Cell Shape and Antibiotic Resistance Are Maintained by the Activity of Multiple FtsW and RodA Enzymes in Listeria monocytogenes

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ABSTRACT Rod-shaped bacteria have two modes of peptidoglycan synthesis: lateral synthesis and synthesis at the cell division site. These two processes are controlled by two macromolecular protein complexes, the elongasome and divisome. Recently, it has been shown that the Bacillus subtilis RodA protein, which forms part of the elongasome, has peptidoglycan glycosyltransferase activity. The cell division-specific RodA homolog FtsW fulfills a similar role at the divisome. The human pathogen Listeria monocytogenes carries genes that encode up to six FtsW/RodA homologs; however, their functions have not yet been investigated. Analysis of deletion and depletion strains led to the identification of the essential cell division-specific FtsW protein, FtsW1. Interestingly, L. monocytogenes carries a gene that encodes a second FtsW protein, FtsW2, which can compensate for the lack of FtsW1, when expressed from an inducible promoter. L. monocytogenes also possesses three RodA homologs, RodA1, RodA2, and RodA3, and their combined absence is lethal. Cells of a rodA1 rodA3 double mutant are shorter and have increased antibiotic and lysozyme sensitivity, probably due to a weakened cell wall. Results from promoter activity assays revealed that expression of rodA3 and ftsW2 is induced in the presence of antibiotics targeting penicillin binding proteins. Consistent with this, a rodA3 mutant was more susceptible to the β-lactam antibiotic cefuroxime. Interestingly, overexpression of RodA3 also led to increased cefuroxime sensitivity. Our study highlights that L. monocytogenes genes encode a multitude of functional FtsW and RodA enzymes to produce its rigid cell wall and that their expression needs to be tightly regulated to maintain growth, cell division, and antibiotic resistance.

IMPORTANCE The human pathogen Listeria monocytogenes is usually treated with high doses of β-lactam antibiotics, often combined with gentamicin. However, these antibiotics only act bacteriostatically on L. monocytogenes, and the immune system is needed to clear the infection. Therefore, individuals with a compromised immune system are at risk to develop a severe form of Listeria infection, which can be fatal in up to 30% of cases. The development of new strategies to treat Listeria infections is necessary. Here we show that the expression of some of the FtsW and RodA enzymes of L. monocytogenes is induced by the presence of β-lactam antibiotics, and the combined absence of these enzymes makes bacteria more susceptible to this class of antibiotics. The development of antimicrobial agents that inhibit the activity or production of FtsW and RodA enzymes might therefore help to improve the treatment of Listeria infections and thereby lead to a reduction in mortality.

KEYWORDS FtsW, Listeria monocytogenes, RodA, SEDS, antibiotic resistance, cell division


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Bacterial cells are surrounded by a mesh of peptidoglycan (PG) that determines their shape and also protects the cells from lysis due to their high internal turgor pressure (1–3). Peptidoglycan is comprised of glycan strands that are cross-linked by short peptides (4). The glycan strands are composed of alternating N-acetylglucosamine and N-acetylmuramic acid residues that are connected by a β-1,4 glycosidic bond (5). The synthesis of peptidoglycan begins in the cytoplasm with the production of the PG precursor lipid II by the proteins MurABCDEF, MraY and MurG (6–9). Lipid II is then transported across the cytoplasmic membrane by the flippase MurJ and Amj (10–12) and subsequently incorporated in the growing glycan strand by glycosyltransferases. The polymerization and cross-linking of the glycan strands are facilitated by the activity of glycosyltransferases and transpeptidases, respectively. Class A penicillin binding proteins (PBPs) are bifunctional enzymes that possess glycosyltransferase and transpeptidase activity, whereas class B PBPs contain only a transpeptidase domain (13–15). In addition, some species such as Escherichia coli, Staphylococcus aureus, and Streptococcus pneumoniae carry genes that encode monofunctional glycosyltransferases (MGTs) that can also incorporate lipid II into the growing glycan strand (16–20).

* Bacillus subtilis * contains genes that encode four class A PBPs and no MGT; however, deletion of all class A PBPs manifests in only small PG changes (21). Recently, it has been shown that members of the SEDS (shape, elongation, division, sporulation) family of proteins, namely, RodA and FtsW, also act as glycosyltransferases (22–25). Both RodA and FtsW form complexes with cognate class B PBPs to enable polymerization and cross-linking of glycan strands (23, 25–28). Interestingly, SEDS proteins and the class B PBPs are more conserved among different bacterial species than class A PBPs are (22).

In rod-shaped bacteria, peptidoglycan is synthesized by two multiprotein complexes, the elongasome that is essential for the cell elongation and the divisome that is crucial for the formation of the division septum (29–32). RodA is part of the elongasome and is essential in many bacteria, including *B. subtilis* and *S. pneumoniae* (33, 34). Depletion of RodA results in the production of enlarged, spherical cells in *B. subtilis* (34). In contrast, FtsW is essential for cell division, and cells depleted for FtsW grow as long filaments (35–37). *B. subtilis* harbors a sporulation-specific member of the SEDS family, SpoVE in addition to RodA and FtsW. SpoVE is dispensable for growth, but it is essential for the synthesis of the spore cortex peptidoglycan (38, 39). Other *Bacillus* species such as *B. cereus* and *B. anthracis* possess four or five FtsW/RodA proteins, and strains of different serotypes of the human pathogen *Listeria monocytogenes* carry genes that encode even up to six FtsW/RodA homologs in their genome. However, their functions have not yet been investigated.

Here, we determined the roles of the different FtsW and RodA homologs for the growth and cell morphology of *L. monocytogenes*. Our results show that *L. monocytogenes* carries genes that encode two FtsW enzymes and three RodA enzymes. The absence of either FtsW1 or of all three RodA proteins is lethal under standard laboratory conditions. *L. monocytogenes* infections are usually treated with high doses of β-lactam antibiotics such as ampicillin, which inhibit the transpeptidase activity of penicillin binding proteins (PBPs) (40). We demonstrate that the expression of two SEDS proteins, FtsW2 and RodA3, is induced in the presence of β-lactam antibiotics likely to compensate for the inhibition of PBPs and that a rodA3 mutant is more sensitive to the β-lactam antibiotic cefuroxime. Antimicrobial agents inhibiting the activity of proteins of the SEDS family could therefore potentially improve the treatment of *Listeria* infections in the future.

**RESULTS**

*L. monocytogenes* 10403S carries genes that encode six FtsW/RodA homologs. So far, FtsW and RodA proteins of the human pathogen *L. monocytogenes* have not been studied. FtsW and RodA are members of the SEDS (shape, elongation, division, sporulation) family of proteins and are multistranding membrane proteins with 8 to 10 transmembrane helices and a large extracellular loop (Fig. 1A). Using BLAST, six proteins with homology to the *B. subtilis* FtsW and RodA proteins could be identified in the

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The genome of *L. monocytogenes* 10403S (Table 1). The protein encoded by *lmo0421* has the weakest homology to *B. subtilis* FtsW and RodA (Table 1; see also Fig. S1 in the supplemental material). *lmo0421* is part of the *sigC* operon, which is comprised of *lmo0422* encoding the PadR-like repressor LstR and *lmo0423* coding for the ECF-type sigma factor SigC (Fig. 1B). The *sigC* operon acts as a lineage II-specific heat shock system (41) and is therefore not present in all *L. monocytogenes* genomes. Due to the weak homology to FtsW and RodA and its absence in *L. monocytogenes* strains of lineage I and III, Lmo0421 was excluded from further analysis.

The *L. monocytogenes* protein Lmo1071 is the closest homolog to *B. subtilis* FtsW with a sequence identity of 48% (Table 1). Furthermore, *L. monocytogenes* Lmo1071 and *B. subtilis* ftsW are found in the same chromosomal context. More specifically, Lmo1071 is located between the *lmo1070* gene, which encodes a protein with homology to the *B. subtilis* YlaN protein, and the *pycA* gene coding for the pyruvate carboxylase, which

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**TABLE 1** Sequence homology between *B. subtilis* and *L. monocytogenes* FtsW/RodA proteins as determined by BLAST

<table>
<thead>
<tr>
<th><em>L. monocytogenes</em> protein</th>
<th><em>B. subtilis</em> FtsW (403 aa)</th>
<th><em>B. subtilis</em> RodA (393 aa)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lmo0421 (416 aa)</td>
<td>46/128 aa (36%) [7e−14]</td>
<td>77/350 aa (22%) [4e−09]</td>
</tr>
<tr>
<td>FtsW1 (Lmo1071) (402 aa)</td>
<td>195/403 aa (48%) [1e−122]</td>
<td>100/333 aa (30%) [7e−35]</td>
</tr>
<tr>
<td>RodA1 (Lmo2427) (391 aa)</td>
<td>124/403 aa (31%) [9e−29]</td>
<td>132/360 aa (37%) [1e−57]</td>
</tr>
<tr>
<td>RodA2 (Lmo2428) (389 aa)</td>
<td>112/374 aa (30%) [1e−33]</td>
<td>159/402 aa (40%) [1e−66]</td>
</tr>
<tr>
<td>RodA3 (Lmo2687) (369 aa)</td>
<td>95/324 aa (29%) [3e−25]</td>
<td>110/356 aa (31%) [3e−44]</td>
</tr>
<tr>
<td>FtsW2 (Lmo2688) (376 aa)</td>
<td>147/342 aa (43%) [5e−67]</td>
<td>95/300 aa (32%) [6e−22]</td>
</tr>
</tbody>
</table>

*The *L. monocytogenes* proteins and their amino acid sizes (aa) are shown in the leftmost column, and the *B. subtilis* FtsW (403 aa) and RodA (393 aa) proteins used for the homology search are indicated at the top of the middle and right columns.*

*The number of amino acids, which were found to be identical between the respective *L. monocytogenes* and *B. subtilis* FtsW/RodA protein are denoted (before the slash) along with the number of amino acids that was utilized by the BLAST algorithm for this comparison (after the slash). The percent identity is given in parentheses, and the corresponding E values are indicated in brackets.*
are also adjacent to ftsW in B. subtilis. This analysis suggests that the lmo1071 gene encodes the cell division protein FtsW. However, L. monocytogenes carries a gene that encodes a second protein, Lmo2688, which shares a higher degree of homology to the B. subtilis FtsW than to the B. subtilis RodA protein (Table 1). Due to these similarities and additional data presented in this study, we refer to Lmo1071 and Lmo2688 as FtsW1 and FtsW2, respectively.

The BLAST search with the B. subtilis RodA sequence as a query sequence yielded the L. monocytogenes protein Lmo2428 as the closest homolog with a sequence identity of 40% (Table 1). In addition to Lmo2428, two additional RodA homologs are present in L. monocytogenes, namely, Lmo2427 and Lmo2687. As presented below, Lmo2427, Lmo2428, and Lmo2687 are likely bona fide RodA homologs and were therefore renamed RodA1, RodA2, and RodA3, respectively. rodA1 is located adjacent to rodA2, but despite their proximity, rodA1 and rodA2 are likely not transcribed as part of the same operon (42). In contrast, rodA3 and ftsW2 are part of the four-gene operon lmo2689-lmo2686. Lmo2689 is similar to a Mg2+-type ATPase, whereas lmo2686 encodes a protein of unknown function. Analysis of around 2,000 genomes of L. monocytogenes strains presently available at NCBI revealed that the five FtsW/RodA homologs named here, FtsW1 and RodA1, RodA2, and RodA3, are conserved in the different strains.

Imo1071 encodes FtsW1 and is essential for the survival of L. monocytogenes. The cell division protein FtsW is essential for growth in the Gram-negative and Gram-positive model organisms E. coli and B. subtilis (35, 36, 39, 43). Depletion of FtsW in these organisms leads to a block in cell division and formation of elongated cells (36, 37). All our attempts to delete the ftsW1 gene in L. monocytogenes 10403S were unsuccessful, suggesting that FtsW1 is also essential for growth in Listeria. Next, strain 10403SΔftsW1 ftsW1 was constructed, in which the expression of ftsW1 is controlled by an IPTG-inducible promoter. While no difference in growth was observed between the wild-type and FtsW1 depletion strain (likely due to leakiness of the inducible promoter) (Fig. 2A), cells depleted of FtsW1 were significantly elongated (Fig. 2B and C). Bacteria depleted of FtsW1 had a median cell length of 3.41 ± 0.16 μm, while wild-type and 10403SΔftsW1 ftsW1 bacteria grown in the presence of 1 mM IPTG had a median cell length of 2.09 ± 0.16 μm.
length of 1.85 ± 0.16 μm and 1.93 ± 0.07 μm, respectively (Fig. 2C). These data indicate that lmo1071 encodes the cell division-specific SEDS protein FtsW.

*L. monocytogenes carries a gene that encodes a second FtsW protein.* To our knowledge, all bacteria analyzed so far possess only one FtsW protein that is essential for cell survival. We identified a second potential FtsW protein, Lmo2688, in *L. monocytogenes*. In contrast to ftsW1, an *L. monocytogenes* ftsW2 deletion strain could be constructed, and no significant growth or cell morphology phenotypes could be observed for the ΔftsW2 deletion strain (Fig. 52). In a previous study, it was reported that the operon comprised of genes lmo2689-lmo2686 is only minimally expressed when *L. monocytogenes* 10403S is grown in BHI broth (44). We reasoned that if ftsW2 does indeed code for a second FtsW protein, it should be possible to delete ftsW1 in a strain in which ftsW2 is artificially expressed from an IPTG-inducible promoter. Indeed, strain 104035ΔftsW1 lftsW2 could be generated in the presence of IPTG. In contrast, we were unable to generate strain 104035ΔftsW1 lftsW2 when any of the other FtsW/RodA homologs Lmo2427 (RodA1), Lmo2428 (RodA2), or Lmo2687 (RodA3) were expressed from the same IPTG-inducible promoter system. While prolonged depletion of FtsW2 in strain 104035ΔftsW1 lftsW2 again had no impact on growth, the cells were significantly elongated in the absence of the inducer compared to the wild type or bacteria grown in the presence of inducer (Fig. 3). These data strongly suggest that ftsW2 encodes a second FtsW enzyme, while the remaining three proteins, Lmo2427, Lmo2428, and Lmo2687, likely function as RodA proteins.

*L. monocytogenes carries genes that encode three RodA homologs.* We were able to assign roles for two of the FtsW/RodA homologs as FtsW-like proteins. However, *L. monocytogenes* carries genes that encode three additional homologs, which show a higher similarity to the *B. subtilis* RodA protein compared to the *B. subtilis* FtsW protein (Table 1). As described above, expression of none of the enzymes Lmo2427, Lmo2428, or Lmo2687 was able to rescue the growth of an ftsW1 deletion strain, indicating that these enzymes likely function as RodA proteins in *L. monocytogenes*, and hence, they were renamed RodA1, RodA2, and RodA3, respectively. All attempts to construct a rodA1 rodA2 rodA3 triple mutant failed, further corroborating that these proteins function as RodA proteins and that at least one of them needs to be present for cell viability. To determine whether the different RodA homologs have distinct functions or whether they are merely duplications, single and double mutant strains were generated. No significant differences with regard to growth and cell length could be observed between the wild-type strain 10403S and single rodA1, rodA2, or rodA3 deletion strains (Fig. S3). Similar observations were made with the rodA double mutant strains 10403SΔrodA1ΔrodA2 and 10403SΔrodA2ΔrodA3 (Fig. 4). However, cells lacking
RodA1 and RodA3 are essential to maintain the rod shape of *L. monocytogenes.* (A) Growth of *L. monocytogenes* 10403S (wt), 10403SΔrodA1ΔrodA2, 10403SΔrodA1ΔrodA3, and 10403SΔrodA2ΔrodA3 strains in BHI broth at 37°C. (B) Microscopy images of wt and mutant *L. monocytogenes* strains. Cells from the strains described above for panel A were stained with the membrane dye Nile red and analyzed by fluorescence and phase-contrast microscopy. Bar, 2 μm. (C) Cell length measurements of wt and mutant *L. monocytogenes* strains. The cell length of 300 cells per strain was measured, and the median cell length was calculated and plotted. Three independent experiments were performed, and the average and standard deviation of the median cell length was plotted. For statistical analysis, a one-way ANOVA coupled with a Dunnett’s multiple comparison test was used (*, \( P \leq 0.05 \)). (D) Microscopy images of wild-type and mutant *L. monocytogenes* strains. Cells from 10403S (wt), 10403SΔrodA1ΔrodA3 (−), and 10403SΔrodA1ΔrodA3 expressing rodA1 (+rodA1), rodA2, or rodA3 from an IPTG-inducible promoter were stained with the membrane dye Nile red, and analyzed by fluorescence and phase-contrast microscopy. Bar, 2 μm. (Continued on next page)
RodA1 and RodA3 were shorter (1.3 ± 0.03 μm) than wild-type cells (1.9 ± 0.06 μm; Fig. 4B and C), indicating that either RodA1 or RodA3 needs to be present for *L. monocytogenes* to maintain its rod shape. RodA3 is part of the lmo2689-lmo2686 operon that is only minimally expressed when *L. monocytogenes* is grown in BHI broth (44). The fact that we observe differences in cell morphology between a rodA1 single mutant and the rodA1 rodA3 double mutant suggests that the function of the two proteins could be additive or that rodA3 expression, which is only minimally expressed in a wild-type strain under standard laboratory growth conditions, might increase upon deletion of rodA1. To test whether rodA3 expression is increased in the absence of other RodA proteins, we fused the promoter upstream of lmo2689 and driving rodA3 expression to lac2 and inserted this fusion into the chromosome of wild-type 10403S, the rodA1 and rodA1 rodA2 deletion strains. The promoter activity was indeed 1.5- to 2-fold higher in the rodA1 and rodA1 rodA2 mutant strains compared to the wild type, as assessed by the increase in the β-galactosidase activity (Fig. 4G). This result indicates that expression of the lmo2689-lmo2686 operon, which encodes FtsW2 and RodA3, is induced in the absence of RodA1, suggesting a coordination of the expression of the different RodA homologs.

To confirm that the decrease in cell length of the double mutant strain 10403SΔrodA1ΔrodA3 depends on the absence of RodA1 and RodA3, complemented strains with IPTG-inducible expression of rodA1 or rodA3 were constructed. Expression of RodA1 restored the cell length to 1.84 ± 0.1 μm, which is comparable to the cell length of wild-type cells (1.76 ± 0.15 μm; Fig. 4E). On the other hand, expression of rodA3 from an ectopic locus and IPTG-inducible promoter in strain 10403SΔrodA1ΔrodA3 led to the formation of longer cells with an average cell length of 2.47 ± 0.01 μm (Fig. 4D and E). These results indicate that induction of RodA3 from the IPTG-inducible promoter likely results in overproduction of the protein compared to expression from the native promoter. To confirm that rodA3 expression is increased when expressed from the IPTG-inducible promoter compared to its native promoter, rodA3 transcript levels were assessed by qRT-PCR in the wild-type strain, the 10403SΔrodA1ΔrodA3 deletion strain, and strain 10403SΔrodA1ΔrodA3 irodA3 grown in the presence of IPTG (Fig. 4H). Significant higher rodA3 transcript levels were detected in the inducible strain in the presence of IPTG compared to the wild-type strain. Similarly, expression of rodA3 from an IPTG-inducible promoter in wild-type 10403S led to the formation of elongated cells with an average cell length of 2.49 ± 0.08 μm, whereas additional expression of rodA1 or rodA2 using the same inducible system had no impact on the cell length of 10403S (Fig. 4S). These results highlight that in particular fine-tuning of RodA3 production is essential for cell length determination in *L. monocytogenes*.

The observation that the rodA1 rodA3 double mutant forms shorter cells suggests that RodA2 is not sufficient to maintain the cell length of *L. monocytogenes*. There are several possible explanations for this. RodA2 might have a reduced activity compared to RodA1 or RodA3. RodA2 might have a function that is different from the functions of RodA1 and RodA3 or the protein levels of RodA2 might be sufficient to maintain cell

**Fig 4** Legend (Continued)

Phase-contrast microscopy. Bar, 2 μm. (E and F) Cell length analysis of 10403SΔrodA1ΔrodA3 complemented strains. Analysis was performed as described above for panel C. (G) β-Galactosidase assay using *L. monocytogenes* strains 10403S (wt), 10403SΔrodA1ΔrodA3, and 10403SΔrodA1ΔrodA3 carrying a P<sub>lmo2689</sub>-lacZ fusion construct. Averages and standard deviations of three independent experiments were plotted. For statistical analysis, a one-way ANOVA coupled with a Dunnett’s multiple-comparison test was used (*, *P* ≤ 0.05). (H) Analysis of rodA3 expression by qRT-PCR. RNA was isolated from strains 10403S (wt), 10403SΔrodA1ΔrodA3 (−), and 10403SΔrodA1ΔrodA3 irodA3 grown in the presence of IPTG. Expression of rodA3 was normalized to the expression of gyrB, and fold changes were calculated using the ΔΔCT method. Averages and standard deviations of three independent experiments were plotted. For statistical analysis, a one-way ANOVA coupled with a Dunnett’s multiple-comparison test was performed (**, *P* ≤ 0.01). (I) Analysis of rodA2 expression using qRT-PCR. Same as panel H but using strains 10403S, 10403SΔrodA1ΔrodA3 (−), and 10403SΔrodA1ΔrodA3 irodA2 grown in the presence of IPTG. Averages and standard deviations of three independent experiments were plotted. For statistical analysis, a one-way ANOVA coupled with a Dunnett’s multiple-comparison test was performed (*, *P* ≤ 0.05).
viability but too low to maintain the rod shape. To investigate this further, a strain was constructed that lacks rodA1 and rodA3 but carries pIMK3-rodA2 to allow for IPTG-inducible expression of rodA2 in addition to the expression of rodA2 from its native locus (10403SΔrodA1ΔrodA3 irodA2). In the absence of the inducer, the cells had a median cell length of 1.2 \pm 0.03 \mu m (data not shown). However, the cell length of strain 10403SΔrodA1ΔrodA3 irodA2 increased to 1.71 \pm 0.8 \mu m when the strain was grown in the presence of IPTG (Fig. 4F). Therefore, additional expression of rodA2, which was verified by qRT-PCR (Fig. 4I), can partially complement the cell length phenotype of the rodA1 rodA3 deletion strain, suggesting that RodA2 has a function similar to that of RodA1 and RodA3 but that it has either a lower activity or is not expressed in sufficient amounts from its native promoter for proper cell length maintenance.

As stated above, several attempts to construct a strain inactivated for all three RodA homologs remained unsuccessful, suggesting that at least one of the proteins RodA1, RodA2, or RodA3 needs to be present for the viability of L. monocytogenes. The results presented so far indicate that RodA1 is the most important RodA homolog considering that RodA2 alone is not sufficient to maintain the rod shape and that RodA3 is only minimally expressed under standard laboratory conditions (44). To understand the impact of RodA enzymes on cell growth and cell division in L. monocytogenes, a strain was constructed that lacks all three rodA genes from its genome but harbors pIMK3-rodA1 to enable IPTG-inducible expression of RodA1 (strain 10403SΔrodA1-3 irodA1). Prolonged depletion of RodA1 in strain 10403SΔrodA1-3 irodA1 led to a growth defect that was not seen when the strain was grown in the presence of the inducer (Fig. 5A). However, the depletion was not efficient enough to see a complete growth inhibition, which would be expected for a strain lacking all three RodA homologs. This is likely caused by residual rodA1 expression from the inducible promoter even in the absence of IPTG. Consistent with this notion, even after prolonged depletion, rodA1 transcripts could still be detected in strain 10403SΔrodA1-3 irodA1 as assessed by qRT-PCR (Fig. S5).
However, cells of the \textit{L. monocytogenes} strain 10403SΔrodA1-3 irodA1 that were grown without IPTG were significantly shorter with a cell length of 1.18 ± 0.08 μm compared to cells of the double mutant 10403SΔrodA1ΔrodA3 or the wild-type strain 10403S (Fig. 5B and D). Interestingly, different cell morphologies could be observed for strain 10403SΔrodA1-3 irodA1 after prolonged RodA1 depletion (Fig. 5C). The placement of the division septum was affected in some cells and daughter cells of different sizes, or cells with two septa were observed (Fig. 5C). These morphological defects could be complemented, and the cell length increased to 1.95 ± 0.04 μm upon the addition of IPTG and expression of RodA1 (Fig. 5D). These data highlight that RodA1 alone is sufficient to maintain the cell shape of \textit{L. monocytogenes}.

**Decreased moenomycin and lysozyme resistance in the absence of RodA homologs.** Next, we wondered whether the absence of FtsW or RodA proteins affects the resistance of \textit{L. monocytogenes} toward the antibiotics penicillin, bacitracin, and moenomycin, which target different steps in the peptidoglycan biosynthesis process. Penicillin binds to the transpeptidase domain of PBPs and inhibits their function, leading to a reduced cross-linking of the peptidoglycan (45, 46). Bacitracin inhibits the dephosphorylation of the bactoprenol carrier, leading to a block in lipid II synthesis (47). The phosphoglycolipid antibiotic moenomycin inhibits the glycosyltransferase activity of bifunctional PBPs and thereby prevents the polymerization of the glycan chain (48).

No significant differences could be observed in terms of resistance against penicillin, bacitracin, or moenomycin for the FtsW1 depletion strain 10403SΔftsW1 iftsW1. This is presumably due to basal level expression of \textit{ftsW1} even in the absence of the inducer. Simultaneous deletion of \textit{rodA1} and \textit{rodA3} resulted in a slight decrease in the MIC for penicillin; however, this difference was not significant (Fig. 6A). On the other hand, strain 10403SΔrodA1ΔrodA3 was two- to fourfold more sensitive to the antibiotic bacitracin (Fig. 6B). This phenotype could be complemented by expressing either RodA1, RodA2, or RodA3 from an IPTG-inducible promoter (Fig. 6B).

As described above, moenomycin inhibits the transglycosylase activity of PBPs, leading to a decreased activity of these enzymes. In the absence of RodA1 and RodA3, cells are more susceptible to reduced activity of PBPs, manifesting in a fourfold-reduced resistance to moenomycin (Fig. 6C). Induction of RodA1 expression in strain 10403SΔrodA1ΔrodA3 resulted in a significantly higher resistance to moenomycin compared to that of wild-type strain 10403S, and expression of RodA2 or RodA3 led to partial or complete complementation of the moenomycin sensitivity (Fig. 6C).

Moreover, resistance to lysozyme, an enzyme that cleaves the linkage between \textit{N}-acetylmuramic acid and \textit{N}-acetylglucosamine residues of the peptidoglycan, was drastically decreased in strain 10403SΔrodA1ΔrodA3 and could be fully restored by expression of RodA1, RodA2, or RodA3 (Fig. 6D). Lysozyme resistance in \textit{L. monocytogenes} is mainly accomplished by two modifications of the peptidoglycan; deacetylation of \textit{N}-acetylglucosamine residues by PgdA or O-acetylation of \textit{N}-acetylmuramic acid residues by OatA (49, 50). To determine whether the activity of PgdA is changed in the absence of RodA1 and RodA3, peptidoglycan was purified from the 10403SΔrodA1ΔrodA3 mutant strain and digested with mutanolysin, and the resulting muropeptides were analyzed by HPLC. Peptidoglycan samples isolated from the wild-type strain 10403S and the complementation strain 10403SΔrodA1ΔrodA3 irodA1 that had been grown in the presence of IPTG were analyzed as controls (Fig. 6E). The main muropeptide peaks were assigned as described previously (51, 52). Peaks 1 and 2 correspond to the acetylated and deacetylated monomeric muropeptides, respectively, whereas peak 3 and peaks 4 to 6 are acetylated and deacetylated muropeptide dimers, respectively. Deletion of \textit{rodA1} and \textit{rodA3} led to a reduction of both monomeric muropeptides and therefore to an increase in cross-linked peptidoglycan fragments by approximately 2% compared to the wild-type strain 10403S, in which 65% of the peptidoglycan was cross-linked (Fig. 6F). However, no significant difference with regard to the deacetylated muropeptides could be observed between wild-type 10403S, strain 10403SΔrodA1ΔrodA3, and the 10403SΔrodA1ΔrodA3 irodA1 complementation strain (Fig. 6F). These results suggest that the lysozyme sensitivity phenotype of strain...
rodA1ΔrodA3 is not caused by changes in the peptidoglycan deacetylation but instead is due to general defects in the peptidoglycan structure.

Cell wall-acting antibiotics induce the promoter of lmo2689. The operon lmo2689-lmo2686, which contains the genes encoding FtsW2 and RodA3, is only minimally expressed under standard laboratory conditions (44). A genome-wide transcriptional analysis performed in L. monocytogenes strain LO28 has shown that lmo2687, lmo2688, and lmo2689 are part of the CesR regulon (53). The cephalosporin sensitivity response regulator CesR is part of the CesRK two-component system that regulates the transcription of several cell envelope-related genes in response to changes in cell wall integrity, such as those caused by the presence of cell wall-acting antibiotics or...
alcohols, including ethanol (53–55). Therefore, we next used the lmo2689 promoter described above to assess whether expression of the lmo2689-lmo2686 operon is induced in the presence of antibiotics that target different processes of the PG biosynthesis or ethanol. Indeed, increased \(\beta\)-galactosidase activity could be measured for cells that had been grown in the presence of subinhibitory concentrations of the \(\beta\)-lactam antibiotics ampicillin, penicillin, and cefuroxime and the phosphoglycolipid moenomycin (Fig. 7A). In contrast, no increase in \(\beta\)-galactosidase activity could be detected upon the addition of vancomycin, lysozyme, or ethanol compared to untreated control cells (Fig. 7A). We also tested whether the presence of MgSO\(_4\) or EDTA has an impact on lmo2689 promoter activity, since lmo2689 encodes a putative Mg\(^{2+}\)-type ATPase. However, the \(\beta\)-galactosidase activity of cells grown in the presence of MgSO\(_4\) or EDTA was comparable to the \(\beta\)-galactosidase activity seen for untreated cells (Fig. 7A). These results indicate that the expression of ftsW2 and rodA3, which are part of the lmo2689-lmo2686 operon, are induced in the presence of various cell wall-acting antibiotics, suggesting that FtsW2 and RodA3 might be important for the intrinsic resistance of \(L.\) monocytogenes against these antibiotics. However, no significant dif-

![Figure 7](http://mbio.asm.org/)

**FIG 7** Cell wall-acting antibiotics increase the lmo2689 promoter activity. (A) Bacteria from mid-logarithmic cultures of strain 10403S pPL3e-\(\text{lmo2689-lacZ}\) were exposed for 2 h at 37°C to different stressors. The activity of the lmo2689 promoter was subsequently determined by performing \(\beta\)-galactosidase activity assays as described in Materials and Methods. Bacteria that had been grown in the absence of a stressor were included as a negative control (\(-\)). The averages of the \(\beta\)-galactosidase activity units and standard deviations from three independent experiments were plotted. For statistical analysis, a one-way ANOVA coupled with a Dunnett’s multiple-comparison test was used (***, \(P = 0.001; \text{****}, P \leq 0.0001)\). (B and C) Absence and overexpression of RodA3 result in decreased cefuroxime resistance. Dilutions of overnight cultures of strains 10403S (wt), 10403SΔrodA1, 10403SΔrodA2, and 10403SΔrodA3 (B) and strains 10403S (wt), 10403S plMK3-rodA1, 10403S plMK3-rodA2, and 10403S plMK3-rodA3 (C) were spotted on BHI agar and BHI agar containing 1\(\mu\)g/ml cefuroxime and incubated for 24 h at 37°C. BHI agar plates were supplemented with 1 mM IPTG for cefuroxime resistance assays shown in panel C. A representative result from three independent experiments is shown. undil., undiluted.
differences in MICs for penicillin and moenomycin could be observed between wild-type 10403S, the ftsW2 or rodA3 single mutant strains, or the ftsW2 rodA3 double mutant (Fig. S6). However, there was a slight reduction in the resistance of the rodA3 single mutant against cefuroxime compared to the wild type (Fig. S6). To further assess whether there is a difference in the cefuroxime resistance between the L. monocytogenes wild-type strain 10403S and the rodA1, rodA2, and rodA3 single mutant strains, dilutions of overnight cultures were spotted on BHI agar plates with or without 1/2 μg/ml cefuroxime. Deletion of rodA1 or rodA2 results in a slightly reduced ability of these strains to grow on BHI plates supplemented with 1 μg/ml cefuroxime compared to the wild-type 10403S strain (Fig. 7B). However, deletion of rodA3 leads to a stronger reduction of growth on BHI plates containing 1 μg/ml cefuroxime compared to the growth of rodA1 and rodA2 single mutants (Fig. 7B). Interestingly, overexpression of RodA3, but not of RodA1 or RodA2, also resulted in decreased resistance toward cefuroxime compared to the wild-type strain 10403S (Fig. 7C). Our results therefore suggest that L. monocytogenes induces the expression of rodA3 and ftsW2 in the presence of β-lactam antibiotics and moenomycin to compensate for the inhibition of the glycosyltransferase and transpeptidase activity of PBPs. In particular, RodA3 seems to play an important function for the intrinsic cephalosporin resistance in L. monocytogenes, and its expression needs to be finely balanced, as both its absence as well as increased expression have detrimental effects on resistance against this antibiotic.

**FtsW and RodA proteins interact with class B PBPs.** Previous studies have shown that members of the SEDS protein family act together with a cognate class B PBP to synthesize and cross-link peptidoglycan (28, 34, 56–58). L. monocytogenes carries genes that encode three class B PBPs, namely PBP B1, PBP B2, and PBP B3. To identify potential protein-protein interactions between the L. monocytogenes class B PBPs and the FtsW/RodA proteins, a bacterial adenylate cyclase two-hybrid (BACTH) analysis was performed. Interactions were detected between the three L. monocytogenes PBP B1, PBP B2, and PBP B3 and all FtsW and RodA homologs (Fig. 8). These results suggest that the FtsW and RodA proteins also form a complex with class B PBPs in L. monocytogenes. However, using this bacterial two-hybrid approach, it was not possible to determine specific SEDS protein and class B PBP pairs.
DISCUSSION

Bacterial cell elongation and cell division need to be tightly regulated to maintain cell shape. This is accomplished by two multiprotein complexes, the elongasome and divisome, which are coordinated by the actin homolog MreB and the tubulin homolog FtsZ, respectively (30–32, 59, 60). The SEDS protein FtsW is part of the divisome and essential for growth as shown for many bacteria, including E. coli, B. subtilis, and S. aureus (28, 35, 36, 39, 43). Our experiments suggested that FtsW1 is also essential in L. monocytogenes; however, a second FtsW protein, FtsW2, can compensate for the loss of FtsW1 if it is expressed from an inducible promoter. FtsW2 is encoded by a gene in the lmo2689-lmo2686 operon that appears to be only minimally expressed when L. monocytogenes 10403S is grown under standard laboratory conditions (44). The expression of the lmo2689-lmo2686 operon is regulated by the two-component system CesRK that is activated by cell envelope stress (53–55). Using an L. monocytogenes strain carrying a P_lmo2689-lacZ promoter fusion, we could detect increased β-galactosidase activity after incubation with subinhibitory concentrations of different β-lactam antibiotics, including penicillin, cefuroxime, and moenomycin. However, expression of the lmo2689-lmo2686 operon was not induced by other cell wall-targeting antibiotics such as vancomycin or the hydrolase lysozyme. This suggests that inhibition of the glycosyltransferase or transpeptidase activity of PBPs leads to activation of the lmo2689-lmo2686 operon, and hence, to the expression of ftsW2 as well as rodA3.

The rod shape-determining protein RodA is part of the elongation machinery. The data presented in this study suggest that L. monocytogenes carries genes that encode not one but three RodA proteins and that depletion of the three RodA enzymes leads to a decreased cell length (Fig. 5). Simultaneous deletion of rodA1 and rodA3 already results in the formation of shorter cells, whereas cells of strains with rodA1 and rodA2 or rodA2 and rodA3 deleted have a cell length that is comparable to that of the wild-type strain 10403S. Taking into consideration that rodA3 is only minimally expressed under standard laboratory growth conditions in L. monocytogenes 10403S (44), the results presented in this study suggest that rodA3 expression becomes induced upon inactivation of RodA1, since we observed morphological differences between the rodA1 single mutant and rodA1 rodA3 double mutant strains. Indeed, β-galactosidase assays confirmed that deletion of rodA1 or rodA1 rodA2 increases the activity of the promoter from which rodA3 is expressed. The data presented in this study also indicate that RodA1 is the “main” RodA enzyme in L. monocytogenes, as no significant phenotypic changes with regard to growth and cell division could be observed as long as RodA1 was present. On the other hand, RodA2 was able to compensate for the loss of RodA1 and RodA3 only when it was overproduced from an inducible promoter. Interestingly, cells of strains 10403S and 10403SΔrodA1ΔrodA3 in which rodA3 is overexpressed from an ectopic locus have an increased cell length compared to the wild type. An explanation for this could be that elevated levels of RodA3 lead to the depletion of proteins needed at the cell division site, resulting in an extended synthesis of PG on the lateral wall. Another possibility could be that RodA3 directly inhibits FtsW1 or displaces FtsW1 at the cell division site, leading to a block in cell division and therefore resulting in the formation of elongated cells.

Recent studies have shown that SEDS proteins act as glycosyltransferases (22, 24). The glycosyltransferase activity of PBPs and MGT can be inhibited by moenomycin, whereas RodA/FtsW enzymes are not affected by moenomycin and are therefore important for moenomycin resistance (24, 61). In good agreement with the importance of SEDS proteins for the intrinsic moenomycin resistance, deletion of the genes encoding two of the three RodA enzymes, RodA1 and RodA3, resulted in an increased moenomycin sensitivity of L. monocytogenes (Fig. 6C).

In B. subtilis, RodA is in a complex with the class B PBP, PBP 2A (also named PbpH), and these two proteins act together to polymerize and cross-link the glycan strands (34, 56). Similarly, FtsW and PBP 2B form a subcomplex as part of the divisome (57, 58). Recently, it was shown that RodA-PBP3 and FtsW-PBP1 act as cognate pairs in the
coccoid bacterium *S. aureus* (28). Depletion of all three RodA enzymes in *L. monocytogenes*, RodA1, RodA2, and RodA3, leads to a drastic reduction in cell length (Fig. 5). A similar phenotype was observed for an *L. monocytogenes* strain depleted for the essential class B PBP, PBP B1 (51). In contrast, the absence of either FtsW1 (Fig. 2) or the class B PBP, PBP B2, in *L. monocytogenes* results in the formation of elongated cells (51). These observations suggest that RodA and FtsW might work in a complex with the cognate PBPs PBP B1 and PBP B2 during cell elongation and cell division, respectively. Indeed, protein-protein interactions between FtsW1 and FtsW2 with PBP B2 and between RodA1, RodA2, and RodA3 with the PBP B1 could be observed (Fig. 8). However, interactions were also detected between the FtsW proteins and PBP B1 and PBP B3 as well as between the RodA proteins and PBP B2 and PBP B3 (Fig. 8). While these data provide the first line of evidence that SEDS proteins and class B PBPs (bPBP) also form complexes in *L. monocytogenes*, additional work is necessary to determine whether specific SEDS-bPBP pairs are formed in *L. monocytogenes*.

Taken together, *L. monocytogenes* has a repertoire of PBPs and multiple members of the SEDS family of proteins to produce its rigid cell wall. The expression and activity of these enzymes need to be tightly regulated in *L. monocytogenes* to maintain its cell shape. Our results suggest that *L. monocytogenes* adapts the expression of a second set of FtsW/RodA enzymes, FtsW2 and RodA3, to environmental stresses such as the presence of β-lactam antibiotics, thereby preventing defects in the peptidoglycan synthesis and subsequent cell lysis.

**MATERIALS AND METHODS**

**Bacterial strains and growth conditions.** All strains and plasmids used in this study are listed in Table S1 in the supplemental material. Strain and plasmid constructions are described in Text S1 in the supplemental material, and all primers used in this study are listed in Table S2. *E. coli* strains were grown in Luria-Bertani (LB) medium, and *L. monocytogenes* strains were grown in brain heart infusion (BHI) medium at 37°C unless otherwise stated. If necessary, antibiotics and supplements were added to the cultures at the following concentrations: for *E. coli* cultures, ampicillin (Amp) at 100 μg/ml and kanamycin (Kan) at 30 μg/ml, and for *L. monocytogenes* cultures, chloramphenicol (Cam) at 10 μg/ml, kanamycin (Kan) at 30 μg/ml, and isopropyl β-D-1-thiogalactopyranoside (IPTG) at 1 mM. We used the *L. monocytogenes* strain 10403S and derivatives thereof. However, we refer to *L. monocytogenes* EGD-e gene and locus tag numbers, as this was the first fully sequenced *L. monocytogenes* strain.

**Growth curves.** Overnight cultures of wild-type *L. monocytogenes* 10403S and the indicated depletion strains were diluted to an optical density at 600 nm (OD600) of 0.01 or 0.05 in 15 ml of BHI medium, and the cultures were incubated at 37°C with shaking. Growth was monitored by determining OD600 readings at hourly intervals. For growth curves with the IPTG-inducible depletion strains 10403SΔrodA1, the strains were cultivated overnight in the presence of 1 mM IPTG. The next day, cells were washed once with fresh medium, diluted 1:50 in 5 ml BHI medium, and grown for 8 to 10 h in the absence of the inducer. The cultures were diluted 1:100 into fresh BHI medium and grown until the next morning at 37°C. The depleted cells were then diluted to an OD600 of 0.01 and grown in the presence or absence of 1 mM IPTG at 37°C. Averages and standard deviations from three independent experiments were plotted.

**RNA extraction and quantitative real-time PCR (qRT-PCR).** For the extraction of RNA from rodA complemented strains, overnight cultures of *L. monocytogenes* strains 10403S, 10403SΔrodA1ΔrodA3, 10403SΔrodA1ΔrodA3 pMK3-rodA1, 10403SΔrodA1ΔrodA3 pMK3-rodA2, and 10403SΔrodA1ΔrodA3 pMK3-rodA3 were diluted in BHI medium (with 1 mM IPTG for the plasmid-containing complemented strains) to an OD600 of 0.05 and incubated at 37°C until the cultures reached an OD600 of 1. For the extraction of RNA from strain 10403SΔrodA1ΔrodA3 irodA1 (ANG5192), bacteria were grown as described for the growth curve assay to deplete RodA1. Next, strain 10403S and depleted cells of 10403SΔrodA1-3 irodA1 were diluted to an OD600 of 0.01 and grown in BHI medium in the presence or absence of IPTG until an OD600 of 0.5. Portions (20 μl) of the cultures were mixed with 47 μl guanidine thiocyanate (GTC) buffer (5 M GTC, 0.5% N-lauryl sarcosine, 0.1 M β-mercaptoethanol, 0.5% Tween 80, 10 mM Tris-HCl [pH 7.5]), bacteria were harvested by centrifugation and subsequently lysed using the FastRNA Pro Blue kit (MP Biomedical). Total RNA was isolated by chloroform extraction and ethanol precipitation and further purified using the RNeasy minikit (Qiagen) and finally treated with Turbo DNase (Invitrogen). cDNA was synthesized from 10 ng of RNA using the Superscript III first strand synthesis kit (Invitrogen). The expression of rodA1, rodA2, and rodA3 in the different strains was assessed using the TaqMan probe-based gene expression assay (Applied Biosystems). Expression of gyrB was used as a control. The cycle threshold (Ct) values obtained for rodA1, rodA2 and rodA3 were normalized to the values obtained for gyrB. The fold changes of gene expression for the different strains were calculated using the ΔΔCt method.

**Determination of MICS.** The MICS for bacitracin, penicillin, moenomycin, and lysozyme were determined using a broth microdilution assay in 96-well plates. Approximately 104 *L. monocytogenes* cells were used to inoculate 200 μl BHI containing twofold dilutions of the different antimicrobials.
starting antibiotic concentrations were 1 mg/ml for bacitracin A, 1 μg/ml for penicillin G, 0.8 or 1.6 μg/ml for moenomycin, 8 μg/ml cefuroxime, and 10 mg/ml for lysozyme. The OD₆₀₀ readings were determined after incubating the 96-well plates for 24 h at 37°C with shaking at 500 rpm in a plate incubator (Thermostar; BMG Labtech). The MIC value refers to the antibiotic concentration at which bacterial growth was inhibited by >90%.

Determination of antibiotic susceptibility using a spot plating assay. Overnight cultures of the indicated L. monocytogenes strains were adjusted to an OD₆₀₀ of 1, and 5-μl portions of serial dilutions were spotted on BHI agar plates or BHI agar plates containing 1 μg/ml cefuroxime and where indicated, 1 mM IPTG. Plates were photographed after incubation at 37°C for 24 h.

Fluorescence and phase-contrast microscopy. For bacterial cell length measurements, 100-μl portions of mid-log cultures were mixed with 5 μl of 100 μg/ml Nile red solution to stain the cell membrane. Following incubation at 37°C for 20 min, the cells were washed once with phosphate-buffered saline (PBS) and resuspended in 50 μl PBS. Portions (1.5 μl) of the different samples were spotted onto microscope slides covered with a thin agarose film (1.5% agarose in distilled water), air dried, and covered with a cover slip. Phase-contrast and fluorescence images were taken using a Zeiss Axio Imager.A1 microscope coupled to an AxioCam MRm and a 100× objective and processed using the Zen 2012 software (blue edition). For the detection of Nile red fluorescence signals, the Zeiss filter set 00 was used. For the cell length determinations, 300 cells were measured for each experiment, and the median cell length was calculated. Averages and standard deviations of the median cell length of three independent experiments were plotted.

Peptidoglycan isolation and analysis. Overnight cultures of L. monocytogenes strains 10403S, 10403SΔrodA1, and 10403SΔrodA1ΔΔrodA3 pLMK3-rodA1 were used to inoculate 1 liter BHI broth (with 1 mM IPTG for the complementation strain 10403SΔrodA1ΔΔrodA3 pLMK3-rodA1) to a starting OD₆₀₀ of 0.06. The cultures were grown at 37°C until they reached an OD₆₀₀ of 1, at which point the cultures were cooled on ice for 1 h. The bacteria were subsequently collected by centrifugation, and peptidoglycan was purified and digested with mutanolysin as described previously (62, 63). Digested muropeptides were analyzed by high-performance liquid chromatography (HPLC) and recorded at an absorption of 205 nm as described previously (62). For quantification, the areas of the main muropeptide peaks were integrated using the Agilent Technology ChemStation software. The sum of the peak areas was set at 100%, and individual peak areas were determined. Averages and standard deviations from three independent extractions were calculated.

β-Galactosidase assay. For determination of the β-galactosidase activity, overnight cultures of strains 10403S pPL3e-P₃ma2689-loacZ, 10403SΔrodA1 pPL3e-P₃ma2689-loacZ, and 10403SΔrodA1ΔΔrodA2 pPL3e-P₃ma2689-loacZ were diluted 1:100 in fresh BHI medium and grown for 6 h at 37°C. Sample collection and preparation were performed as described previously (64). Briefly, OD₆₀₀ readings were determined (for the final β-galactosidase unit calculations) for the different cultures after 6 h of growth, and cells from 1 ml culture were pelleted by centrifugation for 10 min at 13,200 × g, resuspended in 100 μl ABT buffer (60 mM K₂HPO₄, 40 mM KH₂PO₄, 100 mM NaCl, 0.1% Triton X-100 [pH 7.0]), snap-frozen in liquid nitrogen, and stored at −80°C until use. For the identification of substances inducing the expression of the lmo2689-lmo2686 operon, an overnight culture of strain 10403S pPL3e-P₃ma2689-loacZ was diluted 1:100 in fresh BHI medium, and the culture was incubated with shaking at 37°C until an OD₆₀₀ of 0.5 to 0.6 was reached. The culture was divided into several flasks and incubated for 2 h at 37°C in the presence or absence of the following substances: 0.5 μg/ml ampicillin, 0.05 μg/ml penicillin, 0.5 μg/ml vancomycin, 4 μg/ml cefuroxime, 0.05 μg/ml moenomycin, 0.5 mg/ml lysozyme, 1% ethanol, 300 μg/ml MgSO₄, or 300 μg/ml EDTA. Bacteria were pelleted, and samples were frozen as described above.

Samples were thawed, and 1:10 dilutions were prepared in ABT buffer. Fifty-microliter portions of the 1:10 diluted samples were mixed with 10 μl of 0.4 mg/ml 4-methyl-umbelliferyl-β-D-galactopyranoside (MUG) substrate prepared in dimethyl sulfoxide (DMSO) and incubated for 60 min at room temperature (RT). A reaction with ABT buffer alone was used as a negative control. Following this incubation step, 20 μl of each reaction mixture was diluted into 180 μl of ABT buffer in a black 96-well plate, and fluorescence values were measured using an Hitachi F-4500 fluorescence spectrophotometer at 355-nm excitation and 460-nm emission wavelengths. Concentrations from 0.125 μM to 20 μM of the fluorescent 4-methylumbelliferyl (MU) standard were used to obtain a standard curve. β-Galactosidase units were calculated as (picomoles of substrate hydrolyzed × dilution factor) / culture volume [in milliliters] / OD₆₀₀ × minute). The amount of hydrolyzed substrate was determined from the standard curve as (emission reading – y intercept) / slope.

Bacterial two-hybrid assays. Protein-protein interactions between the different FtsW/RodA homologs and class B PBPs were analyzed using the bacterial adenylate cyclase two-hybrid (BACTH) assay (65). The indicated pUT18b/pUT18c and pK72 derivatives were cotransformed into E. coli strain BTH101. Transformants were selected on LB agar plates containing 100 μg/ml ampicillin, 30 μg/ml kanamycin, 0.1 mM IPTG, and 50 μg/ml X-Gal. Images were taken after incubation for 24 h and 48 h at 30°C.

SUPPLEMENTAL MATERIAL

Supplemental material for this article may be found at https://doi.org/10.1128/mBio.01448-19.

TEXT S1, DOCX file, 0.02 MB.
FIG S1, EPS file, 1.2 MB.
FIG S2, TIF file, 3 MB.
FIG S3, TIF file, 4.2 MB.
REFERENCES


July/August 2019 Volume 10 Issue 4 e01448-19 mbio.asm.org

mbio.asm.org 17


