Bifunctionality of a biofilm matrix protein controlled by redox state

Citation for published version:

Digital Object Identifier (DOI):
10.1073/pnas.1707687114

Link:
Link to publication record in Edinburgh Research Explorer

Document Version:
Publisher's PDF, also known as Version of record

Published In:
Proceedings of the National Academy of Sciences

General rights
Copyright for the publications made accessible via the Edinburgh Research Explorer is retained by the author(s) and / or other copyright owners and it is a condition of accessing these publications that users recognise and abide by the legal requirements associated with these rights.

Take down policy
The University of Edinburgh has made every reasonable effort to ensure that Edinburgh Research Explorer content complies with UK legislation. If you believe that the public display of this file breaches copyright please contact openaccess@ed.ac.uk providing details, and we will remove access to the work immediately and investigate your claim.
Bifunctionality of a biofilm matrix protein controlled by redox state

Sofia Arnaouteli1,2, Ana Sofia Ferreira3–5, Marieke Schor6–8, Ryan J. Morris9, Keith M. Bromley10, Jeanyoung Jo11, Krista L. Cortez12, Tetyana Sukhodub13, Alan R. Prescott3, Lars E. P. Dietrich1, Cait E. MacPhee10,2 and Nicola R. Stanley-Wall12,2

1Division of Molecular Microbiology, School of Life Sciences, University of Dundee, Dundee DD1 5EH, United Kingdom; 2School of Physics and Astronomy, The University of Edinburgh, Edinburgh EH9 3FD, United Kingdom; 3Department of Biological Sciences, Columbia University, New York, NY 10027; and 4Centre for Advanced Scientific Technologies, School of Life Sciences, University of Dundee, Dundee DD1 5EH, United Kingdom.

Biofilms are communities of microbial cells that are encapsulated within a self-produced polymeric matrix. The matrix is critical to the success of biofilms in diverse habitats; however, many details of the composition, structure, and function remain enigmatic. Biofilms formed by the Gram-positive bacterium Bacillus subtilis depend on the production of the secreted film-forming protein BslA. Here, we show that a gradient of electron acceptor availability through the depth of the biofilm gives rise to two distinct functional roles for BslA and that these roles can be genetically separated through targeted amino acid substitutions. We establish that monomeric BslA is necessary and sufficient to give rise to complex biofilm architecture, whereas dimerization of BslA is required to render the community hydrophobic. Dimerization of BslA, mediated by disulfide bond formation, depends on two conserved cysteine residues located in the C-terminal region. Our findings demonstrate that bacteria have evolved multiple uses for limited elements in the matrix, allowing for alternative responses in a complex, changing environment.

biofilm matrix | Bacillus subtilis | BslA | redox | hydrophobicity

B. subtilis encodes a monomeric BslA parologue called YweA (14). Deletion of yweA does not impact the overall morphology or hydrophobicity of the biofilm (8); however, deletion in combination with removal of bslA exacerbates the biofilm defect of the single bslA deletion (8, 14). Contrary to the marginal contribution of YweA to biofilm formation, but consistent with the high level of amino acid sequence similarity, in vitro recombinant YweA undergoes the partial structural rearrangement at an interface to reveal the hydrophobic cap and forms an elastic protein film, albeit with limited stability (14). One notable difference between the primary amino acid sequences of BslA and YweA is that the BslA-like variants possess a short C-terminal extension that contains two conserved cysteine residues in a “CxC” configuration. Cysteine residues play an important role in the function of diverse proteins in a wide range of cellular processes (15), and therefore we...

Significance

The biofilm matrix is a critical target in the hunt for novel strategies to destabilize or stabilize biofilms. Knowledge of the processes controlling matrix assembly is therefore an essential prerequisite to exploitation. Here, we highlight that the complexity of the biofilm matrix is even higher than anticipated, with one matrix component making two independent functional contributions to the community. The influence the protein exerts is dependent on the local environmental properties, providing another dimension to consider during analysis. These findings add to the evidence that bacteria can evolve multifunctional uses for the extracellular matrix components.


This article is a PNAS Direct Submission.

Freedly available online through the PNAS open access option.

1S.A., A.S.F., and M.S. contributed equally to this work.

2To whom correspondence may be addressed. Email: n.r.stanleywall@dundee.ac.uk or cait.macphee@ed.ac.uk.

This article contains supporting information online at www.pnas.org/lookup/suppl/doi:10.1073/pnas.1707687114/-/DCSupplemental.
evaluated whether the BslA CxC motif played a significant biological role or was functionally redundant. Our analysis indicates that in addition to BslA having two structural forms (cap in/cap out) (11), it also has two functional forms mediated not by the hydrophobic cap region, but by the cysteines at the C terminus: Monomeric BslA dictates biofilm structure, whereas surface hydrophobicity requires at least dimeric protein. Thus, we show that the cysteine residues are crucial for full BslA function and surmise that, in the native biofilm, electron acceptor availability influences BslA oligomerization: In the oxygen-rich, surface-exposed region, the predominant form is a dimer, whereas the anoxic environment in the depths of the biofilm prevents BslA dimerization and allows for nutrient uptake. This work gives an example of a biofilm matrix protein with two functions that can be genetically separated and where the activity is controlled by redox state.

Results

BslA Disulfide Bond Formation. Recombinant BslA\textsubscript{42–181} forms a mixture of predominantly monomeric and dimeric protein in vitro, with a small amount of tetramer observed (12) (Fig. S1). The requirement of the cysteine residues (C178 and C180) for oligomerization of BslA was assessed in vitro by using purified recombinant protein where the cysteine residue(s) were either replaced with alanine or where the C-terminal 10 amino acids were removed (Fig. S1). Replacement of either C178 or C180 with alanine abolished tetrameric BslA (Fig. S1A and C), but dimers, which could be disrupted by the addition of \(\beta\)-mercaptoethanol, still formed (Fig. S1). In contrast, when both cysteines were replaced with alanine, or the C-terminal 10 amino acids were deleted, the protein was restricted to a monomeric form (Fig. S1).

Secondary structure analysis of the proteins by circular dichroism (CD) spectroscopy indicated that each of the BslA variants had the same overall fold as the wild-type protein, indicating that the inability to form dimers or tetramers was not due to a disruption of the protein structure (Fig. S2).

Next, we tested to see whether BslA formed dimers and/or tetramers in vivo, to explore the possibility that the conserved CxC motif at the C terminus of BslA plays an in vivo role in BslA oligomerization. Proteins were extracted from the wild-type biofilm either in the presence of Cu(II)-(o-phenanthroline)$_3$, which cross-links disulfide bonds (16), or 10 mM DTT, a reducing agent. Western blotting revealed immunoreactive bands consistent with monomeric (~14 kDa), dimeric (~28 kDa), and tetrameric (~56 kDa) forms of BslA in the absence of reducing agent (Fig. L4), whereas in the presence of 10 mM DTT, only monomeric BslA was detected (Fig. LB). The bslA deletion strain (NRS2097) was used as a control for antibody specificity and did not reveal any interacting bands. We generated a series of strains to express the variant bslA coding regions in the \textit{B. subtilis} bslA deletion strain (Table S1). Analysis of proteins extracted from the mature biofilms by immunoblot showed the same BslA monomer, dimer, and tetramer pattern in vivo as that observed in vitro for the recombinant proteins (compare Fig. S1 with Fig. 1A). Strains generating C178A (NRS5177) and C180A (NRS5178) variant BslA formed dimers, but not tetramers, whereas the double C178A, C180A mutant (NRS5179) and the BslA\textsubscript{Δ172–181} (NRS2957) truncation variants were restricted to the monomeric state (Fig. L4). In each case, only monomeric BslA was detected by Western blot analysis when 10 mM DTT was added during protein extraction (Fig. 1B). These

Fig. 1. BslA is a bifunctional protein. (A and B) Western blot analysis of BslA in a native (A) and reduced (B) state using proteins extracted from biofilms (SI Materials and Methods). (C–L) Architecture and hydrophobicity of biofilms. (C–H) Strains used were 3610 (wild-type; NCIB3610) (C), bslA\textsuperscript{−} (NRS2097) (D), and the bslA mutant genetically complemented with the following variants: CxC (NRS2299) (E), AxC (NRS1577) (F), CxA (NRS5178) (G), AxA (NRS5179) (H), and ΔC\textsubscript{term} (NRS2957) (I). Biofilms depicted in J–L are the result of coculturing strains NRS2299 and NRS5179. Under each biofilm is an image of a water droplet on the upper surface of the biofilm, and the values of the contact angle are in Table S2.

Arnaouteli et al. PNAS Published online July 11, 2017 | E6185
data demonstrate that BslA forms dimers and tetramers in vivo in a C178- and C180-dependent manner.

**Genetic Separation of Roles in Biofilm Architecture and Hydrophobicity.**

We next tested whether there was a biological consequence of restricting BslA disulfide bond formation in vivo. Deletion of bslA results in a flat, featureless, wetting biofilm; our analysis revealed that production of the BslA*<sub>C178A</sub>* variants resulted in a wetting biofilm. The wild-type and the bslA*<sub>C178A</sub>* variants showed the same wettability (Table S2; refs. 8 and 12). Each of the cysteine-to-alanine mutations, BslA*<sub>C178A,C180A</sub>* (NRS5177) and BslA*<sub>C180A</sub>* (NRS5178), displayed a nonwetting phenotype, although the contact angle calculated for the BslA*<sub>C178A,C180A</sub>* (NRS5177) strain was lower than that measured for the wild-type strain (18°). However, when 90% of the cells produced BslA, the wild-type strain formed a nonwetting biofilm where the water droplet had a high contact angle (124.6 ± 2.9°), whereas the bslA*<sub>C178A</sub>* mutant was wetting (101.6 ± 2.7°) (Table S2). In sharp contrast, the architectural complexity of the strains formed using the strains indicated could re-instate biofilm complexity of a bslA mutant to a level that was visually comparable to the wild-type strain (Fig. 1 C–F). We then assessed whether the biofilms formed were hydrophobic (22). The wild-type strain formed a nonwetting biofilm in which the water droplet had a high contact angle (124.6 ± 2.9°), whereas the bslA*<sub>C178A</sub>* mutant was wetting (101.6 ± 2.7°) (Table S2; refs. 8 and 12). Each of the single cysteine-to-alanine mutations, BslA*<sub>C178A</sub>* (NRS5177) and BslA*<sub>C180A</sub>* (NRS5178), displayed a nonwetting phenotype, although the contact angle calculated for the BslA*<sub>C178A</sub>* (NRS5177) strain was consistently lower than that measured for the wild-type strain (18°). Given the observation that surface hydrophobicity is associated with the ability to form dimeric protein (Fig. 1 C–F), we predicted that tetrmeric BslA may be in a monomeric form in this region.

**Sharing BslA Molecules in the Biofilm.**

Because hydrophobicity of the biofilms is at the macroscale, where BslA comprises a “common” or “public” good that can be shared by the population (19), the nutrient exchange between cells producing wild-type BslA was needed to achieve maximum nonwetting values. To determine this proportion, cells expressing either the wild-type bslA (NRS2299) or the BslA*<sub>C178A,C180A</sub>* (NRS5179) form were grown in an oxic environment, and the hydrophobicity of the resulting mature biofilm was measured (Fig. 1 L–K). When the strains were mixed in equal proportions, a nonwetting biofilm surface could be sustained (116.2 ± 2.8°). However, when 90% of the cells produced BslA*<sub>C178A,C180A</sub>* and BslA*<sub>C178A</sub>* (or both in the case of functional redundancy), the biofilm hydrophobicity remained above that of the bslA*<sub>C178A</sub>* mutant, but there was a step change in the wettability of the surface (50.5 ± 1.3°). Finacly, wetting reached a value indistinguishable from that measured for the fully monomeric protein when 99% of the cells produced BslA*<sub>C178A,C180A</sub>* (Table S2). These findings demonstrate that noncontributing bacteria can be tolerated during formation of the hydrophobic layer, as long as they represent <50% of the population.

**Formation of the Hydrophobic Layer Depends on Thiol-Disulfide Oxidoreductases and Is Enhanced in an Oxic Environment.**

In the *B. subtilis* extracytoplasmic space, disulfide bond formation is catalyzed by one of two thiol-disulfide oxidoreductases (TDRs) named BdB and BdhD (20–22). We predicted that if BslA was actively oligomerized, then disruption of either bdbA or bdbD (or both in the case of functional redundancy) would produce a structured, but wetting, biofilm similar to the phenotype displayed by the monomeric BslA variants. To test this hypothesis, we constructed bdbA*<sub>NRS5552</sub>* and bdbD*<sub>NRS5554</sub>* (A bdbC bdbD operon deletion), and bdbA*<sub>NRS5553</sub>* deletion strains and assessed biofilm formation and surface hydrophobicity (Fig. 2 A–C and Table S1). Consistent with our hypothesis, each of the strains formed biofilms that were morphologically indistinguishable from the parental strain NCIB3610 (Figs. 1C and 2A–C), but measurement of surface wettability revealed that the double bdbA bdbCD*<sub>NRS5554</sub>* (B) and bdbACD*<sub>NRS5553</sub>* (C). Under each biofilm is an image of a water droplet on the upper surface of the biofilm; contact angle values are in Table S2. (D) Measurement of the oxygen concentration (µM) and redox potential (mV) as a function of the depth of the biofilm, with 0 mV being set at the biofilm surface (see SI Materials and Methods for details). (E–G) Time course of water uptake by a mature biofilm visualized by using pigmented water: before treatment, 0 min (E); 2 min after exposure (F); and 15 min after exposure (G). In G, 5-µL colored water droplets demonstrate retention of upper biofilm hydrophobicity.

**Arnaouteli et al.**

PNAS | www.pnas.org/cgi/doi/10.1073/pnas.1707687114

E6186
consequence of protein misfolding or disruption of protein production in vivo, because CD spectroscopy demonstrated similar secondary structures in the variant proteins (Fig. S24), and immunoblot analysis revealed comparable levels of the BslA cysteine mutants to the wild-type protein (Fig. L4). Therefore, we considered two nonmutually exclusive hypotheses: (i) Mutation or deletion of the C-terminal cysteine residues impairs the innate ability of BslA to form a stable elastic film that depends on lateral interactions between the monomers (12), and consequently the ability to render the biofilm nonwetting; and (ii) BslA_C178A,C180A cannot form a dense layer over the surface of the biofilm as observed for the wild-type protein (12). The ability of recombinant BslA_C178A, BslA_C180A, BslA_C178A,C180A, and BslA_C172–181 to form stable elastic protein films in vitro was assessed by using multidrop analysis, coupled with quantification of the vinkle relaxation speed (12). Each of the variant proteins formed a stable protein film at the oil–water interface with no significant differences compared with wild-type BslA (Fig. S2B). Furthermore, transmission electron microscopy (TEM) indicated that the ability of the variant proteins to form an ordered 2D lattice at an interface was not impeded (Fig. S2 C–E).

Next, in situ localization of BslA was assessed by using immunofluorescence staining of biofilm cross-sections coupled with confocal microscopy (12). The strains tested were the wild type, the bslA mutant, and the bslA mutant complemented with either the wild-type or bslA_C178A,C180A coding region. In each case, the strains were modified to express the fluo-
protein to the coding region to allow the YweA variants (NRS5136), BslA-linked fluo-
protein to the coding bslA β coding region. In each case, the bslA variant (NRS5136) (hereafter YweA_BslA171–181). We additionally generated chimeric constructs, where each of the cysteine residues in the BslA C-terminal region was individually, and in combination, mutated to alanine (Table S1). The wild-type YweA, chimeric YweA_BslA171–181 and YweA_BslA171–181 C178A,C180A recombinant proteins were purified from Escherichia coli, and the secondary structure was assessed by CD spectroscopy. This analysis revealed that the C-terminal extension did not significantly affect folding of the protein compared with the parental YweA protein (Fig. S5A). The oligomerization state of the YweA_BslA171–181 chimeric protein was assessed in vitro by SDS/PAGE (Fig. S4 B and C) and size-exclusion chromatography (SEC) (Fig. S4D), which showed that the chimeric YweA_BslA171–181 protein formed dimers that were reduced to a mutant, and the mutant. BslA mutant complemented with the wild-type BslA (Fig. S2B). Furthermore, transmission electron microscopy (TEM) indicated that the ability of the variant proteins to form an ordered 2D lattice at an interface was not impeded (Fig. S2 C–E).

Next, in situ localization of BslA was assessed by using immunofluorescence staining of biofilm cross-sections coupled with confocal microscopy (12). The strains tested were the wild type, the bslA mutant, and the bslA mutant complemented with either the wild-type or bslA_C178A,C180A coding region. In each case, the strains were modified to express the fluorochrome to the coding region to allow the YweA variants (NRS5136), BslA-linked fluorochrome to the coding bslA β coding region. In each case, the bslA variant (NRS5136). In sharp contrast, appending the BslA C-terminal 11 amino acids to YweA did not alter the stability or organization of the protein film formed in vitro. Podrant drop analysis, coupled with quantification of wrinkle relaxation speed, revealed that YweA, YweA_BslA171–181, and YweA_BslA171–181 C178A,C180A each had an average relaxation time of ~25 s (Fig. S5B), substantially less stable than the BslA elastic film (>600 s; Fig. S5B). This result means that the proteins can form elastic films, but they are unstable under compression. Consistent with the film stability, TEM showed that each protein was able to form an organized lattice on a surface (Fig. S5 C–E). Together, these findings indicate that we can generate YweA oligomers in vitro by the addition of β-mercaptoethanol. Bands with the apparent molecular weight expected for dimers were also formed when either one of the two cysteine residues remained (YweA_BslA171–181 C178A and YweA_BslA171–181 C180A) (Fig. S5D), but for the monomer, only the BslA-C178A–C180A chimera was observed with the appending BslA C-terminal 11 amino acids to YweA (Fig. S4D). Unlike BslA, we did not detect formation of tetramers for the YweA_BslA171–181 chimeric protein. Notably, fusion of the BslA C-terminal 11 amino acids to YweA did not alter the stability or organization of the protein film formed in vitro. Podrant drop analysis, coupled with quantification of wrinkle relaxation speed, revealed that YweA, YweA_BslA171–181, and YweA_BslA171–181 C178A,C180A each had an average relaxation time of ~25 s (Fig. S5B), substantially less stable than the BslA elastic film (>600 s; Fig. S5B). This result means that the proteins can form elastic films, but they are unstable under compression. Consistent with the film stability, TEM showed that each protein was able to form an organized lattice on a surface (Fig. S5 C–E). Together, these findings indicate that we can generate YweA oligomers in vitro by the addition of BslA C-terminal 11 amino acids, but although they form an ordered 2D lattice, the chimeric proteins retain the fast film-relaxing properties of YweA (14).

**Oligomeric YweA Yields a Hydrophobic Biofilm.** To assess the impact of engineering YweA to form intermolecular disulfide bonds in vivo, we constructed a suite of plasmids designed to produce the YweA chimeric proteins in *B. subtilis*. The constructs were generated such that secretion through the Sec-system was directed by the BslA signal sequence (the variants are hereafter referred to as YweA_BslA171–181, YweA_BslA171–181 C178A, YweA_BslA171–181 C180A and YweA_BslA171–181 C178A,C180A) (Fig. S4A). The plasmids carrying the required coding regions were introduced into the bslA mutant at the ectopic *amyE* locus (Table S1). Western blot analysis of proteins extracted from the biofilm, by using an anti-YweA antibody, revealed that only in the presence of both cysteine residues were monomeric complexes (Fig. S3B). This result means that the proteins can form elastic films, but they are unstable under compression. Consistent with the film stability, TEM showed that each protein was able to form an organized lattice on a surface (Fig. S5 C–E). Together, these findings indicate that we can generate YweA oligomers in vitro by the addition of BslA C-terminal 11 amino acids, but although they form an ordered 2D lattice, the chimeric proteins retain the fast film-relaxing properties of YweA (14).
structure retained more architectural similarities with the bslA mutant, rather than the wild-type NCIB3610 strain (Fig. 4B). Expression of YweAΔ171-181 thus results in an unstructured, yet nonwetting, phenotype. The slightly lower contact angle measured (114.8 ± 1.1° vs. 124.6 ± 2.9° for the structured, wild-type biofilms) may indicate that biofilm architecture makes some contribution to overall hydrophobicity, as has been suggested elsewhere (18). In contrast, when the C-terminal extension was mutated such that one (NRS5515 and NRS5516) or both (NRS5210) cysteine residues were replaced with alanine, yielding monomeric BslA in vivo, the colonies formed retained both the wetting and unstructured phenotypes exhibited by the bslA mutant (compare Fig. 1D with Fig. 4B). Thus, dimeric chimeric YweA containing the two cysteine residues is able to reinstate biofilm hydrophobicity, whereas monomeric chimeric YweA is unable to reinstate biofilm architectural complexity.

Hydrophobicity and Architecture Play a Role in Resistance to Chemical Attack. The ability to genetically separate biofilm structure from hydrophobicity allowed us to assess whether protection from external insult is conferred to the bacteria by blocking access of the chemical and/or mediated by the architectural complexity. B. subtilis biofilms are nonwetting when challenged with selected commercial biocides (6), with chlorhexidine gluconate being the reactive agent of a number of such biocides. Analysis revealed that 1% (vol/vol) chlorhexidine gluconate is nonwetting on the biofilm: values of the contact angle are in Table S2 and strains are as in A.

The mechanism revealed here for controlling protein function through oxidation allows us to classify BslA as a bifunctional protein with genetically separable roles in biofilm formation, mediated by cysteine residues in the C terminus. BslA is a key component of the B. subtilis biofilm and plays a role in both biofilm architecture and hydrophobicity (8, 12, 23). Dimerization of BslA directly facilitates the development of the nonwetting layer and relies on a cysteine motif (CxC) at the C terminus.

Discussion

The ability to genetically separate biofilm structure from hydrophobicity allowed us to assess whether protection from external insult is conferred to the bacteria by blocking access of the chemical and/or mediated by the architectural complexity. B. subtilis biofilms are nonwetting when challenged with selected commercial biocides (6), with chlorhexidine gluconate being the reactive agent of a number of such biocides. Analysis revealed that 1% (vol/vol) chlorhexidine gluconate is nonwetting on the biofilm: values of the contact angle are in Table S2 and strains are as in A.

Cell survival after exposure to chlorhexidine gluconate. (A) An image of a 1% (vol/vol) chlorhexidine gluconate droplet on the upper surface of the biofilm for strain WT (NRS5132), bslA mutant (NRS5131), and the bslA mutant complemented with BslAΔ171-181 C178A C180A (+AxA; NRS5136); the values of the contact angle are in Table S2. (B) The strains described above were exposed to 1% (vol/vol) chlorhexidine gluconate, and the percentage survival was calculated. (C) Percentage sporulation was calculated for the strains detailed in A. The error bars represent the SD from the mean.
Monomeric variants of BslA yield biofilms that are architecturally complex, but lack hydrophobicity, whereas, conversely, transplantation of the BslA C terminus onto the normally monomeric nonfunctional paralogue YweA allows the chimeric protein to dimerize and consequentially rehabilitate hydrophobicity, but not architecture, to a bslA mutant. These findings are consistent with the accumulation of BslA at the air–biofilm interface only when it can dimerize, as observed by high-resolution in situ immunofluorescence microscopy (Fig. 3). The BslA layer is thus shared by the entire community and can form over and shield nonproducing bacteria (Fig. 1 J–L). By virtue of being able to separate the role of BslA in biofilm architecture from hydrophobicity, we have shown that both architectural complexity and the hydrophobic layer contribute to protecting the residents from biocides, thus providing an evolutionary advantage to the resident cells. Finally, we have demonstrated that an effective hydrophobic barrier can be generated by a subpopulation of the biofilm, and this finding raises the question of why the whole population has evolved to produce BslA (12) when other biofilm matrix molecules are produced in a bimodal manner (24).

A model can be postulated that explains formation of a BslA layer that is more than one molecule (or dimer) deep at the air interface (Fig. 6). It is known that BslA dimers are orientated longitudinally (tail-to-tail), with only one cap of each dimer able to interact with the air interface at a time (11). The orientation of tetrameric forms of the protein is unclear; however, because dimeric protein is sufficient to give rise to the observed effects, it is not considered further here. Based on the premise that the hydrophobic cap of one dimer can serve as a hydrophobic interface for another dimer, it leads to a scenario where the integument of the biofilm could comprise the dimeric proteins layered against each other (Fig. 6). Furthermore, because monomeric and dimeric BslA are able to coexist in vitro (Fig. 1), the orientation of lateral interactions between BslA molecules is independent from the protein oligomerization state, because both monomeric and dimeric protein are able to flip between cap-in and -out conformations. Thus, the bottom of the biofilm is wetting not just because the protein is monomeric, but because the cap region is also exposed to water; likewise, the top of the biofilm is hydrophobic, not just because BslA forms dimers and tetramers, but because the cap region is also exposed to air. The mechanism(s) by which monomeric BslA gives rise to an architecturally complex biofilm, and the reasons why dimeric protein (at least) is required to give rise to a hydrophobic coat, remain to be elucidated. We have previously observed a correlation between architectural complexity of the biofilm and the ability of BslA variants to form a stable elastic film (14); these previous results are supported by our current findings that chimeric YweA, which forms an unstable film in vitro, can reinstate biofilm hydrophobicity, but not complex architecture. We speculate

![Fig. 6. Model of BslA function. (i) Schematic of a biofilm cross-section depicting the oxygen and redox gradient through the depth of the structure. The blue layer at the air interface represents the BslA hydrophobic coat with a water droplet on top (red circle), and the hatched lines at the base represent BslA in a form that allows water and nutrient uptake into the community. The bacteria are green ovals, and the agar surface is the gray zone at the base of the biofilm. (ii) Oligomerization of BslA is mediated by thiol-oxidoreductases that reside in the membrane and extracytoplasmic space. The electrons (e−) released by oxidation upon formation of the disulfide bond flow into the respiratory chain. BslA is shown as a blue oval in the biofilm matrix (gray). For simplicity, only one disulfide bond has been depicted (S–S). The reduced form of the protein is represented by the (−SH) annotation. (iii) Oligomerization of BslA is also likely to occur using molecular oxygen as the electron acceptor. (iv) Depicted is a model for how the BslA coat might present in the biofilm as a mixture of oligomers. The ability of BslA to present in a cap-in and -out configuration is represented, where the cap-out form is adopted by the molecules at a hydrophobic interface.](Image 0x1 to 19x816)
that the stable elastic film formed by monomeric BslA facilitates an association with another component(s) of the biofilm matrix—for example, the exopolysaccharide. Moreover, consistent with this proposal, an association between different molecular components of the *B. subtilis* biofilm matrix can be presumed, because loss of any individual element leads to impaired structure (19).

**Bifunctionality Through Dimerization.** Cysteine residues, possessing a thiol group (15), have specialized roles in a wide range of cellular processes and control protein folding and stability, multimerization, and function through disulfide bond formation (25). It is clear from our secondary structural analysis (Fig. S2) that the role for disulfide bond formation in modulating BslA activity is not linked with either protein stability or folding, but is instead associated with imparting new function through multimerization. This function is in contrast to the fungal hydroporphins, where disulfide bonds stabilize the structure of the protein (26), and is more analogous to the mechanism used to control activity of the von Willebrand factor during blood clotting (25). Previous bioinformatic analyses revealed that Firmicutes, including *B. subtilis*, limit the number of proteins that contain cysteine residues (27). Consistent with this conclusion, there are no essential components that require disulfide bond formation in the *B. subtilis* biofilm because deletion of the known extracytoplasmic thiol oxidoreductases, bdbA and bdbB, does not lead to pleiotropic defects. It is only when the integrity of hydrophobicity is assessed that differences in the surface wettability are uncovered (Table S2). It has been proposed that in Firmicutes, proteins that contain disulfide bonds have roles in “niches” functions that are not linked with essential cellular processes—for example, genetic competence that allows the uptake of exogenous DNA (21, 28) and production of the S-linked protein sublancin (34). The full details of growth conditions are provided in *SI Materials and Methods*. The analysis of components that are not linked with essential cellular processes that require disulfide bond formation in the *B. subtilis* biofilm because deletion of the known extracytoplasmic thiol oxidoreductases, bdbA and bdbB, does not lead to pleiotropic defects. It is only when the integrity of hydrophobicity is assessed that differences in the surface wettability are uncovered (Table S2). It has been proposed that in Firmicutes, proteins that contain disulfide bonds have roles in “niches” functions that are not linked with essential cellular processes—for example, genetic competence that allows the uptake of exogenous DNA (21, 28) and production of the S-linked protein sublancin (34).

It is well established that oxygen gradients stratify natural, mixed-species biofilms by driving distribution of microorganisms with different respiratory requirements (32–34). Furthermore, the availability of electron acceptors, including oxygen, can drive structuring of biofilm morphology, as has been shown for *Pseudomonas aeruginosa* (35, 36). Therefore, these findings expand the role that oxygen gradients can play in biofilm formation by highlighting an ability to modulate protein function. The ability to respond to localized oxygen heterogeneity in this manner provides an efficient mechanism for bacteria to maximize resource utilization by generating bifunctionality through redox sensitivity. Furthermore, BslA dimerization in response to the oxygen gradient solves the conundrum of how *B. subtilis* obtains nutrients when it is surrounded by a layer of BslA (12) [i.e., the anoxic base of the biofilm is hydrophilic despite the abundance of BslA (Fig. 6)]. We predict that bifunctionality of matrix components will emerge as a common theme across the species. Consistent with this proposal, the *Vibrio cholerae* biofilm matrix protein, RmbA, is proteolytically cleaved to a form that promotes recruitment of cells to the biofilm in an exopolysaccharide-independent manner; effectively, the proteolytic event changes the function of RmbA (37). Additionally, flagella synthesized by *E. coli* are used, not only for motility, but also for imparting structural rigidity to the community by entwining the bacterial cells (38). Control of bifunctionality for each of these examples is distinct and raises the question of how many different mechanisms have evolved to maximize use of a limited number of components.

**Materials and Methods**

Details of all methods used are provided in full in *SI Materials and Methods*.

**Growth Conditions.** The *B. subtilis* strains used and constructed in this study are detailed in Table S1. The full details of growth conditions are provided in *SI Materials and Methods*. Biofilm colonies were grown on M5gg medium (5) solidified with 1.5% Select Agar (Invitrogen) at 30 °C for 48 h.

**Strain Construction.** All strains, plasmids, and primers used are presented in Tables S1, S3, and S4 and were constructed by using standard techniques. See *SI Materials and Methods* for full details.

**ACKNOWLEDGMENTS.** We thank Drs. L. Hobley and L. Caims for initial observations; Prof. F. Sargent for helpful discussions; Dr. A. Ostrowski and Ms. E. Bislett for plasmids and strains; and Profs. Ben-Yehuda and van Dijl for the anti-YweA antibody and the bdbDC mutant, respectively. This work was supported by Biotechnology and Biological Sciences Research Council Grants BB/L00680/1, BB/L006979/1, BB/M013774/1, and BB/N022254/1. The Dundee Imaging Facility, Dundee, supported by Wellcome Trust Technology Platform Award 097945/B/11/Z, helped with experiments. J.J. was supported by NIH Training Grant 5T32GM008798; L.E.P.D. was supported by NIH Grant R01AI103369.