydrolysed by a c-di-GMP-specific phosphodiesterases (PDE). DGC activity is conferred by the GGDEF functional domain, whereas PDE activity is performed by unrelated EAL or HD-GYP domains (Römling & Amikam, 2006). Notably, individual bacterial genomes frequently encode numerous GGDEF and EAL/HD-GYP proteins (Galperin, 2004, 2005), implying that the c-di-GMP network is a highly complex and tightly regulated intracellular signalling system. The observation that most GGDEF and EAL domains are linked directly or through a two-component phosphorylation cascade (Galperin, 2006) to input signal domains (including PAS, blue-light-sensing, Cache, CHASE and MASE domains) implies that numerous environmental and internal signals can be integrated into the c-di-GMP network.

*Bordetella bronchiseptica* is a Gram-negative bacterium that causes respiratory tract infections in mammals, producing atrophic rhinitis in pigs, kennel cough in dogs and snuffles in rabbits (Goodnow, 1980). *B. bronchiseptica* has a variety of virulence factors and strategies that allows the host infection. Each factor such as pertactin (PRN), filamentous haemagglutinin (FHA), adenylate cyclase (AC), the type three secretory system (TTSS) and LPS are likely to perform specific functions required for successful colonization (Harvill et al., 1999, 2000; Sisti et al., 2002; Skinner et al., 2004; Inatsuka et al., 2010). The BvgAS two-component system plays a central role in the regulation of some of these factors such as PRN, FHA, AC and TTSS (Mattoo & Cherry, 2005). This system comprises a

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Abbreviations: AC, adenylate cyclase; c-di-GMP, bis-(3′–5′)-cyclic-dimeric guanosine monophosphate; Ct, threshold cycle; CV, crystal violet; DGC, diguanylate cyclase; FHA, filamentous haemagglutinin; NA, nicotinic acid; PDE, phosphodiesterase; PRN, pertactin; SEM, scanning electron microscopy; TTSS, type three secretory system.

Two supplementary tables, listing plasmids and strains used and primers used in PCRs, are available with the online version of this paper.

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histidine kinase sensor protein, BvgS, and a DNA-binding response regulator protein, BvgA. In response to environmental signals, BvgAS undergoes a series of phosphorylation signal transduction events that ultimately lead to differential transcription of target genes (Mattoo & Cherry, 2005). Growth at 37 °C in low concentrations of nicotinic acid (NA) and magnesium sulfate leads to the Bvg\textsuperscript{+} or virulent phase, in which BvgAS activates expression of most known virulence factors. When the Bordetella sp. are grown at low temperatures (below 26 °C) or in the presence of millimolar concentrations of NA or magnesium sulfate, BvgAS is inactivated, resulting in the Bvg\textsuperscript{−} or avirulent phase, in which transcription of most virulence factor genes is repressed and the expression of other factors is induced, resulting in the maximal expression of motility loci and genes required for the production of urease (Akerley & Miller, 1993; Akerley et al., 1992; McMillan et al., 1996). Intermediate phase, called Bvg\textsuperscript{I} (Bvg intermediate), occurs transiently during shifts between the Bvg\textsuperscript{+} and Bvg\textsuperscript{−} states and can be induced by the addition of magnesium sulfate or NA at concentrations lower than those needed to fully induce the Bvg\textsuperscript{−} phase (Cotter and Miller, 1997). The Bvg\textsuperscript{I} phase is characterized by the expression of a subset of the Bvg\textsuperscript{+}−phase genes (such as flaB and pml) and Bvg\textsuperscript{I}-specific genes (such as bipA and bcfA) (Cotter and Miller, 1997; Stockbauer et al., 2001).

The ability of this genus to form biofilms has been reported in previous work, with other authors reporting the ability of \textit{B. bronchiseptica} to form biofilm-like structures on abiotic surfaces regulated by the two-component system BvgAS (Irie et al., 2004; Mishra et al., 2005). Static growth with intermediate NA concentrations presented the best conditions for biofilm formation (Mishra et al., 2005). Like in other biofilms, extracellular DNA and exopolysaccharide are important for biofilm formation in \textit{B. bronchiseptica} (Conover et al., 2011). Sloan and colleagues even observed these structures \textit{in vivo} in the nasal epithelium of mice infected with \textit{B. bronchiseptica}. Those structures present a polysaccharide essential for \textit{in vivo} biofilm development (Sloan et al., 2007). However, the exact mechanism of this process and the bacterial factors involved has not been yet determined.

Although the cyclic-di-GMP signalling system has been characterized in several types of bacteria regulating biofilm formation and motility, the understanding of this important signalling mechanism is limited in \textit{Bordetella} sp. So far there are no reports relating the c-di-GMP network to a specific phenotype in \textit{B. bronchiseptica}. In the published genome of \textit{B. bronchiseptica} RB50 strain there are four hypothetical proteins with EAL domains, ten with GGDEF domains and five with both domains (Amikam & Galperin, 2006). A recent study has identified a GGDEF diguanylate cyclase type protein with ability to synthesize c-di-GMP from the genome sequence of \textit{B. pertussis} Tohama I. Deletion of the gene encoding this enzyme diminished the capacity of \textit{B. pertussis} to adhere to abiotic surfaces (Wan et al., 2009).

In the present work, we demonstrated that c-di-GMP signalling is present in \textit{B. bronchiseptica} by introducing genes coding for proteins with proven PDE or DGC activity. Phenotypes previously linked with the presence of c-di-GMP in other bacteria were analysed, particularly biofilm formation and motility in soft agar. We also describe BB3576, a probable DGC, involved in swimming motility regulation and biofilm formation. The results reported here strongly suggest that c-di-GMP regulates these phenotypes in \textit{B. bronchiseptica}.

**METHODS**

**Bacterial strains and growth conditions.** Strains and plasmids used in this study are listed in Table S1 available with the online version of this paper. \textit{B. bronchiseptica} strains were grown on Bordet Gengou agar (Britainia) supplemented with 10% (v/v) defibrinated fresh sheep blood (BGA medium) at 37 °C for 48 h and replated in the same medium for 24 h. \textit{Escherichia coli} DH5-\textsuperscript{α} and S17-1 and \textit{Pseudomonas fluorescens} P90-1 strains were routinely cultured with liquid LB medium in a test tube or on solidified LB with 1.5% (w/v) agar. Proteins with DGC (PA1120) and PDE (PA3947) domains were overexpressed in \textit{B. bronchiseptica} 9.73 by using vectors with the inducible tac promoter to assess the consequences of alterations in c-di-GMP levels. Plasmids were introduced into \textit{B. bronchiseptica} or in \textit{Pseudomonas fluorescens} P90-1 by electroporation and transformants were selected in the presence of gentamicin (50 μg ml\textsuperscript{-1}).

\textit{B. bronchiseptica} protein BB3576 was overexpressed in \textit{B. bronchiseptica} by using broad-host-range plasmid pBBR1MCS-5 with a constitutive promoter npt\textsuperscript{II} (Dombrecht et al., 2001) cloned by us in \textit{Sal} and \textit{XbaI} sites of the pBBR1MCS-5 multiple cloning site. Proof reading Pfx taq polymerase was employed to amplify the BB3576 gene from \textit{B. bronchiseptica} 9.73 with primers BB3576F\textsuperscript{XhoI} (5′AGTC-CTCGAGGACGGGGTCGGATAAGGATA3′) and BB3576R\textsuperscript{KpnI} (5′CTCGAGGATCCTGCGAAGGCGAT3′). PCR conditions were 94 °C for 4 min (1 cycle), followed by 35 cycles of 94 °C for 20 s, 58 °C for 20 s, and 68 °C for 2 min and a final extension of 68 °C for 5 min. Underlined portions indicated restriction enzyme sites. Underlined portions indicated restriction enzyme sites. The PCR product was digested with \textit{XhoI} and \textit{KpnI} and cloned into pBBR1MCS-5-npt\textsuperscript{II} (renamed pEmpty) that had been digested with the same enzymes, to generate pBB3576. Constructs were confirmed by sequencing. Plasmids were transferred into \textit{B. bronchiseptica} 9.73 or into \textit{Pseudomonas fluorescens} P90-1 by electroporation and transformants were selected in the presence of gentamicin (50 μg ml\textsuperscript{-1}).

**Biofilm assays.** \textit{B. bronchiseptica} biofilm formation assays using static cultures were performed as described previously (Irie et al., 2004) from overnight cultures into Stainer–Scholte (SS) liquid medium (Stainer & Scholte, 1970). The overnight culture was diluted to OD\textsubscript{560} 0.1, pipetted into each well of a sterile 96-well U-bottom microtitre plate (both polycarbonate and PVC surfaces) and incubated statically at 37 °C with NA or magnesium sulfate at different concentrations. 1 mM IPTG and gentamicin (50 μg ml\textsuperscript{-1}) were added, when appropriate.

For \textit{P. fluorescens} biofilms an aliquot (1.5 μl) of an overnight culture grown in LB was transferred into 100 μl K10T-1 medium in a 96-well plate (353911; BD Falcon) and grown statically for 6 h at 30 °C. K10T-1 medium, used in prior studies as a biofilm-promoting, phosphate-rich medium, contains 50 mM Tris/HCl (pH 7.4), 0.2% (w/v) Bacto tryptone, 0.15% (v/v) glycerol, 0.6 mM MgSO\textsubscript{4} and 1 mM K\textsubscript{2}HPO\textsubscript{4} and was prepared as described previously (Newell et al., 2011).
In all assays planktonic bacteria were removed and remnant cells were stained with 0.1% crystal violet solution (CV). The stain was dissolved by adding 120 μl 33% acetic acid solution. A 100 μl sample was transferred to a microplate and then quantified by measuring OD595. Each data point results from an average for six wells and each experiment was repeated at least three times with similar results. Figures are representative of one of those replicates.

**Measurements of c-di-GMP levels.** c-di-GMP levels were analysed via LC-MS. Strains of interest were grown in BGA media for 24 h. Four replicates of each strain was harvested and resuspended in 250 μl extraction buffer [methanol:acetonitrile:water (40:40:20) plus 0.1 M formic acid at −20 °C and incubated at −20 °C for 30 min. The cell debris was pelleted for 5 min at 4 °C, and the supernatant containing the nucleotide extract was saved. Samples were immediately adjusted to a pH of approximately 7.5 with 15% (NH4)2HCO3 and stored on dry ice prior to analysis. The resultant extract was analysed via LC-MS using the LC-20AD HPLC system (Shimadzu) coupled to a Finnigan TSQ Quantum Discovery MAX triple-quadrupole mass spectrometer (Thermo Electron) as previously described (Newell et al., 2011).

**Motility assays.** SS soft-agar motility plate [0.35% (p/v) agar] supplemented with MgSO4 40 mM and 1 mM IPTG was used to determine the motility of bacterial strains as previously described (Fernández et al., 2005). The diameter of the migration zone was measured after 18 h of incubation at 37 °C.

**Scanning electron microscopy (SEM).** Bordetella strains were cultured statically on glass coverslips partially submerged vertically in 1.5 ml plastic tubes (Mishra et al., 2005). The glass coverslips were placed such that an air–liquid interface was established. After 48 h the coverslip was removed and washed with sterile PBS (KH2PO4 3 mM, Na2HPO4 10 mM, NaCl 120 mM), and the bacteria were fixed with 2.5% glutaraldehyde. Samples were dehydrated in a graded ethanol series (20, 50, 70, 90 and 100 % for 60 min each), dried by critical point liquid carbon dioxide (EMITECH, K850) and sputter coated with gold. The surface topographies of the biofilm were visualized with a scanning electron microscope (Philips SEM 505), and the images were processed [Image Soft Imaging System ADDA II (SIS)].

**RNA extraction and qPCR quantification.** RNA preparation from bacteria was performed using the Illustra RNAspin kit (GE). Samples were placed on ice, and quantification of RNA was performed using a ND-1,000 NanoDrop spectrophotometer at 260 nm. Measurements of A260/A280 were used to determine the purity of the RNA. DNase (Promega) treatment was performed according to manufacturer’s instructions in order to eliminate contaminating DNA. The synthesis of cDNA was performed with a Reverse Transcription System Kit (Promega) according to the manufacturer’s protocol using random primers. For each sample 1 μg RNA was used. The reaction was incubated at room temperature for 10 min, and reverse transcription was performed in a thermal cycler at 42 °C for 15 min and 95 °C for 5 min. qPCR conditions were 95 °C for 10 min (1 cycle), followed by 40 cycles of 60 °C for 30s, 95 °C for 15 s and a final increasing temperature cycle between 55 and 95 °C for 10 s when melt curve data was obtained. Samples were placed on ice for 5 min to stop the reaction. Samples that had not undergone the reverse transcription process were used as controls for genomic DNA absence in real-time PCR experiments. Only samples with threshold cycle (Ct) values above mock values were used in further experiments. Real-time PCR were performed using the SYBR green master mix 2× (Bio-Rad). Primers employed are summarized in Table S2. All samples, including a negative control using mock samples instead of DNA, were run in triplicates. The data were analysed using Ct calculations using aCt expression levels as a normalizer. Results were expressed as fold increase over values from bacteria growth in SS media without additional NA.

**Statistical analyses.** All the results were compared by ANOVA followed by the Tukey test. A value of P<0.01 was considered significant. To identify significant differences in RNA expression, Ct values were analysed using the REST program.

**RESULTS**

**B. bronchiseptica biofilm formation is enhanced by diguanylate cyclase activity**

Because some authors have described that not all proteins with GGDEF domains have DGC activity, we first decided to use a protein with known in vitro and in vivo DGC activity in our studies (Kulesekara et al., 2006). Protein PA1120 with DGC activity was overexpressed in B. bronchiseptica 9.73 (Bb-DGC) by using a vector with the inducible tac promoter. Clone Bb-DGC grown in IPTG-containing media overexpressed PA1120 and this strain was able to grow in a batch culture at the same rate as the parental strain (data not shown). The ability to form biofilm was evaluated by the crystal violet method in 96-well polycarbonate U-bottom and polyvinylchloride (PVC) microtitre plates as described in Methods. Biofilm formation is regulated by the BvgAS two-component system (Irie et al., 2004; Mishra et al., 2005). Hence, we determined the amount of biofilm biomass formed by strains under Bvg-modulated-phase conditions in the presence of NA (0–8.0 mM). This chemical compound serves as an environmental modulator of BvgAS activity (Akerley et al., 1992), at 0 mM NA the BvgAS system should be fully activated or in Bvgplus phase and at 8 mM NA the BvgAS system should be fully inactivated or in Bvgminus phase. In our hands, B. bronchiseptica 9.73 (RBWT) strain showed biofilm formation on both polycarbonate and PVC surfaces and the biofilm pellicle was enhanced in intermediate modulation conditions in agreement with results for B. bronchiseptica RB50 strain (Irie et al., 2004). In Fig. 1(a) results obtained on polycarbonate surface are shown and are similar to PVC results (not shown). As expected for a high c-di-GMP intracellular concentration, overexpression of PA1120 in Bb-DGC significantly enhanced pellicle formation at NA concentrations from 0 to 4.0 mM (Fig. 1a) compared with the parental strain. This difference was observed only when IPTG-supplemented SS was used. Surprisingly, when PA1120 was overexpressed biofilm formation was particularly exacerbated in the Bvgminus phase (4.0 mM NA; Fig. 1a). We observed no biofilm formation in 8.0 mM NA media, but planktonic growth in that condition was significantly slower compared with that for media without additional NA (data not shown). On the other hand, overexpression of PA3947 with PDE activity produced a biologically significant decrease in the biofilm formation as compared with the parental strain only in 1.0 mM NA (Fig. 1a).

The BvgAS system is downregulated by NA and by magnesium sulfate. For that reason, we performed biofilm quantification with different magnesium sulfate concentrations.
corresponding to Bvg\textsuperscript{plus}, Bvg\textsuperscript{i} and Bvg\textsuperscript{minus} phases, as reported previously (Williams & Cotter, 2007). We observed that biofilm formation was also enhanced in Bb\textsuperscript{-DGC} at Bvg\textsuperscript{i} (16 mM) and Bvg\textsuperscript{minus} (32 mM) magnesium sulfate-induced phases compared with the parental strain (Fig. 1b).

In order to confirm that NA concentrations corresponded to established phases in Bb\textsuperscript{WT} like in the sequenced B. bronchiseptica strain RB50, mRNA extraction and quantification was performed. Bacteria cultures grown in SS with NA at concentrations between 0 and 4.0 mM were subject to mRNA purification. Levels of cya\textit{A} (AC, Bvg\textsuperscript{plus} phase factor), bip\textit{A} (Bvg\textsuperscript{i} phase factor) and fla\textit{A} (flagellin, Bvg\textsuperscript{minus} phase factor) mRNA were normalized to rec\textit{A} and compared. Results obtained confirmed that with NA in the concentrations assayed all the virulence phases were detected, 0.5 mM NA and 1 mM NA correspond to Bvg\textsuperscript{i} phase and 4 mM NA corresponds to Bvg\textsuperscript{minus} phase. (Fig. 2).

**Overexpression of a diguanylate cyclase in B. bronchiseptica induced increased intracellular c-di-GMP levels**

In order to confirm that PA1120 overexpression in Bb\textsuperscript{-DGC} correlated with increased DGC activity \textit{in vivo}, intracellular c-di-GMP levels were determined. Cultures with or without IPTG induction were subjected to c-di-GMP extraction and analysis. As shown in Fig. 3, Bb\textsuperscript{-DGC} in the presence of IPTG presented significantly higher c-di-GMP levels than the strain grown under non-inducing conditions, supporting the hypothesis that biofilm phenotypes
observed in Bb-DGC were a consequence of increased c-di-GMP level.

Scanning electron microscopy of B. bronchiseptica cells adhered to glass coverslips

To further investigate the consequences of DGC activity in biofilm development, biofilms formed at the air–liquid interface in biphasic cultures on glass coverslips were observed by SEM. As expected for Bvgi conditions, at 48 h all strains grown in 1.0 mM NA presented thick multilayered stack of cells alternated with stacked cells aggregated in clusters similar to those observed by other authors (Fig. 4) (Mishra et al., 2005). Wild-type cells grown in Bvg\textsuperscript{plus} phase (0 mM NA) formed a thin layer with small aggregates, whereas cells grown in Bvg\textsuperscript{minus} phase (4.0 mM NA) appear as diffuse, interspersed bacteria (Fig. 4). Interestingly, SEM analysis of Bb-DGC biofilms revealed stacked bacteria more frequently and with bigger dimensions, resulting in an architecture that appeared to encase the bacterial microcolonies. These structures were observed in all virulence phases tested. In the case of Bb-PDE, cells grown at Bvg\textsuperscript{plus} (0 mM NA) or Bvg\textsuperscript{minus} (4.0 mM NA) phase were spread around the disks with large regions remaining uncolonized. Altogether these results further corroborate those from CV quantification for Bb-DGC, with the exception that no differences were observed at 1.0 mM NA between Bb-PDE and BbWT in this analysis.

BvgA is not necessary for diguanylate-cyclase-dependent biofilm formation

Bacterial proteins that mediate c-di-GMP turnover and signal transduction are often composed of multiple domains, allowing for a variety of regulatory inputs (Galperin et al., 2001). In particular, interplay between c-di-GMP network and two-component systems has been observed in many bacteria (Lai et al., 2009; Mikkelsen et al., 2009). B. bronchiseptica biofilm formation was dependent on Bvg phase conditions and c-di-GMP signalling as described above, indicating a probable connection between the two regulatory systems.

As described above, biofilm formation was dependent on Bvg phase condition even if high c-di-GMP intracellular levels were induced. A hypothesis to explain this observation is that the BvgAS system controls c-di-GMP levels. However, quantification of intracellular c-di-GMP levels under different Bvg-modulated conditions shows no significant differences between c-di-GMP concentrations (Fig. 5a), thus we must reject this hypothesis.

Although c-di-GMP concentration was apparently independent of direct BvgAS regulation, we assessed the effect of a \textit{bvgA} mutant in a strain overexpressing a DGC. We

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**Fig. 4.** SEM images of \textit{B. bronchiseptica} biofilms. BbWT (upper row of panels), Bb-DGC (middle row of panels) and Bb-PDE (bottom row of panels) were grown statically on vertically submerged coverslips in SS medium alone (left column of panels), SS supplemented with 1.0 mM NA (middle column of panels) or SS supplemented with 4.0 mM NA (right column of panels). After 48 h of growth, the biofilms formed at the air–liquid interface were visualized by SEM.
overexpressed PA1120 with DGC activity in *B. bronchiseptica* ΔBvgA (*Bb*ΔBvgA), a mutant locked in the BvgA\textsuperscript{−} phase and previously constructed by our group (Fernández et al., 2005). All strains were assayed for biofilm formation in 96-well polycarbonate U bottom plates. As expected, *Bb*ΔBvgA showed poor biofilm formation in all Bvg modulatory conditions, similar to the BvgA\textsuperscript{−} phase (Fig. 5b). However, when PA1120 in *Bb*ΔBvgA-DGC was overexpressed, significantly higher biofilm formation was detected at NA concentrations lower than 8.0 mM.

Biofilms produced by DGC-expressing bacteria in a ΔBvgA background were analysed by SEM. As shown in Fig. 5(c), *Bb*ΔBvgA-DGC in 1.0 mM NA was the only strain and condition that formed a uniform multilayered stack of cells, but the volume of the structure was smaller than that for *Bb*-DGC, corroborating the CV determinations (Fig. 4). As expected, *Bb*ΔBvgA showed no distinct region of biofilm formation and cells were spread evenly across the coverslips (Fig. 5c).

**c-di-GMP regulates swimming motility in *B. bronchiseptica***

In several bacteria c-di-GMP suppresses swimming, swarming and twitching motility (Jenal & Malone, 2006; Römling & Amikam, 2006). Flagellar expression and motility in *B. bronchiseptica* is regulated by the BvgAS two-component system and is maximal in the BvgA\textsuperscript{−} phase (Akerley et al., 1992). Therefore, we evaluated strain motility in the presence of modulating concentrations of magnesium sulfate. As expected, all strains showed motility in soft agar in modulated conditions. However, when DGC overexpression was induced by IPTG in WT reduced motility was observed (Fig. 6). This phenotype was observed also in a ΔBvgA background. *Bb*-PDE showed no significant differences from the wild-type strain with regard to motility.

**BB3576: a hypothetical GGDEF protein regulating swimming motility and biofilm formation in *B. bronchiseptica***

The *B. bronchiseptica* genome contains 15 proteins with GGDEF domains. As observed above, DGC overexpression in *B. bronchiseptica* inhibits swimming motility in soft agar. In *E. coli*, swimming is regulated by c-di-GMP through diverse DGCs and PDEs. Deletion of genes encoding GGDEF proteins Yead, YedQ, YdN, YejA and YneF in *E. coli* increased swimming motility (Sanchez-Torres et al., 2011).
Also, YeaJ, YedQ and YfiN overexpression negatively regulate motility without impairing it completely (Pesavento et al., 2008). These results suggested that some proteins with DGC activity are involved in fine-tuning regulation of flagellar activity. Among these proteins, YeaJ also has a Cache domain similar to the domain found in regulation of flagellar activity. Among these proteins, YeaJ proteins with DGC activity are involved in fine-tuning based on three replicates.

Fig. 6. Motility phenotypes of B. bronchiseptica strains. The diameters of migration zones of the wild-type, overexpression strains and mutants were measured and expressed relative to wild-type diameter after 18 h of incubation at 37 °C on SS motility plates supplemented with 32 mM magnesium sulfate. One hundred per cent motility in BbWT was 12 mm. The results are based on three replicates.

As was observed for Bb-DGC, overexpression of BB3576 should inhibit swimming motility in Bvg− phase. The BB3576 gene was cloned into a broad-host-range plasmid pBB1RMCS-5 under control of the nptII constitutive promoter and transferred to Bb-DGC to obtain Bb-BB3576. These bacteria showed reduced swimming motility in soft agar compared with wild-type B. bronchiseptica. Swimming of Bb-BB3576 was enhanced in Bvg+ phase (1.0 mM NA) compared with B. bronchiseptica transformed with the empty vector (Fig. 7c). Furthermore, biofilm formation for BbΔBvgA–BB3576 in Bvg+ phase was enhanced compared with BbΔBvgA transformed with the empty vector (Fig. 7c).

BB3576 complements a diguanylate cyclase mutant phenotype

The BB3576 protein expressed in B. bronchiseptica resulted in phenotypes consistent with this protein being an active DGC. To confirm that BB3576 has DGC activity, we transformed the P. fluorescens ΔDGC (PsΔ4) strain with the pBB3576 plasmid. Strain PsΔ4 has the genes coding for four DGC proteins deleted from its genome and is not able to produce biofilm under static growth conditions (Newell et al., 2011). A previous study showed that complementation with one DGC protein was sufficient to restore biofilm formation to this strain (Newell et al., 2011). Biofilm formation for the P. fluorescens strains was evaluated in a 96-well plate grown statically for 6 h at 30 °C in K10T-1 medium (Fig. 8). When PsΔ4 was complemented with a DGC-encoding-gene gcbB, biofilm formation was restored as previously described (Newell et al., 2011). When a plasmid carrying BB3576 was introduced, biofilm formation was also observed, suggesting a DGC activity for this protein in concordance with the results described above (Fig. 8).

DISCUSSION

The signalling molecule c-di-GMP has been reported to regulate phenotypes like biofilm formation, motility and virulence. It is generated from two GTP molecules by GGDEF-domain-containing DGC enzymes, and degraded by PDE enzymes containing either EAL or HD-GYP protein domains. Despite the frequent occurrence of these protein domains encoded in bacteria genomes, information on mechanisms and physiological roles regarding their function and regulation is sparse. Many of these proteins have also other domains, suggesting that c-di-GMP activity is regulated by these additional domain functions. So we can imagine that cell c-di-GMP turnover is regulated through the consensus of various external and internal factors. The balance of these signals ultimately regulates biofilm formation, motility and virulence.

In the present work we showed that c-di-GMP signalling is involved in B. bronchiseptica biology. We overexpressed proteins with demonstrated in vitro and in vivo activity in order to establish if c-di-GMP regulation was present in this microbe. We overexpressed PA1120 or PA3947 with known DGC and PDE activities, respectively, in wild-type B. bronchiseptica. As shown in Fig. 1, PA1120 with a GGDEF functional domain overexpression leads to an enhanced biofilm phenotype compared with the wild-type strain under all conditions tested. Biofilm formation was...
quantified by the CV method and confirmed by SEM. These findings suggest that an increase in the levels of this DGC and in intracellular c-di-GMP levels causes an enhanced production of factors that promote bacterial binding to abiotic surfaces and/or inter-bacterial adherence.

As mentioned above, biofilm formation is regulated by BvgAS in *B. bronchiseptica*. Nicotinic acid or magnesium sulfate can modulate BvgAS activity in vitro through the three phases, virulent (Bvg+) intermediate (Bvgi) and avirulent (Bvg−). Interestingly, although for all modulator conditions Bb-DGC showed more biofilm formation than the parental strain, the difference is bigger in Bvg− phase (4.0 mM NA). Irie et al. (2004) suggested that while AC activity inhibits biofilm formation, FHA is necessary for full biofilm development. Both proteins are present in Bvg+ phase but only FHA is present in Bvg+ phase and both are absent in Bvg− phase (Mattoo & Cherry, 2005). This is in agreement with results showing that Bvg+ phase is the condition where major biofilm formation is observed in *B. bronchiseptica*. Nevertheless, it is noteworthy that with overexpression of a non-physiological DGC, and in the absence of FHA during growth in the Bvg− phase, a biofilm is still established by the Bb-DGC strain. The group of factors involved in biofilm regulation and presumably activated by c-di-GMP might be sufficient for establishment of this phenotype regardless of virulence factors like FHA.

In concordance with this finding, when PA1120 was overexpressed in a ΔBvgA background, biofilm formation was observed. However, the biofilm magnitude was significantly weaker than in wild-type background and SEM analysis showed only biofilm architecture in 1.0 mM NA. These results are surprising, since neither BbΔBvgA nor BbΔBvgA-DGC is expected to respond to different concentrations of known BvgAS modulators, thus the interplay between NA and the c-di-GMP network may be present in *B. bronchiseptica* through mechanisms not yet explored. We can speculate that BvgAS regulates the c-di-GMP network regulating protein expression, particularly those proteins directly involved in c-di-GMP signalling. Interestingly, the BvgR regulatory protein, which represses the expression of virulence genes in Bvg+ phase in *Bordetella*, contains an EAL domain (Merkel et al., 1998). The expression of this protein is stimulated by the BvgAS.
system, strongly suggesting a relationship between the BvgAS system and c-di-GMP that requires further investigation.

In other bacteria where c-di-GMP function has been determined, low c-di-GMP levels are frequently associated in planktonic phenotypes with flagellar expression. As shown above, DGC overexpression in *B. bronchiseptica* enhanced biofilm formation, probably as a consequence of high c-di-GMP levels, which may also repress motility in *Bb*-DGC when a flagellar system is present. It is known that *B. bronchiseptica* shows motility in Bvg<sup>minus</sup> modulated conditions like high-sulfate concentrations. Motility assays in soft agar plates showed that *Bb*-DGC exhibited significantly diminished motility. This result is in concordance with behaviour of other bacteria and with a c-di-GMP network that regulates the transition between sessile and motile lifestyles of bacteria. Moreover, we described for the first time, to our knowledge, in *B. bronchiseptica* a protein with a GGDEF domain that probably had diguanylate cyclase activity *in vivo*. Real-time PCR results clearly demonstrated that BB3576 expression was higher in Bvg<sup>minus</sup> phase compared with Bvg<sup>plus</sup> conditions. However, NA regulation appears to be dominant over BB3576 activity for biofilm formation, even in a ΔBvgA background, since differences in biofilm quantification of strains overexpressing BB3576 were only significant at NA concentrations inducing the Bvg<sup>1</sup> phase. One possible explanation is that conformational changes in the expressed BB3576 protein may be required for optimal DGC function. BB3576 has two predicted domains, a DGC domain and an extracellular sensory Cache domain (Ca<sup>2+</sup> channels, chemotaxis receptors). In general, Cache domains sense stimuli present in the periplasm and transmit signals to an output domain such as GGDEF, resulting in a specific adaptive response (Anantharaman & Aravind 2000; Galperin 2006). We speculate that BB3576 regulates biofilm and motility when a ligand binds to the Cache domain. The nature of this ligand remains unknown at the moment. Diguanylate cyclase activity was demonstrated *in vivo* for BB3576 as shown in Fig. 8. Overexpression of BB3576 in a *P. fluorescens* strain with a low-DGC-activity background restored biofilm formation. The partial complementation achieved by BB3576 may be explained by the absence from the growth media of the unknown ligand.

Recently, Amarasinghe and co-workers described YeaJ in *Salmonella enterica* serovar Typhimurium as an active DGC membrane protein involved in motility regulation and exopolysaccharide production (Amarasinghe et al., 2013). This protein, like BB3576, has a GGDEF domain with demonstrated DGC activity and a putative Cache domain. They proposed that the association of a protective monoclonal IgA antibody with the O-antigen induces outer membrane stress triggering a c-di-GMP signalling pathway that effectively promotes a less motile and non-invasive biofilm state, thereby rendering the bacterium unable to invade intestinal epithelial cells. The particular expression profile of BB3576 in Bvg<sup>plus</sup>, Bvg<sup>i</sup> and Bvg<sup>minus</sup> phases is in concordance with putative motility regulation of the bacteria during Bvg<sup>minus</sup> phase. Flagellar synthesis and function is regulated in bacteria at different levels by c-di-GMP (Wolfe & Visick, 2008). This newly described protein BB3576 might fine tune flagellar motor function using c-di-GMP as a second messenger in response to chemosensory activity of the Cache domain, as reported for *E. coli* (Pesavento et al., 2008).

Although further research is needed to elucidate c-di-GMP regulation and signalling in *B. bronchiseptica*, we demonstrated here for the first time, to our knowledge, its role regarding the control of *B. bronchiseptica* biofilm formation and motility. More over we would now argue that c-di-GMP is involved in motility regulation in response to as yet unknown ligands that may be sensed by BB3576.

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