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http://dx.doi.org/10.1111/mmi.12813

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Staphylococcus aureus DivIB is a peptidoglycan-binding protein that is required for a morphological checkpoint in cell division

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Summary

Bacterial cell division is a fundamental process that requires the coordinated actions of a number of proteins which form a complex macromolecular machine known as the divisome. The membrane-spanning proteins DivIB and its orthologue FtsQ are crucial divisome components in Gram-positive and Gram-negative bacteria respectively. However, the role of almost all of the integral division proteins, including DivIB, still remains largely unknown. Here we show that the extracellular domain of DivIB is able to bind peptidoglycan and have mapped the binding to its β subdomain. Conditional mutational studies show that divIB is essential for Staphylococcus aureus growth, while phenotypic analyses following depletion of DivIB results in a block in the completion, but not initiation, of septum formation. Localisation studies suggest that DivIB only transiently localises to the division site and may mark previous sites of septation. We propose that DivIB is required for a molecular checkpoint during division to ensure the correct assembly of the divisome at midcell and to prevent hydrolytic growth of the cell in the absence of a completed septum.

Introduction

Cell division in bacteria requires the coordinated action of a number of proteins which form a complex macromolecular machine known as the divisome (Errington et al., 2003). Many components of the divisome have been shown to be essential for viability: 10 genes involved in cell division are essential in Bacillus subtilis (Kobayashi et al., 2003), Escherichia coli (Buddelmeijer and Beckwith, 2002) and Caulobacter crescentus (Goley et al., 2011), while eight division genes are essential in Streptococcus pneumoniae (Song et al., 2005; van Opijnen et al., 2009). The tubulin homologue FtsZ is the most highly conserved of the division proteins, and FtsZ recruitment into the Z-ring at midcell is the first step in the division process. The Z-ring acts as a scaffold for the recruitment and assembly of subsequent essential and accessory divisome proteins. The divisome is composed of FtsZ-associated proteins (FtsA, ZapA, FtsE/X, [ZipA ZapB ZapC; E. coli], [EzrA, SepF; B. subtilis]), and membrane-spanning proteins (including FtsK, FtsW, FtsQ/DivIB, FtsL, FtsB/DivIC, FtsI/PBP2B, FtsN [E. coli]), many of which are involved in the biosynthesis of septal peptidoglycan (Errington et al., 2003; Schmidt et al., 2004; Ishikawa et al., 2006; Ebersbach et al., 2008).

While key components of the divisome, such as FtsZ, are highly conserved throughout bacterial species, others have diverged significantly (Angert, 2005). This diversity of cell division mechanisms carried out by the set of cell division proteins that comprise the divisome in each species is likely to be influenced by bacterial shape and envelope structures. Most studies of cell division have focused on the rod-shaped model organisms E. coli and B. subtilis. In rods, there are three phases of cell wall synthesis: elongation due to lateral peptidoglycan synthesis, involving MreB/Mbl (Daniel and Errington, 2003; Figge et al., 2004); pre-septal elongation (Typas et al., 2012) and septation due to FtsZ-driven peptidoglycan synthesis at the midcell (Errington et al., 2003), with each process involving two distinct protein complexes. A comprehensive analysis of sequenced bacterial genomes found a correlation between a lack of mreB and non-rod shape, with exceptions of some cyanobacteria and the Chlamydia (Daniel and Errington, 2003). Using coccus-shaped bacteria to study cell division may therefore prove a simpler model due to the lack of cylindrical elongation of the cell wall and thus elimination of potential overlapping roles of cell wall synthesis machineries (Turner et al., 2010).

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Indeed, the human pathogen *Staphylococcus aureus* does not undergo an elongation growth phase but instead synthesises peptidoglycan only at the septum in an FtsZ-dependent manner (Pinho and Errington, 2003), with the septum becoming the nascent hemispherical poles of the daughter cells following cleavage of the septal cell wall. Atomic Force Microscopy (AFM) has been used to study *S. aureus* peptidoglycan architecture and dynamics, and revealed a thickening of peptidoglycan, described as a ‘piecrust’, midcell at the site of the presumptive septum (Turner et al., 2010). After subsequent completion of the septum the piecrust remains as orthogonal ‘ribs’ due to hydrolytic turnover of the cell wall, marking the location of previous division planes.

*Staphylococcus aureus* is a close relative of *B. subtilis*, and homologues of all genes essential for vegetative division in *B. subtilis* are found to be conserved in *S. aureus* (Steele et al., 2011). Accordingly, while there is likely to be a conservation of the cell division process among prokaryotes, much can be learned from comparative studies of morphologically diverse bacteria. There is also a direct interest in studying cell division in coccus-shaped bacteria, as many species are prevalent human pathogens (e.g. *S. pneumoniae, S. aureus, Neisseria meningitidis, Neisseria gonorrhoeae*), and an understanding of cell growth and division in these bacteria may aid in the identification of novel antimicrobial targets.

While there is a degree of conservation of division proteins throughout bacterial species, differences in the essentiality of some of these proteins have been reported in different species. The *ftsQ* gene of *E. coli* is essential, with thermosensitive mutants forming aseptate filaments or filaments with partially formed septa when grown at the non-permissive temperature (Begg et al., 1980; Carson et al., 1991). In *B. subtilis, divIB* is only essential for vegetative growth at high temperatures but is required for sporulation at all temperatures (Beall and Lutkenhaus, 1989; Harry et al., 1993). *Streptomyces coelicolor divIB* is dispensable for mycelial growth but is necessary for sporulation septation to allow the conversion of aerial hyphae into spores (McCormick and Losick, 1996). In *S. pneumoniae, divIB* was found to be non-essential for growth in rich media, although deletion resulted in an altered morphology to longer chains that lysed earlier after the onset of stationary phase, and was essential for nutrient-limited growth (Le Gouellec et al., 2008). A recent large-scale transposon mutagenesis screen of *S. aureus* has suggested that *divIB* is essential for cell viability (Chaudhuri et al., 2009).

Although cell division has been well studied for many decades, the biochemical role of each of the membrane-spanning divisome proteins, with the exception of FtsL (Nguyen-Disteche et al., 1998) and FtsW (Mohammadi et al., 2011), is mostly unknown. A trimeric complex of DivIB, DivIC and FtsL in Gram-positives, and their homologues FtsQ, FtsB and FtsL in Gram-negatives, is conserved in all species for which division protein interactions have been investigated, suggesting functional importance (Buddelmeijer and Beckwith, 2004; Noirclic-Savoye et al., 2005; Daniel et al., 2006). There are strong interdependencies between DivIB, DivIC and FtsL for the stabilisation of this heterocomplex and recruitment to the division site, as well as midcell localisation of penicillin-binding protein (PBP) 2B (FtsI) (Daniel et al., 1998; 2000; 2006; Ghigo et al., 1999; Weiss et al., 1999; Daniel and Errington, 2000; Buddelmeijer et al., 2002). The use of artificial septum targeting and mutagenesis experiments has allowed a model to be constructed that suggests that the DivIB/DivIC/FtsL trimeric complex may play a direct or indirect role in peptidoglycan metabolism at the septum through interactions with PBP2B (Rowland et al., 2010). Interestingly, no DivIB orthologue is found in bacteria lacking cell walls, implying a role in peptidoglycan synthesis or remodelling (Margolin, 2000). Further evidence to support this has previously been reported; the inability of a *B. subtilis divIB* null mutant to sporulate results in a thickening of the polar septa, akin to mutants deficient in sporulation-specific cell wall hydrolases (Thompson et al., 2006). Additionally, coordinate expression of *divIB* and *murB* from the highly conserved *dcw* (division and cell wall) cluster, containing many genes involved in peptidoglycan biosynthesis and cell division, is necessary for growth and sporulation in *B. subtilis* (Real and Henriches, 2006). Finally, an *S. pneumoniae ΔdivIB* mutant shows increased sensitivity to β-lactam antibiotics, whose primary target is the transpeptidase domain of PBPs (Le Gouellec et al., 2008).

DivIB consists of an N-terminal cytoplasmic segment, a single membrane-spanning region and an extracytoplasmic domain. The extracytoplasmic region of DivIB is comprised of three subdomains, α, β and γ (Fig. 1A), as determined by nuclear magnetic resonance spectroscopy of *Geobacillus stearothermophilus* DivIB, small-angle X-ray scattering of *S. pneumoniae* DivIB, and X-ray crystallography of *E. coli* and *Yersinia pestis* FtsQ (Robson and King, 2006; van den Ent et al., 2008; Masson et al., 2009). The α domain shows homology to the POTRA (polypeptide transport-associated) domain, which is thought to act as a molecular chaperone in both prokaryotes and eukaryotes (Sanchez-Pulido et al., 2003). The β domain was shown to contain a rare left-handed connection between parallel β-sheets by NMR spectroscopy (Robson and King, 2006). The γ domain is unstructured and highly variable in length, ranging from ~ 20 residues (e.g. *B. subtilis*) to over 60 residues (e.g. *S. pneumoniae* and *S. aureus*) and is absent from some species (e.g. *Haemophilus influenzae* and *Legionella pneumophila*).
**Fig. 1.** DivIB is a peptidoglycan-binding protein.

A. Schematic representation of the domain architecture of *B. subtilis* and *S. aureus* DivIB. The extracytoplasmic region is separated into three domains, α, β and γ. The numbers correspond to the amino acids at the domain boundaries based on structural alignments with *G. stearothermophilus* DivIB.

B and C. Sedimentation analysis of SaDivIB and BsDivIB, corresponding to the α, β and γ subdomains, binding to *S. aureus* (B) and *B. subtilis* (C) purified peptidoglycan. Recombinant protein was incubated with increasing concentrations of purified peptidoglycan for 2 h at 37°C. Samples were then separated into supernatant (S) and pellet (P) fractions prior to separation using SDS-PAGE.

D. Sedimentation analysis of truncated SaDivIB proteins binding to *S. aureus* purified peptidoglycan. Schematics of the truncations with corresponding amino acid residues are shown on the left, while Coomassie-stained gels of the separated supernatant (S) and pellet (P) fractions are shown on the right.

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Our previous work has revealed that DivIB forms part of the division complex (Steele et al., 2011); however, its role in cell division, and specifically in peptidoglycan metabolism, is still currently unknown. In this study we have shown that *B. subtilis* and *S. aureus* DivIB bind directly to peptidoglycan and represent a novel class of peptidoglycan-binding protein. Furthermore, the binding domain of *S. aureus* DivIB has been mapped. We have used conditional mutation analysis to show that DivIB is required for division of *S. aureus*, being necessary for septal completion, but not initiation. This provides a tool to determine the morphological checkpoints during septation.

**Results**

The extracellular domain of DivIB is a novel peptidoglycan-binding protein

DivIB is a bitopic membrane protein composed of an N-terminal cytoplasmic domain, a membrane-spanning domain and a C-terminal extracytoplasmic region. Domain swapping experiments in *E. coli* and *B. subtilis* have shown that the extracytoplasmic domain of FtsQ and DivIB is topologically separate and sufficient for cell division (Guzman et al., 1997; Katis and Wake, 1999). To investigate putative DivIB biochemical function, the extracytoplasmic domain of DivIB from *B. subtilis* (BsDivIB; residues 54–263) and *S. aureus* (SaDivIB; residues 195–439) were produced as his-tagged recombinant proteins (Supplementary Fig. S1A) and tested for the ability to bind purified peptidoglycan using a sedimentation assay (see Experimental procedures). SaDivIB efficiently bound purified native peptidoglycan in a substrate-concentration-dependent manner (Fig. 1B). Binding of BsDivIB to native peptidoglycan was also observed, although precipitation of the recombinant protein was observed under the conditions used (Fig. 1C). Furthermore, both BsDivIB and SaDivIB bound to non-native peptidoglycan, indicating that the binding ability of DivIB is not affected by the composition of the peptide stem, which contains mesodiaminopimelic acid at residue 3 in *B. subtilis* or L-Lysine, to which a pentaglycine cross bridge binds, in *S. aureus* (Fig. 1B and C). Indeed, it was observed that SaDivIB showed stronger affinity for non-native peptidoglycan compared to native peptidoglycan. This may be due to the availability of binding sites due to lower cross-linking of stem peptides in *B. subtilis* peptidoglycan. Affinity for peptidoglycan was not due to non-specific interactions since binding was not observed for cytochrome C, which has a comparable isoelectric point to SaDivIB (9.5 and 9.34 respectively) or BSA (Supplementary Fig. S1B).

To further determine the domain(s) involved in peptidoglycan affinity, truncations of SaDivIB were tested for the ability to bind peptidoglycan (Fig. 1D). Truncations were made based on alignments with the domain architecture for *G. stearothermophilus* DivIB to attempt to reduce protein misfolding and produced as his-tagged recombinant proteins (Supplementary Fig. S1A). Sedimentation assays revealed that both the α and γ domains are dispensable for peptidoglycan binding of *S. aureus* DivIB. Progressive removal of the N-terminus of the β domain did not abolish affinity for peptidoglycan, inferring that the binding site of SaDivIB lies within the C-terminus of the β domain (residues 333–372). Additionally, removal of the extreme C-terminus of the β domain did not affect the binding of SaDivIB, further mapping the peptidoglycan binding site to residues 334–344 of the β domain. However, all truncations tested in this study showed some degree of affinity for peptidoglycan, and so it cannot be ruled out that another binding site is present, but not essential, for binding under the conditions used in this study. Since the assay used to perform these experiments is qualitative, conclusions could not be drawn about the affinity of DivIB binding to peptidoglycan. Thus, a semi-quantitative method was used to investigate this further.

To investigate peptidoglycan binding semi-quantitatively, SaDivIB was conjugated to the fluorescent dye Cy2 and the peptidoglycan binding kinetics were examined (see Experimental procedures). It was found that a significant amount of non-specific peptidoglycan binding of Cy2-BSA occurred without addition of 0.05% (v/v) Tween 20, and so was subsequently included in the binding buffer in all experiments (Supplementary Fig. S1C, Li and Howard, 2010). SaDivIB bound to purified *S. aureus* peptidoglycan in a concentration-dependent and saturable manner. This binding was dependent on pH, with highest affinity observed at pH5 and greatly reduced binding at higher pH (Fig. 2A).

To determine if increased affinity for peptidoglycan at lower pH correlates with physiologically relevant conditions, protonation of *S. aureus* cell walls was investigated by measurement of the total amount of cell wall-bound fluorescence using FITC, a pH-sensitive dye with an optimal pH range of 7–9 (Calamita et al., 2001). Unprotonated bacterial cell walls result in available linkage sites for FITC, while cell walls possessing a lower pH greatly reduces the concentration of aliphatic amines which results in lower FITC binding. Here, similar results for FITC conjugation to cell walls were observed for *S. aureus* to that previously reported for *B. subtilis* (Calamita et al., 2001). Cell walls were more readily labelled at pH 8 after dissipation of the proton motive force (pmf), using DCCD, resulting in loss of the low pH cell wall and an equilibrium of pH of the cell wall and surrounding environment: de-energised cells show an increase in FITC binding because of unprotonation of the cell walls by pmf disruption (Supplementary Fig. S2A and B). Hence, optimal binding of Cy2-SaDivIB to

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Peptidoglycan at pH 5 is likely to reflect the physiological conditions of the native protein. Peptidoglycan binding of DivIB was abolished by the addition of 1 M NaCl, indicating ionic interactions between DivIB and substrate. Addition of Mg\(^{2+}\) cations did not affect DivIB affinity for peptidoglycan. It was found however that a higher amount of Cy2-SaDivIB was dissociated from peptidoglycan during the wash stages in the absence of magnesium cations compared to the presence of cations (4 ± 0.2% lost compared to 1 ± 0.1% at the highest Cy2-SaDivIB concentration tested), suggesting that magnesium cations may act to stabilise the interaction between DivIB and peptidoglycan.

The presence of teichoic acids was found to reduce the affinity of a known peptidoglycan-binding protein (Utsui and Yokota, 1985) (S. aureus Cy2-PBP1) for peptidoglycan (data not shown). To investigate if the same was true for Cy2-SaDivIB, binding kinetics were analysed using either SDS- and pronase-treated broken S. aureus cell walls (peptidoglycan plus teichoic acids), or purified S. aureus peptidoglycan that had been chemically stripped of teichoic acids (Fig. 2B). An apparent K\(_d\) of 550 ± 56 nM could be calculated, representing the concentration of Cy2-SaDivIB giving half-maximum binding, for binding to cell walls (peptidoglycan plus teichoic acids). A K\(_d\) of 134 ± 9 nM was observed for binding to peptidoglycan stripped of teichoic acids, indicating higher affinity for the peptidoglycan backbone. To confirm that differences in binding affinity was due to teichoic acids and not caused by chemical modification of cell walls during the purification process, purified S. aureus ΔtagO peptidoglycan, which is devoid of teichoic acids due to deletion of the enzyme responsible for the first step in of wall teichoic acid synthesis, was used as substrate. An apparent K\(_d\) of 221 ± 81 nM was calculated, indicating that the presence of teichoic acids decreases the affinity of DivIB for peptidoglycan, presumably due to masking of available binding sites.

S. aureus DivIB localises transiently at midcell

Immunoblot analysis of native B. subtilis DivIB showed the protein to be associated with the cytoplasmic membrane, and also the cell wall in vivo (Harry et al., 1993). The ability of S. aureus DivIB to bind to cell wall in vivo was therefore determined using α-DivIB antiserum. S. aureus DivIB associated with both cytoplasmic membrane and cell wall fractions (Fig. 3A). It is unlikely that detection of DivIB in the cell wall fraction was due solely to contamination with unfractinated cells and/or membranes, as immunoblot analysis using antiserum against S. aureus YneS, a known membrane-bound protein (J. Garcia-Lara, unpublished) showed only minimal detection in the cell wall fraction.

Bacterial two-hybrid analysis has previously indicated that DivIB is a component of the S. aureus divisome (Steele et al., 2011). Initial attempts to determine the subcellular localisation of DivIB utilised a C-terminal GFP fusion protein (ALB2; SH1000 divIB-gfp pGL485). Unexpectedly, no obvious midcell localisation of DivIB-GFP was observed. Instead, two or three discrete peripheral foci on each cell, or each hemisphere of dividing cells, were detected (Fig. 3B). A line of fluorescence was also sometimes observed that connected two of the peripheral foci. It may be that this localisation pattern is due to the degradation of GFP due to fusion to the C-terminus of DivIB and

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thus export outside the cytoplasm. However, immunofluorescence microscopy with α-DivIB antibodies showed a similar localisation pattern at that seen for DivIB-GFP (data not shown).

To fully confirm localisation of *S. aureus* DivIB, and to exclude any potential polar effects on downstream genes due to expression of the fusion proteins, an N-terminal YFP fusion protein was constructed. Strain ALB26-yfp (SH1000 ΔdivIB geh::PSpac eYFP-divIB) expresses a single copy of yfp-divIB under the control of PSpac ectopically inserted at lipase based on the pCL84 integrase system (Lee et al., 1991). YFP-DivIB was found to localise in a range of different patterns, including two foci or line of fluorescence at the presumptive midcell, as single focus at the cell membrane, or as uniform fluorescence throughout the membrane of the cell (Fig. 3C). These results confirm the localisation patterns observed using DivIB-GFP and immunolocalisation, suggesting that DivIB localisation at midcell in *S. aureus* may only be transient.

**DivIB is essential for *S. aureus* growth**

*Staphylococcus aureus* divIB, SAOUHSC_01148, was identified to be putatively essential by a high-density transposon screen for genes important for cell viability (Chaudhuri et al., 2009). Bioinformatic analysis of the *S. aureus* divIB chromosomal regions indicated that the gene is part of the dcw cluster and is located directly upstream of ftsA and ftsZ (Fig. 4A). Initial attempts to confirm essentiality of divIB involved construction of a *S. aureus* conditional mutation. However, due to the complexity of transcription of the dcw cluster and likely polar effects on downstream ftsA2, the role of divIB could not be established using this method (data not shown).

To overcome this, and to determine the role of divIB, a conditional mutant was constructed where a full-length copy of divIB under the control of PSpac was inserted ectopically at the geh locus, allowing an in-frame deletion of the gene from its native chromosomal location without disruption of expression of downstream genes (Fig. 4B). To ensure minimal expression from PSpac in the absence of inducer, lacI was constitutively overexpressed from a multicopy plasmid, pGL485 (Cooper et al., 2009), resulting in strain ALB27 (geh::PSpac-divIB ΔdivIB pGL485). ALB27 did not grow in the absence of inducer (IPTG), whereas in the presence of IPTG ALB27 had a growth rate comparable to wild-type strain VF17 (SH1000 pGL485) both on solid and in liquid media (Fig. 4C). ALB27 (geh::PSpac-divIB ΔdivIB pGL485) was also unable to grow on agar plates in the absence of IPTG.
absence of IPTG when incubated at 30°C (data not shown). Therefore, *divIB* is essential for growth of *S. aureus*.

Depletion of DivIB results in increased cell size

To investigate the effect of DivIB depletion on cellular morphology, ALB27 (*geh::P<sub>spec</sub>-divIB ΔdivIB pGL485*) was examined following growth in the absence or presence of the inducer IPTG. In the presence of inducer, cells showed a similar morphology to wild-type cells (Fig. 5A). However, after 2 h incubation in the absence of inducer, ALB27 cells showed an increased cell size. It is important to note that this morphology differs to that previously observed for *S. aureus* depleted of FtsZ (Pinho and Errington, 2003) or EzrA (Steele *et al.*, 2011), which results in very large spherical single cells. DivIB-depleted *S. aureus* cells showed a range of phenotypes, including misplacement of septa resulting in ‘hamburger’ cells due to initiation of new rounds of septum formation in parallel planes without the...
completion of previous rounds of septation, bulging of the cell wall and eventual lysis (Fig. 5A). Measurement of cells found that in the presence of 1 mM IPTG, the mean cell diameter of ALB27 was similar to wild-type VF17 cells (mean diameter = 1 ± 0.2 μm, n = 768 and 0.9 ± 0.1 μm, n = 363 respectively). In the absence of inducer, cells showed an increased cell size (mean diameter = 1.5 ± 0.4 μm, n = 980). A small proportion of ALB27 cells showed an increased cell size (> 1.25 μm) even at 1 mM IPTG, indicating that expression of DivIB from the Spac promoter doesn’t fully restore cellular morphology. However, this phenotypic change was most notable in the absence of inducer, with a high proportion of very large cells up to 3.5 μm in diameter seen (Fig. 5B). Western blot analysis shows undetectable levels of DivIB after growth in the absence of inducer (Fig. 5C), indicating the observed morphology is due to depletion of DivIB.

**DivIB is required for completion, but not initiation, of septum formation**

Previous work has shown that *S. aureus* synthesises cell wall specifically at the septum, and that nascent cell wall synthesis is dispersed or does not occur in the absence of early components of the divisome (Pinho and Errington, 2003; Steele *et al.*, 2011). To investigate if DivIB plays a
role in the synthesis of cell wall, a fluorescent derivative of vancomycin (Van-Fl) was used to label nascent peptidoglycan in DivIB-depleted cells. Almost all wild-type S. aureus cells (VF17; SH1000 pGL485) and ALB27 (geh::Pspa-divIB ΔdivIB pGL485) grown in the absence or presence of IPTG showed septal peptidoglycan synthesis (Fig. 6A). However, different staining morphologies were observed for VF17 and ALB27 grown in the presence of inducer compared to ALB27 cells grown in the absence of IPTG. Forty-eight per cent of VF17 cells and 43% of ALB27 cells grown in the presence of IPTG showed either a ring or line of fluorescence at midcell, and 23% and 22%, respectively, showed an ‘x’ or ‘y’ staining pattern, characteristic of separating newly formed daughter cells (Fig. 6B, Turner et al., 2010). A large proportion (75%) of ALB27 cells grown in the absence of inducer also showed a midcell staining pattern. In addition, 13% of DivIB-depleted cells showed multiple or aberrant fluorescent rings. These unusual staining patterns were observed exclusively in cells > 1.25 μm, indicating misplacement of the cell wall biosynthesis machinery. Further analysis of midcell staining found that 72% and 52% of VF17 and induced ALB27 cells showed a ring of fluorescence at the division site which corresponds to a ring of new peptidoglycan, and 28% and 33% (VF17 and ALB27 respectively) showed a fluorescent line across the cell, corresponding to a plate of nascent peptidoglycan that is the completed septum (Fig. 6C). In the absence of IPTG, ALB27 cells showed a ring of fluorescence that appeared to be equivalent to the cell diameter. Only a small proportion of DivIB-depleted cells appeared to form complete septa (12%), presumably due to residual DivIB present from prior to DivIB-depletion. Growth of S. aureus has been proposed to occur in between cell division events via specific hydrolysis of existing cell wall material (Turner et al., 2010). A distinct ring of nascent peptidoglycan between two cells was also often observed, indicating that cells are undergoing hydrolytic growth of the cell wall in the absence of the formation of complete septa. Thus, in the absence of DivIB, initiation of septum formation is not affected, resulting in the synthesis of a large ‘band’ (piecrust) of nascent peptidoglycan at midcell. However the ensuing formation of the septal plate is blocked.

Scanning electron microscopy of ALB27 (geh::Pspa-divIB ΔdivIB pGL485) grown in the absence of IPTG revealed a band of cell wall at midcell which was not detectable in wild-type cells (VF17) or ALB27 cells grown in the presence of IPTG (Fig. 7A), and may represent the piecrust. This is likely due to the continued hydrolytic growth and turnover of the existing cell wall of DivIB-depleted cells in the absence of new septum formation, revealing cell wall architecture not observed in wild-type cells. Transmission electron microscopy of DivIB-depleted cells also confirmed the misplacement of septa, resulting in more than one initiation site within dividing cells, bulging of the cell wall and cell lysis (Fig. 7B).

To investigate the architecture of the cell wall in the absence of DivIB in more detail, atomic force microscopy (AFM) of purified sacculi of ALB27 (geh::Pspa-divIB ΔdivIB pGL485) cells grown in the absence of inducer was performed. Thick bands of peptidoglycan were observed, confirming the formation of piecrusts in cells depleted of DivIB (Fig. 7C). Incomplete septa were also occasionally seen, and may represent cells that were at different stages of the cell cycle when cell division was blocked by depletion of DivIB. Thus, investigation of the macromolecular architecture of the cell wall in the absence of DivIB confirms the results observed for fluorescence microscopy, resulting in the initiation of septation and the formation of the piecrust. However, completion of septum formation is severely affected in the absence of DivIB.

Localisation of cell division proteins in the absence of DivIB

The significant increase in cell size and misplacement of septa in S. aureus cells depleted of DivIB suggests that recruitment of the divisome to the midcell may be altered in the absence of this protein. The effect of DivIB depletion on the ability of divisome components to localise to midcell was therefore investigated.

In B. subtilis, EzrA localises to the midcell in an FtsZ-dependent manner where it is thought to be a negative regulator of Z ring formation (Levin et al., 1999). Time-lapse microscopy has shown that EzrA localises concomitantly with FtsZ, with a time delay of at least 20% of the cell cycle before late proteins, including DivIB, assemble at midcell (Gamba et al., 2009). Previous analysis of the role of EzrA in S. aureus has shown that the protein likely acts as a scaffold for the assembly of the divisome (Jorge et al., 2011; Steele et al., 2011). It was therefore investigated if depletion of DivIB, a late division protein, affected the localisation of the early protein EzrA in S. aureus. Localisation of EzrA in VF104 (ezrA-GFP+ pGL485) and ALB30 (ezrA-GFP+ geh::Pspa-divIB ΔdivIB pGL485) was determined using a C-terminal GFP+ fusion. Fluorescence was detected as a ring or line at the septum in almost all VF104 cells and ALB30 grown in the presence of IPTG (Fig. 8A). Midcell localisation of EzrA-GFP+ was also observed for the majority of ALB30 cells grown in the absence of IPTG with a cell diameter < 1.25 μm (Fig. 8B). However, for ALB30 cells with a diameter > 1.25 μm, a striking localisation pattern was observed, with fluorescence almost exclusively observed as multiple or aberrantly formed rings. Interestingly, EzrA-GFP+ ring size appeared to be equivalent to the cell diameter for large DivIB-depleted cells. Furthermore, the localisation pattern...
Role of DivIB in peptidoglycan biosynthesis.

A. Van-Fl labelling of nascent cell wall synthesis in VF17 (WT; SH1000 pGL485) and ALB27 (geh::PSpac-divIB ΔdivIB pGL485) grown for 120 in the presence (1) or absence (0) of 1 mM IPTG. Scale bar = 4 μm.

B. Frequency of Van-Fl staining cellular phenotypes of VF17 (WT; SH1000 pGL485) and ALB27 (geh::PSpac-divIB ΔdivIB pGL485) grown for 120 in the presence (1) or absence (0) of 1 mM IPTG. Cells were given one of five Van-Fl staining phenotypes in relation to cell diameter. The number of cells measured was 278, 362 and 421 respectively.

C. Frequency of midcell Van-Fl staining cellular phenotypes of VF17 (WT; SH1000 pGL485) and ALB27 (geh::PSpac-divIB ΔdivIB pGL485) grown for 120 in the presence (1) or absence (0) of 1 mM IPTG. Midcell Van-Fl staining phenotypes were assigned as a plate or ring of nascent peptidoglycan as determined by analysis of Z stacks of cells. The number of cells measured was 134, 153 and 306 respectively.

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Fig. 7. Role of DivIB in cellular morphology.
A and B. Scanning (A) and transmission (B) electron micrographs of VF17 (WT, SH1000 pGL485) and ALB27 (geh::Pspac-divIB ΔdivIB pGL485) grown for 120 min in the presence (1) or absence (0) of 1 mM IPTG. Scale bar in A = 2 μm. White arrowheads in A depict bands of peptidoglycan observed at midcell. Black arrowheads in B show sites aberrant sites of septum initiation.
C. AFM height (H) and phase (P) images of VF17 (WT; SH1000 pGL485) and ALB27 (geh::Pspac-divIB ΔdivIB pGL485) sacculi purified from cells grown in the presence (1) and absence (0) of IPTG. Scale bar = 1 μm. Scales: WT H 150 nm; ALB27 (1) H 150 nm; ALB27 (0) left hand panel H 250 nm; right hand panel H 150 nm.

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of EzrA-GFP+ suggests that EzrA is still recruited to midcell, perhaps through interactions with FtsZ.

Recruitment of all known division proteins to the midcell occurs in an FtsZ-dependent manner (Errington et al., 2003). In order to determine FtsZ localisation in the absence of DivIB, and to investigate if EzrA is recruited to midcell in an FtsZ-dependent DivIB-independent manner,
Fig. 8. cont.

C

EzrA-GFP+

α-FtsZ

Overlay

D

E

WT

% frequency

0 5 10 15 20 25 30 35 40 45 50

WT

foci

dispersed

midcell

1

% frequency

0 5 10 15 20 25 30 35 40 45 50

1

foci

dispersed

midcell

0

% frequency

0 2 4 6 8 10 12 14 16 18 20

0

aberrant rings

foci

dispersed

midcell

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presence of IPTG (Fig. 8C). Additionally, FtsZ immuno-fluorescence in ALB33 cells grown in the absence of inducer showed the formation of large, sometimes aberrant, midcell rings which coincided with EzrA-GFP+ localisation. Thus, while FtsZ can polymerise into the Z ring and recruit EzrA to midcell in the absence of DivIB, constriction of the Z ring and progression of the division cycle is blocked.

Although *ezrA* is not essential in *B. subtilis*, deletion of *ezrA* in combination with *gpsB* results in severe defects in lateral and septal peptidoglycan synthesis as a result of perturbed PBP1 localisation (Claessen et al., 2008). Direct interactions have been observed between EzrA and GpsB in both *B. subtilis* and *S. aureus* (Claessen et al., 2008; Steele et al., 2011). It was therefore investigated if GpsB showed a similar localisation pattern to EzrA in DivIB-depleted *S. aureus* using a C-terminal GpsB-GFP+ fusion protein. GpsB-GFP+ fluorescence was observed as a line or ring in the majority of wild-type (VF94, *gpsB-GFP*+ pGL485) and ALB31 (*gpsB-GFP*+ *geh::Pspac-divIB ΔdivIB* pGL485) cells grown in the presence of IPTG (Fig. 8D). A bright focus of fluorescence was also often observed between two daughter cells that were undergoing separation, indicating that GpsB remains at the site of division after septum formation is complete. In ALB31 cells grown in the absence of inducer, a larger proportion of cells showed a dispersed fluorescence pattern compared to VF94 (33% compared to 8% respectively; Fig. 8E). Dispersed localisation of GpsB-GFP+ in DivIB-depleted cells was independent of cell size, indicating that, unlike EzrA, DivIB is required for localisation of GpsB at midcell.

Depletion of DivIB in *S. aureus* cells does not affect initiation of septation, but results in a cessation of completion of septum formation. To investigate if the inability to form complete septa in the absence of DivIB is due to mislocalisation of cell wall synthetic enzymes (PBPs), a fluorescent derivative of penicillin, Bocillin 650/665, was used. *S. aureus* encodes four PBPs, three of which have previously been shown to localise to midcell in wild-type cells (Pinho and Errington, 2005; Pereira et al., 2007; Attilano et al., 2010). Midcell localisation of the PBPs was observed for both control VF17 (SH1000 pGL485) cells and ALB27 (*geh::Pspac-divIB ΔdivIB* pGL485) cells grown...
in the presence and absence of IPTG (Fig. 8F). Staining of nascent cell wall with Van-Fl revealed that the PBPs localised at the leading edge of forming septa. Furthermore, PBPs were located to aberrant rings in DivIB-depleted cells. Thus the inability of S. aureus cells to complete septum formation is not due to mislocalisation of cell wall synthetic enzymes, but due to depletion of DivIB.

A strong interdependency between DivIB, DivIC and FtsL has been previously established (Daniel et al., 1998; 2006; Ghigo et al., 1999; Daniel and Errington, 2000; Buddelmeijer et al., 2002). It is therefore possible that the inability of S. aureus to complete septum formation is not due directly to depletion of DivIB, but may be due to the instability of the DivIB/DivIC/FtsL complex. To investigate this, localisation of DivIC in DivIB-depleted cells was performed (Fig. 8G). However, DivIC-GFP+ fluorescence was observed as punctate foci or as a diffuse signal in wild-type cells (AFK5, divIC-GFP+ pGL485). Fluorescence was also diffuse in AFK24 (divIC-GFP+ geh::Pspec− divIB ΔdivIB pGL485) cells grown in the presence or absence of IPTG, with no defined localisation pattern observed. Thus, the role of S. aureus DivIC in septum completion could not be established.

**Discussion**

DivIB is a bitopic protein that consists of an N-terminal domain, a membrane-spanning domain and an extracytoplasmic region that is comprised of three separate domains (α, β and γ). In this study we have shown that the extracytoplasmic domain of S. aureus and B. subtilis DivIB binds peptidoglycan, and that both the α and γ domains are dispensable for this function. Although peptidoglycan hydrolase activity of DivIB has been previously suggested (Thompson et al., 2006), no such enzymatic activity was detected in this present study (data not shown). Domain replacement studies have shown that the extracytoplasmic domain of B. subtilis DivIB, or the orthologous periplasmic domain of E. coli FtsQ, is essential for function (Buddelmeijer et al., 1998; Katis and Wake, 1999; Chen et al., 2002), suggesting that affinity for peptidoglycan may be important for DivIB function. Although dispensable for interaction with the cell wall, the α domain is important for septal localisation (Goehring et al., 2007; Wadsworth et al., 2008) and interactions with a range of division proteins (Karimova et al., 2005; D’Ullisse et al., 2007; Goehring et al., 2007; Grenga et al., 2010). The extreme C-terminus of the γ domain, while not required for septal localisation, is also needed for function and protein–protein interactions in E. coli and B. subtilis (Chen et al., 2002; Karimova et al., 2005; Robson and King, 2006; Goehring et al., 2007). Thus, while the α and γ domains of DivIB are not necessary for peptidoglycan binding, they are essential to ensure correct localisation and interaction with the rest of the divisome. Furthermore, the β domain has been shown to be important for interaction with division proteins (Goehring et al., 2007; Masson et al., 2009; Rowland et al., 2010) and for function (Harry et al., 1993; Le Gouellec et al., 2008). The ability of S. aureus DivIB to bind peptidoglycan via the C-terminal region of the β domain (as predicted from alignments with G. stearothermophilus DivIB) does not interfere with domains previously reported as important for function in other species.

Several proteins involved in cell division have been previously characterised as containing a peptidoglycan-binding domain. FtsN is a bitopic cell division protein, with only the periplasmic SPOR (Pfam 23)-containing domain essential for function (Dai et al., 1996). FtsN has been shown to bind peptidoglycan (Ursinus et al., 2004; Muller et al., 2007), with the SPOR domain of E. coli FtsN sufficient to mediate midcell localisation (Moll and Thanbichler, 2009; Arends et al., 2010). Midcell localisation of three E. coli proteins, DamX, DedD and RlpA, is also dependent on the presence of a SPOR domain (Gerding et al., 2009). PASTA domains (Pfam 03793) are found mainly in Gram-positive species and are present in the C-terminus of high-molecular-weight PBPs (Yeats et al., 2002). Crystal structure analysis of S. pneumoniae PBP2x in complex with the β-lactam cefuroxime indicates that PASTA domains recognise unlinked peptidoglycan through van der Waal’s forces (Gordon et al., 2000). Three groups recently reported the characterisation of C. crescentus DipM, a cell division-specific peptidoglycan hydrolase (Goley et al., 2010; Moll et al., 2010; Poggio et al., 2010). Bioinformatic analysis of DipM revealed presence of LysM domains (Pfam 01476), with removal of these domains markedly impairing recruitment to midcell (Moll et al., 2010). LysM domains have also been shown to be present in the cell division-associated protein E. coli NlpD (Uehara et al., 2010), and the SOS-inducible division inhibitors Mycobacterium tuberculosis Rv2719c (Chauhan et al., 2006) and B. subtilis YneA (Mo and Burkholder, 2010). However, S. aureus DivIB shows no homology to any peptidoglycan-binding domain previously described for a cell division protein, or indeed to any protein without a recognisable peptidoglycan-binding domain, while structural alignments reveal homology only within the POTRA (α) domain. Therefore, it is likely that DivIB represents a novel class of peptidoglycan-binding protein. This function is conserved, at least among closely related Gram-positive species (this study). The ability of FtsQ to bind peptidoglycan would give insights into the conservation of function among species which have low sequence homology to DivIB of Gram-positive species.

Construction of an S. aureus conditional-lethal mutation of divIB has shown that this gene is essential for growth in this organism. The orthologous ftsQ of E. coli is also

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essential for growth (Begg et al., 1980; Carson et al., 1991), while divIB essentiality studies in the Gram-positives B. subtilis and S. pneumoniae have found the gene to be dispensable under certain conditions (Beall and Lutkenhaus, 1989; Harry et al., 1993; Le Gouellec et al., 2008), suggesting some functional redundancy between different organisms.

The ability of EzrA and FtsZ to localise at midcell in the absence of DivIB indicates that DivIB is not involved in the early stages of the division process. However, DivIB-depleted S. aureus cells were blocked in progression of the division cycle, showing that while early components of the divisome are recruited in a DivIB-independent manner, the assembly of the complete divisome is needed for the physical act of septum formation. It may be that DivIB is directly or indirectly involved in the regulation of activity of cell wall synthesising proteins, most likely through protein–protein interactions. Extensive studies have also shown that DivIB/FtsQ interacts with many division proteins (e.g. Di Lallo et al., 2003; Buddelmeijer and Beckwith, 2004; Karimova et al., 2005; Noirclic-Savoye et al., 2005; Steele et al., 2011). Further investigation is needed to fully understand the importance of DivIB interactions with divisome components in regulating cell wall metabolism.

Interestingly, in large DivIB-depleted cells Z-ring diameter was apparently equivalent to the cell diameter, indicating FtsZ constriction did not occur without septum formation. Using membrane-targeted FtsZ in an in vitro liposome system it has been shown that Z-rings can undergo constriction in the absence of any other protein (Osawa et al., 2008). However, complete division of liposomes was not observed, indicating that while FtsZ alone is sufficient for Z-ring formation and initiation of constriction, a component(s) of the divisome is required for completion of septation.

While S. aureus DivIB is not required for recruitment of early division proteins, it was found that GpsB localises in a DivIB-dependent manner, indicating a possible hierarchy of midcell assembly of S. aureus division proteins with GpsB being a late recruited protein. E. coli FtsQ is required for FtsI (Pbp3) localisation (Weiss et al., 1998), while there are strong interdependencies between DivIB, DivIC and FtsL for their recruitment to the division site (Daniel et al., 1998; Daniel and Errington, 2000). It has been suggested that GpsB midcell recruitment may be dependent on DivIB/DivIC/FtsL/Pbp2B in B. subtilis (Tavares et al., 2008), although no interaction has been observed between DivIB and GpsB in S. aureus (Steele et al., 2011). Thus, requirement of DivIB for GpsB localisation may be through indirect interactions with another component(s) of the divisome.

Although cell division has been studied for many decades, the role of late division proteins in septum formation are still poorly understood. In this study we have shown that in S. aureus the septum appears to be formed in two stages with DivIB-independent synthesis of a large ring or ‘band’ of peptidoglycan equivalent to the diameter of the dividing cell, followed by completion of the septum, which requires DivIB. In ovococci such as S. pneumoniae, two types of division-specific cell wall synthesis have been previously described, with synthesis of peripheral cell wall occurring prior to septum formation. Isolation of temperature-sensitive mutants or treatment of ovococci with division-inhibiting concentrations of antibiotics results in filamentation of cells (Higgins et al., 1974; Gibson et al., 1983; Lleo et al., 1990), indicating some longitudinal growth in the absence of septation and suggesting a model of cell wall synthesis with similarities to that reported for rod-shaped bacteria. S. aureus only undergoes a single mode of peptidoglycan synthesis (Pinho and Errington, 2003). Thus, to our knowledge this is the first example of a true coccus which undergoes two phases of division-specific cell wall synthesis.

Recent AFM analysis of purified S. aureus sacculi has found the peptidoglycan architecture to be comprised of a thickening of peptidoglycan, described as a ‘piecrust’ at the site of the presumptive septum (Turner et al., 2010). After division, this structure remains as orthogonal ‘ribs’, marking the location of previous division planes. The initial ring of peptidoglycan synthesis observed in DivIB-depleted S. aureus correlates to the cell wall piecrust which may act as a buttress to stabilise the cell wall during the remodelling process to form the new septum. A similar phenomenon has been observed indirectly in S. aureus cells depleted of PBP1, with depleted cells showing signs of initiation of septation but only a small percentage with completed septa (Pereira et al., 2007). This observation appears to be specific for PBP1, as PBP2-depleted cells are not affected in formation of septa, although are affected in septum placement (Pinho et al., 2001), while PBP3-deleted S. aureus shows no morphological defects (Pinho et al., 2000). Thus, DivIB may act in concert with PBP1 to ensure correct formation of septum through either direct interaction with PBP1 or its substrate to regulate enzymatic activity and/or by indirect interactions with other components of the S. aureus divisome.

Based on the results presented in this study, we propose that DivIB is required for a morphological checkpoint for the completion of septum formation in S. aureus. The divisome assembles at midcell through direct interactions; FtsZ, EzrA and probably the PBPs are recruited independently of DivIB, although some DivIB is likely recruited, perhaps in an inactive form, based on previous interaction studies (Steele et al., 2011). Assembly of these proteins at midcell is sufficient to initiate septation, resulting in the formation of the piecrust, a thick band of peptidoglycan that has been suggested to act as a brace to allow dividing cells to withstand changes in cell pressure during hydrolytic

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growth of the nascent septal peptidoglycan (Turner et al., 2010). In DivIB-depleted cells, the piecrust was formed but progression of septum completion was blocked, suggesting that DivIB acts as a checkpoint to stop cells undergoing hydrolytic growth, leading to eventual lysis, in the absence of completed septa. Initiation of septum completion may occur through direct interactions of DivIB with the piecrust, and/or with DivI acting as a molecular connector for the recruitment and assembly of early and later division proteins (such as GpsB), to allow septum completion. It should be noted that DivIC and/or FtsL may also be required for this function, although this could not be established during this study. The misplacement of septa in DivIB-depleted cells also implies that DivIB may play a role in correct septum placement, perhaps through recognition of the piecrust peptidoglycan architecture that marks previous division planes. It could be speculated that the localisation pattern observed for YFP-DivIB in this study correlates to accumulation of DivIB at specific peptidoglycan architectures: after division the thick band of peptidoglycan (piecrust) that is present during septum formation remains as orthogonal ribs, marking the location of previous division planes. The peptidoglycan ribs remain as half or quarter ribs in subsequent divisions due to each daughter cell inheriting an old cell pole from previous rounds of division (Turner et al., 2010). Localisation of DivIB on piecrusts and ribs would result in discrete foci or a line pattern, depending on the orientation and the Z plane sectioning through the cell. Interestingly, DivIB localisation in S. pneumoniae was restricted to old hemispheres immediately after division rather than future division sites (Noircierc-Savoye et al., 2005), suggesting a difference in old and nascent peptidoglycan structure and/or architecture that is specifically recognised by DivIB. It has also been recently shown that Shigella flexneri FtsQ is required for the localisation of the IcsA autotransporter at the cell poles, and that the extracytoplasmic domain of FtsQ is required for this localisation (Fixen et al., 2012), further implying a role for DivIB/FtsQ in correct localisation of protein complexes within the cell, perhaps through direct recognition of specific cell wall features.

Thus, work in this study has revealed that DivIB is an important component of the bacterial divisome. Furthermore, investigation of the role of conserved division proteins in organisms of different cellular morphologies provides a useful tool to determine the morphological checkpoints during septation.

**Experimental procedures**

**Bacterial strains, plasmids, and oligonucleotides**

The bacterial strains and plasmids used in this study are shown in Table 1, while oligonucleotide sequences used are shown in Table 2.

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**Growth conditions and media**

Escherichia coli, S. subtilis and S. aureus strains were grown in Luria–Bertani broth (LB; Oxoid), nutrient broth (NB; Oxoid) or brain heart infusion broth (BHI; Oxoid), respectively, at 37°C unless otherwise stated. For growth on solid media, 1.5% (w/v) agar was added. When necessary, the medium was supplemented with erythromycin (5 μg ml⁻¹), chloramphenicol (30 μg ml⁻¹), tetracycline (5 μg ml⁻¹), ampicillin (100 μg ml⁻¹), kanamycin (50 μg ml⁻¹), spectinomycin (100 μg ml⁻¹), 5-bromo-4-chloro-3-indolyl β-D-thiogalactopyranoside (X-Gal, 80 μg ml⁻¹) or isopropyl β-D-thiogalactopyranoside (IPTG, 1 mM).

Transformations of S. aureus RN4220 were carried out as previously described (Schenk and Laddaga, 1992). Phage transductions of S. aureus using Φ11 were carried out as described by Novick and Morse (1967). General DNA manipulation and transformation of E. coli was performed using the method of Sambrook and Russell (2001).

**Construction of an S. aureus divIB-inducible strain**

Attempts to make a DivIB null mutant were carried out using the thermosensitive plasmid pMAD (Amaud et al., 2004). PCR fragments containing ~1 kb flanking regions of divIB were amplified from genomic DNA of SH1000 using primers ALB27/ALB28 and ALB29/ALB30 which encoded an internal KpnI restriction site to allow in-frame fusion of the upstream and downstream regions. After KpnI digestion and ligation of the two PCR products the resulting DNA fragment underwent a second PCR reaction using primers ALB27/ALB30. This resulting DNA fragment was digested with BamHI and EcoRI and cloned into pMAD to create pALB29. The plasmid was electroporated into RN4220 at 30°C and subsequently transduced into SH1000 to produce strain ALB16. Several attempts were carried out to isolate a colony in which the deletion of divIB was completed due to a two-step homologous recombination event by passing of ALB16 at 42°C. However, only a single-crossover event, resulting in the integration of pALB29 into the chromosome, was achieved. Deletion of genes by two-step homologous recombination of pMAD relies of the assumption that deletion of the target gene does not affect cell viability. To ensure resolution of pALB29 from the chromosome was not being hindered by the essentiality of divIB for cell growth, a chromosomal ectopic copy of divIB under the control of Pspac was introduced to allow inducible expression of divIB during growth at the permissive temperature. The DNA fragment corresponding to the RBS and coding region of divIB under the control of Pspac was PCR amplified from pALB21 using primers ALB127/ALB128. The PCR product was digested with Smal and BamHI and cloned into pCL84 (Lee et al., 1991). The resulting plasmid, pALB49, was transformed into RN4220 containing pCL112Δ19, a constitutively expressed multi-copy plasmid containing the integrase gene without the attP site (Lee et al., 1991). Correct integration of the plasmid into the chromosome was verified by PCR using primers ALB127/ALB128 and by disruption of lipase production on Baird-Parker medium (Oxoid). The chromosomal region, including the plasmid insertion, was then transferred to ALB16 via Φ11 transduction at 30°C. The
resulting strain contained pALB29 inserted in the chromosome due to a single-crossover event and \( P_{\text{spa}}-\text{divIB} \) inserted ectopically at lipase. Colonies in which the deletion of \( \text{divIB} \) due to a double-crossover event, resulting in the excision of the integrated plasmid, were then selected by passing recombinants at 42°C in the absence of erythromycin. Colonies that showed erythromycin sensitivity and were not blue on X-gal were screened by PCR using primers ALB27/ALB30, and deletion of \( \text{divIB} \) was confirmed by Southern blotting to produce strain ALB26. To allow controlled expression of \( \text{divIB} \) from \( P_{\text{spa}} \), pGL485, a multi-copy plasmid carrying lacI (Cooper et al., 2009), was introduced into ALB26 by \( \Phi 11 \) transduction in the presence of 1 mM IPTG to create strain ALB27.

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**Table 1.** Plasmids and bacterial strains used in this study.

<table>
<thead>
<tr>
<th>Plasmid</th>
<th>Relevant genotype/markers</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>pMAD</td>
<td><em>E. coli</em>-S. aureus shuttle vector with temperature-sensitive origin of replication in S. aureus and promoterless bgaB; (Amp', Ery')</td>
<td>Amaud et al. (2004)</td>
</tr>
<tr>
<td>pCL84</td>
<td><em>S. aureus</em> recombination vector with attP site of L54a; (Spec', Tet')</td>
<td>Lee et al. (1991)</td>
</tr>
<tr>
<td>pGL485</td>
<td>Chloramphenicol-resistant derivative of pMJ8426; (Spec', Cam')</td>
<td>Cooper et al. (2009)</td>
</tr>
<tr>
<td>pGL601</td>
<td>pET-21d SaDivIB; (Amp')</td>
<td>This study</td>
</tr>
<tr>
<td>pGL617</td>
<td>pMUTIN-GFP+ divIC; (Amp', Ery')</td>
<td>This study</td>
</tr>
<tr>
<td>pALB17</td>
<td>pET-21d SaIγ (Amp')</td>
<td>This study</td>
</tr>
<tr>
<td>pALB18</td>
<td>pET-21d SaIγ (Amp')</td>
<td>This study</td>
</tr>
<tr>
<td>pALB21</td>
<td>pAIH1 carrying a 1349 bp fragment containing RBS and coding region of <em>S. aureus</em> divIB; (Amp', Tet')</td>
<td>This study</td>
</tr>
<tr>
<td>pALB22</td>
<td>pAIH1 carrying an 803 bp fragment containing RBS and 5' region of <em>S. aureus</em> DivIB; (Amp', Tet')</td>
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<tr>
<td>pALB23</td>
<td>pET-21d BsDivIB; (Amp')</td>
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<tr>
<td>pALB29</td>
<td>pMAD containing a 0.95 Kb fragment of the upstream region of <em>S. aureus</em> divIB fused in frame to a 1.2 Kb fragment of the downstream region of <em>S. aureus</em> divIB; (Amp', Ery')</td>
<td>This study</td>
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<td>pET-21d SaIγ Δ263–291; (Amp')</td>
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</tr>
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<td>pALB40</td>
<td>pET-21d SaIγ Δ345–372; (Amp')</td>
<td>This study</td>
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<tr>
<td>pALB47</td>
<td>pCL84 ( P_{\text{spa}}-\text{divIB} ); (Spec', Tet')</td>
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<tr>
<td>pKASBAR-kan</td>
<td>pUC18 containing attP and kan cassette; (Amp', Kan')</td>
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<tr>
<td>pALB53*</td>
<td>pMUTIN4 yfp-divIB; (Amp')</td>
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<td>pKASBAR-kan ( P_{\text{spa}}-\text{yfp-divIB} ); (Amp', Kan')</td>
<td>This study</td>
</tr>
</tbody>
</table>

**E. coli**

- BL21 (DE3) F::ompT hsdS2 (r- m-) gal dcm lacY1 (DE3)
- Lab strain

**B. subtilis**

- 168 trpC2
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**Source**

- 2011, 1041–1064 (2011)
- 2011, 1041–1064 (2011)

**Genotype/Markers**

- Ery', erythromycin resistant; Tet', tetracycline resistant; Kan', kanamycin resistant; Cam', chloramphenicol resistant; Amp', ampicillin resistant; Spec', spectinomycin resistant.
### Table 2. Primers used in this study.

<table>
<thead>
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<td>S. aureus divIB extracytoplasmic domain</td>
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<tr>
<td>GLUSH341C3’</td>
<td>ATAATACTCGAGATTATTCTTACTTGATTGTTTGTTG</td>
<td>S. aureus divIB extracytoplasmic domain</td>
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<tr>
<td>GLUSh378C5’</td>
<td>ATAATAGGTACCTGGAGGTACAAGCAATGAAAAATAATAGTAG</td>
<td>Upstream region of S. aureus divIC</td>
</tr>
<tr>
<td>GLUSh378C3’</td>
<td>ATAATACGCCGTTTTTGAATCTTACCTTATCCTTATTTGAATTTGTT</td>
<td>Coding region of S. aureus divIC</td>
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<td>ALB12</td>
<td>ATAATACCATGCTTCACTTGTAAATTGCGCATG</td>
<td>S. aureus divIB β domain</td>
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<td>ALB14</td>
<td>ATAATACCATGCTTCACTTGTAAATTGCGCATG</td>
<td>S. aureus divIB γ domain</td>
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<td>S. aureus divIB β domain</td>
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<td>ATAATACCATGCTTCACTTGTAAATTGCGCATG</td>
<td>B. subtilis divIB extracytoplasmic domain</td>
</tr>
<tr>
<td>ALB18</td>
<td>ATAATACCATGCTTCACTTGTAAATTGCGCATG</td>
<td>B. subtilis divIB extracytoplasmic domain</td>
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<td>ALB19</td>
<td>TTTTTTGGATCCTTAATTATTCTTACTTGATTGTTTG</td>
<td>Upstream flanking region of S. aureus divIB</td>
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<td>ALB22</td>
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Restriction sites are underlined.
Construction of fluorescent derivatives of S. aureus DivIB and DivIC

To create an N-terminal YFP fusion of DivIB, yfp was amplified from SU492 (B. subtilis ftsZ-yfp) (Feucht and Lewis, 2001) using primers yfp_for and yfp_rev and ligated to divIB, which had been amplified from SH1000 genomic DNA using primers ALB139 and ALB140, using an Xhol cut site that had been introduced during PCR amplification. The product was digested with HindIII and BamHI and inserted into pMUTIN4 (Vagner et al., 1998) resulting in plasmid pALB53. A PCR fragment including yfp-divIB under control of the Spac promoter was then amplified from pALB53 using primers ALB141 and ALB140. To insert P_spac-yfp-divIB ectopically at the lipase gene of the S. aureus chromosome, a high copy number of pCLB4 (Lee et al., 1991) was created by amplifying a DNA fragment containing attP and the tet cassette from pCLB4 using primers ALB135/ALB136 and inserting into pUC18 using SphI and EcoRI cut sites, creating pKASBAR. The tet cassette was then removed and replaced with the kan cassette by HindIII digestion and ligating. The resulting plasmid, pKASBAR-kan, was then digested with EcoRI and BamHI to allow insertion of P_spac-yfp-divIB to create plasmid pALB54-kan.

The resultant plasmid, pALB54-kan, was firstly electroporated into RN4220 containing pCL112Δ19 (Lee et al., 1991) before being transduced into ALB26 (SH1000 geh::P_spac-divIB ΔdivIB) and kanamycin-resistant/tetracycline-sensitive colonies were selected. The resulting strain, ALB26-yfp (SH1000 geh::P_spac-yfp-divIB ΔdivIB), expressed an IPTG-inducible single copy of yfp-divIB.

To construct a C-terminal GFP fusion of DivIC, divIC was amplified from SH1000 using primers GLUSh378C3’ and GLUSh378C3’and ligated into pMUTIN-Gfp+ (Kaltwasser et al., 2002). The resulting plasmid, pGL617, was transformed into S. aureus RN4220. Integration of the plasmid into the chromosome occurred via a single-crossover event, resulting in divIC-gfp fusion under the control of the native divIC promoter and a native copy of divIC under the control of P_spac. The plasmid insertion was transferred into VF17 via ɸ11 transduction to create strain AFK5, and into ALB27 to create strain A FK24.

Generation of antibodies

Anti-DivIB and anti-FtsZ polyclonal antibodies were obtained from a rabbit immunised with purified his-tagged recombinant S. aureus DivIB and FtsZ (BioServ UK, UK).

Fluorescence imaging

For fluorescence microscopy, cells from a mid-exponential-phase culture were fixed with formaldehyde and glutaraldehyde as previously described (Pinho and Errington, 2003). For phenotypic imaging of IPTG-inducible strains, cells were depleted of the appropriate protein as described in Steele et al. (2011) before fixation of cells. Immunofluorescence imaging was carried out as basically described in Pinho and Errington (2003). Permeabilisation of the cell wall was carried out by lysozostaphin digestion at a range of concentrations (20–200 ng ml⁻¹) for 1 min. Primary antibodies were used at the following dilutions: rabbit anti-FtsZ at 1:2000 and rabbit anti-DivIB at 1:100. The secondary antibody used was anti-rabbit IgG Alexa Fluor 594 conjugate (Invitrogen). Fluorescence images were acquired using an Olympus IX70 deconvolution microscope and SoftWoRx 3.5.0 software (Applied Precision).

Electron microscopy

The DivIB conditional mutant strain (ALB27) was grown with 0.2 mM IPTG until mid-exponential phase. The culture was washed three times with BHI, diluted in pre-warmed BHI to an initial OD600 of 0.01 and grown with or without 1 mM IPTG for 2 h. All samples were fixed overnight in ice-cold 3% (v/v) gluteraldehyde in 0.1 M sodium phosphate buffer pH 7.4. Cell pellets were washed twice in the same buffer before post-fixation with 2% (w/v) osmium tetroxide for 1 h. Following a further buffer-wash step, cells were dehydrated using a graded ethanol series. For SEM samples, cells were then air dried from hexamethydisilazane using a 1:1 mix of ethanol and hexamethydisilazane, followed by 100% (v/v) hexamethydisilazane. Once dried, samples were mounted on 12.5 mm stubs, attached with carbon-sticky tabs and coated in Edwards S150B sputter coater with approximately 25 nm gold. Samples were analysed in a Philips XL-20 scanning electron microscope at an accelerating voltage of 20 kV. For TEM samples, ethanol-dried samples were incubated in propylene oxide before infiltration of the samples was carried out at room temperature overnight using a 1:1 mix of propylene oxide and araldite resin. Samples were then cut as before and stained with 3% uranyl acetate and 0.5% (w/v) lead citrate for 48–72 h at 60°C. Electron micrographs were taken using a Gatan digital camera.

Preparation of S. aureus and B. subtilis sacculi

Sacculi were prepared using the method previously described (Turner et al., 2010). Briefly, exponentially growing cultures (OD600 ~ 0.5) were collected, boiled for 7 min and broken by FastPrep. Broken cells were then suspended in 5% (w/v) SDS and boiled for 25 min. Insoluble material was collected by centrifugation and the pellet was resuspended in 4% (w/v) SDS and subsequently boiled for 15 min. SDS was removed from samples by repeated washing with distilled water. The resulting pellets were then resuspended in Tris-HCl (50 mM pH 7) containing 2 mg ml⁻¹ pronase and incubated at 60°C for 90 min, followed by a single dH2O wash step. To removed teichoic acids, pellets were resuspended in 250 μl hydrofluoric acid and incubated overnight at 4°C, before being washed six times in distilled water. Samples were stored at −20°C.

Atomic force microscopy

AFM was carried out as previously described (Turner et al., 2010). A dilution of sacculi were dried onto freshly cleaved
mica and washed three times with Milli-Q water using a stream of nitrogen. Tapping mode with silicon tips in ambient conditions using a Multimode or Dimension AFM with an Extended Nanoscope Illa controller (Veeco Instruments) was performed. Images were analysed using Gwyddion and ImageJ.

**Cell wall binding assays**

The ability of DivIB to bind to peptidoglycan was investigated using the method based on Kern et al. (2008). Briefly, samples of a total volume of 200 μl, in binding buffer (20 mM sodium citrate pH 5 10 mM MgCl₂), containing 0.1 mg ml⁻¹ protein and different concentrations of peptidoglycan (0.5, 0.25, 0.125 and 0.0625 mg ml⁻¹) were incubated for 2 h at 37°C. Peptidoglycan, and any associated protein, was separated from unbound protein by centrifugation at 14 000 r.p.m. for 10 min before washing twice in buffer (20 mM sodium citrate pH 5 10 mM MgCl₂). Equal amounts of supernatant and pellet were then separated on an 11% (w/v) SDS-PAGE gel.

To investigate binding of fluorescent protein to purified peptidoglycan, recombinant proteins were firstly labelled with Cy2 bis-reactive dye (GE Healthcare) using the method described in Schlag et al. (2010). Unconjugated dye was separated from labelled protein by dialysis against excess 50 mM sodium phosphate 0.5 M NaCl (pH 7.2) before storage of the conjugated protein at −20°C. To investigate the peptidoglycan binding kinetics of Cy2-labelled protein, 0.25 mg ml⁻¹ peptidoglycan was incubated with a range of concentrations of Cy2-labelled protein in a final volume of 200 μl in various binding buffers containing 0.05% (v/v) Tween 20 Tween 20 (either 20 mM sodium citrate pH 5, 20 mM potassium phosphate pH 7.2 or 20 mM Tris pH 9.5 ± 10 mM MgCl₂) at room temperature for 5 min. Insoluble peptidoglycan and associated protein was removed by centrifugation and the remaining pellet was washed in the appropriate binding buffer to remove non-specifically bound protein. Bound fluorescent protein was released using 200 μl of 10% (w/v) SDS in two SDS wash steps to ensure complete release of all peptidoglycan-bound protein. Cy2-BSA was included as a negative control. Binding was determined by fluorescence measurement at 525 nm using a Victor™ X3 multilabel reader, and the concentration of bound Cy2-labelled protein was calculated.

**Acknowledgements**

We are grateful to Chris Hill for assistance with electron microscopy, and to Kasia Wacnik and Bartek Salamaga for the construction of pKASBAR. This work was funded by the Biotechnology and Biological Sciences Research Council (Grant BB/H011005/1). The authors declare no conflict of interest.

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Supporting information

Additional supporting information may be found in the online version of this article at the publisher’s web-site.