Contribution of the FtsQ Transmembrane Segment to Localization to the Cell Division Site

Dirk-Jan Scheffers, Carine Robichon, Gert Jan Haan, Gregory Koningstein, Edwin van Bloois, Jon Beckwith, and Joen Luirink

Molecular Microbiology, Institute for Molecular Cell Biology, Vrije Universiteit Amsterdam, De Boelelaan 1085, 1081 HV Amsterdam, The Netherlands; Department of Microbiology and Molecular Genetics, Harvard Medical School, 200 Longwood Avenue, Boston, Massachusetts 02115; and Swammerdam Institute for Life Sciences, Molecular Cytology, Kruislaan 316, 1098 SM Amsterdam, The Netherlands

Received 8 May 2007/Accepted 3 August 2007

The Escherichia coli cell division protein FtsQ is a central component of the divisome. FtsQ is a bitopic membrane protein with a large C-terminal periplasmic domain. In this work we investigated the role of the transmembrane segment (TMS) that anchors FtsQ in the cytoplasmic membrane. A set of TMS mutants was made and analyzed for the ability to complement an ftsQ mutant. Study of the various steps involved in FtsQ biogenesis revealed that one mutant (L29/32R;V38P) failed to functionally insert into the membrane, whereas another mutant (L29/32R) was correctly assembled and interacted with FtsB and FtsL but failed to localize efficiently to the cell division site. Our results indicate that the FtsQ TMS plays a role in FtsQ localization to the division site.

Bacteria are capable of localizing integral membrane proteins (IMPs) to specific sites in the cytoplasmic membrane. A wealth of studies has shown specific localization patterns for IMPs involved in cell division, chemotaxis, sporulation, and cell wall synthesis in model organisms, such as Escherichia coli, Bacillus subtilis, Caulobacter crescentus, Staphylococcus aureus, and Streptococcus pneumoniae (14, 20, 21, 25, 31). It is not known how these IMPs find their destination: the Sec machinery that inserts IMPs into the cytoplasmic membrane is localized along the lateral wall in E. coli and B. subtilis, and proteins seem to insert in a random fashion into the membrane before being localized to their destination (5, 34). A diffusion and capture model has been proposed in which an IMP diffuses randomly through the membrane until it is captured at its destination by an as-yet-unknown factor (30). Such a factor could be the lipid composition of the membrane, as the distribution of lipids throughout the bacterial membrane is not homogeneous, with cardiolipin-enriched domains at the poles and the cell division site (23, 27, 28).

One of the best-studied sets of localizing IMPs consists of IMPs involved in E. coli cell division. These IMPs need to be targeted to mid-cell, where they will form part of the divisome, a complex consisting of 14 cytoplasmic (FtsZ, FtsA, and ZapA), inner membrane (ZipA, FtsE, FtsK, FtsQ, FtsL, FtsB, FtsW, FtsI, and FtsN), and periplasmic (AmpC) proteins that form a ring and mediate cell constriction, synthesis of the septal cell wall, and cell separation (14). The divisome forms in two steps, starting with the assembly of the FtsZ ring followed by a well-defined time gap after which all the essential cell division IMPs, such as FtsK, FtsQ, FtsL, FtsB, FtsW, FtsI, and FtsN, assemble (1). The assembly of these proteins was long thought to occur in a hierarchical manner observing the order of proteins as listed. Recent studies using a premature targeting assay have revealed that various downstream proteins can recruit upstream proteins, which has led to a more comprehensive model in which FtsK recruits a subcomplex consisting of FtsQ, -L, and -B, which in turn recruits an FtsW/FtsI subcomplex, after which FtsN and AmpC are recruited (15, 16).

FtsQ plays a central role in the assembly of the divisome. FtsQ is a bitopic membrane protein consisting of a short cytoplasmic domain (residues 1 to 24), a fairly long transmembrane segment (TMS; residues 25 to 49), and a periplasmic domain (residues 50 to 276) (Fig. 1). Two-hybrid analyses have suggested that FtsQ interacts with itself, FtsA, -K, -X, -L, -B, -W, -I, and -N, and YmgF, a protein of unknown function (9, 11, 22). This number of interactions, 10, is greater than for any other division protein tested (a maximum of five interaction partners for FtsI,-N, and -L). The interaction with FtsA and FtsK depends on the N-terminal domain of FtsQ, whereas all other interactions require only the periplasmic domain of FtsQ (11, 22). This is in accordance with domain swap experiments that showed that the periplasmic domain of FtsQ is essential for FtsQ localization and recruitment of downstream proteins (2, 7, 19) but that the cytoplasmic domain and the TMS can be exchanged for unrelated domains. The proteolytically sensitive and unstructured γ-subdomain of the periplasmic domain (29) plays an important role in the interaction of FtsQ with FtsB...
and FtsL (17). This interaction is independent of localization to the cell division site and can be identified by communoprecipitation (co-IP) experiments (3). Mutants in the α-subdomain of the periplasmic domain are affected in localization to the cell division site but are still capable of recruiting downstream proteins (17).

Since the original finding that the FtsQ TMS can be swapped for the unrelated TMS from MalF (19), it has been assumed that the TMS functions as a rather inert membrane anchor but does not fulfill any FtsQ-specific role. However, a closer inspection of the results of the swap experiments reveals that FtsQ containing the TMS of either MalF or FtsL is capable of complementing an ftsQ temperature-sensitive mutant but that these mutants grow as filaments at the restrictive temperature (19). Also, green fluorescent protein (GFP) fusions to FtsQ swap constructs containing the MalF TMS show a twofold reduction in localization efficiency compared to wild-type FtsQ (7). In both studies, the capacity of swap constructs to support growth was used as the major criterion for functionality, but these results also support a role for the FtsQ TMS in FtsQ function, as the swap constructs are not fully efficient in these results also support a role for the FtsQ TMS in FtsQ growth was used as the major criterion for functionality, but does not fulfill any FtsQ-specific role. However, a closer inspection of the results of the swap experiments reveals that FtsQ containing the TMS of either MalF or FtsL is capable of complementing an ftsQ temperature-sensitive mutant but that these mutants grow as filaments at the restrictive temperature (19). Also, green fluorescent protein (GFP) fusions to FtsQ swap constructs containing the MalF TMS show a twofold reduction in localization efficiency compared to wild-type FtsQ (7). In both studies, the capacity of swap constructs to support growth was used as the major criterion for functionality, but these results also support a role for the FtsQ TMS in FtsQ function, as the swap constructs are not fully efficient in localization to the cell division site, consistent with a role for the FtsQ TMS in division site localization.

**MATERIALS AND METHODS**

**Strains, plasmids, and growth conditions.** Strains and plasmids are listed in Table 1. Strain Top10F’ was used for routine plasmid handling and expression of ftsQ from pBAD24, strain MJC129 was used for complementation experiments, strain LMC500 was used for GFP-FtsQ localization, and strain MRE600 was used to obtain translation lysate for in vitro translation experiments.

Bacteria were grown in Luria-Bertani broth (LB; per liter, 10 g tryptone, 5 g yeast extract, 5 g NaCl) unless indicated otherwise. Solid medium was LB with agar (1.5%, wt/vol). Antibiotics were used at appropriate concentrations: ampicillin (100 μg/ml), chloramphenicol (30 μg/ml), and tetracycline (12.5 μg/ml). t-Arabinose and D-glucose were used at concentrations indicated to modulate expression of ftsQ constructs from the pBAD24 expression vector.

For co-IP assays, the strains were grown in NZY liquid broth or agar (as described elsewhere [6]) supplemented with chloramphenicol (10 μg/ml) and ampicillin at low concentration (25 μg/ml) and with t-arabinose or D-glucose at 0.2% final concentration, to induce or repress, respectively, the expression of FtsQ from pJCl0.

**Plasmid construction.** Mutations were introduced into FtsQ using nested PCR and plasmids pC4Meth108FtsQ-TAG40 or pC4Meth108FtsQ (37) as templates. Primers FtsQfw, FtsQ108Bamrev, and nested PCR primers were also used (sequences available at http://www.bio.vu.nl/vakgroepen/molmic/publications.html). The FtsQ L29R mutation. Mutated FtsQ derived from the pC4Meth108FtsQ plasmids was used to clone the FtsQ mutants into pBAD24-FtsQ using the internal Asp718 restriction site in ftsQ. The ftsQ coding sequence was cloned into pBAD24 from pBAD24-FtsQ using EcoRI and HindIII, resulting in pBAD24-FtsQ. The FtsQ expression of FtsQ constructs from the pBAD24-FtsQ constructs were verified by sequencing. pCR45 to pCR50 were constructed by inserting EcoRI-XbaI-digested PCR products, generated using pBAD24-FtsQ* as a template and primers EcoRI-fitsQfor and XbaI-fitsQrev, into EcoRI-XbaI-digested pDSW204.

**FtsQ complementation assay.** Overnight cultures of strain MJC129 [ftsQ1ftsA3] harboring the pBAD24 vector encoding FtsQ or FtsQ mutants, or pLD104 encoding the FFQ domain swap construct (19), were diluted to an optical density at 660 nm (OD660) of 0.01 in prewarmed LB containing 0.02% arabinose and grown at 30°C (control) and 42°C, and growth was monitored. Also, exponentially growing cells from cultures grown at 30°C without arabinose were diluted.
and spotted on LB agar with appropriate antibiotics and arabinose (0.01%, wt/vol) and incubated at 30°C or 42°C.

In vitro transcription, translation, and cross-linking. Truncated mRNA was prepared as described previously (33) from HindIII-linearized pC4Meth-108FtsQ*-TAG40 plasmids encoding FtsQ or FtsQ mutants. In vitro translation was performed in an E. coli cell- and membrane-free extract, and inner membrane vesicles prepared from the E. coli wild-type strain MC4100 (18.6 μg total protein) were used to allow targeting described elsewhere (37), generating [35S]methionine-labeled FtsQ nascent chains of 108 amino acids in length, with the photoactivatable cross-linker (Tmd)Phe incorporated at position 40 through cross-linking adducts were analyzed by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and phosphorimagining as described elsewhere (33).

Assay for in vivo membrane assembly. Strain Top10F′ harboring the pBAD24 vector encoding FtsQ or FtsQ mutants was grown to early log phase. Cells were induced for 3 min with 0.2% l-arabinose, labeled with [35S]methionine (30 μCi/ml) for 5 min, and converted to spheroplasts as described previously (12). Aliquots of the spheroplast suspension were incubated with or without proteinase K (0.4 mg/ml) for 1 h on ice. Subsequently, phenylmethylsulfonyl fluoride (0.33 mM) was added to inhibit proteinase K, and proteins were acid precipitated and immunoprecipitated with antiserum against OmpA, trigger factor, or FtsQ, as described elsewhere (38). Samples were analyzed by SDS-PAGE, and proteins were visualized by phosphorimagining.

GFP-FtsQ fluorescence microscopy. Strain LMC500 harboring the pTHV-FtsQ* vector, encoding FtsQ or FtsQ mutants, was grown in glucose minimal medium (GB1) (8). GFP-FtsQ* induction was constitutive from the weakened Para promoter without induction. Exponentially growing cells were fixed and mounted on 1% agarose pads, and microscopy was performed as described elsewhere (8), using an Olympus BX-60 fluorescence microscope equipped with a UPLFLN 100×/1.3 numerical-aperture oil objective and a Photometrics CoolSnap-fx charge-coupled-device camera.

<table>
<thead>
<tr>
<th>Strain or plasmid</th>
<th>Relevant characteristics</th>
<th>Source or reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>E. coli strains</td>
<td></td>
<td>Laboratory collection</td>
</tr>
<tr>
<td>MC4100</td>
<td>araD139 ΔlacU169 relA1 rpsL150 thi mot fab5301 deoC7 ptsF25 rbsR</td>
<td></td>
</tr>
<tr>
<td>MJIC129</td>
<td>KS272 ftsQ(Ts) recA:cat</td>
<td></td>
</tr>
<tr>
<td>Top10F′</td>
<td>F' [lacI15 Tn10(Tet')] mcrA (ntr-hsdRMS-mcrBC) φ80lacZM15 lacX74 recA1 araD139 (ara-leu7697 galU galK rpsL endA1 supG Str*</td>
<td>Invitrogen</td>
</tr>
<tr>
<td>LMC500</td>
<td>araD139 Δ(argF-lac)U169 deoC1 fab5301 ptsF25 rbsR relA1</td>
<td></td>
</tr>
<tr>
<td>MRE600</td>
<td>RNase 1 gene</td>
<td></td>
</tr>
<tr>
<td>JOE309</td>
<td>MC4100 ara“</td>
<td></td>
</tr>
<tr>
<td>JOE417</td>
<td>ftsQ E14:kan/pc10</td>
<td></td>
</tr>
<tr>
<td>CR306-313</td>
<td>JOE309 ftsQ E14:kan Δ(att-L-lom):bla lacZ pCR45-pCR50/pJC10</td>
<td>This work (each strain carries a different integration plasmid encoding a Flag-tagged ftsQ version)</td>
</tr>
<tr>
<td>SU202</td>
<td>lexA71::Tn5 recA+ subD11FΔ(lacIP312YAZ)Δ169/F′ lacPlacDΔM15::Tn9 op408/op7 lacZ</td>
<td></td>
</tr>
<tr>
<td>MM39</td>
<td>araD lacDΔU169 malDΔ44Sta</td>
<td></td>
</tr>
</tbody>
</table>

Plasmids*  
pBS-FtsQ    | bla ftsQ | Laboratory collection |
pBAD24     | araC P_{BAD} blu | 18 |
| pLD104     | araC P_{BAD} pffQ blu | 19 |
pBAD24-FtsQ* | araC P_{BAD} ftsQ* blu | This work |
pTHV038    | lacP P_{psd-down} gff-mut2 blu | 8 |
pTHV039    | lacP P_{psd-down} gff-mut2-fsQ blu | 1 |
pTHV-FtsQ* | lacP P_{psd-down} gff-mut2-fsQ* blu | This work |
pC4Meth108FtsQ | lacP P_{psd-down} ftsQ{5\cdot1-108}Met4-HindIII | 37 |
pC4Meth108FtsQ* | lacP P_{psd-down} ftsQ{5\cdot1-108}Met4-HindIII | This work |
pC4Meth108FtsQ-TAG40 | lacP P_{psd-down} ftsQ{TAG40}{5\cdot1-108}Met4-HindIII | This work |
pC4Meth108FtsQ*-TAG40 | lacP P_{psd-down} ftsQ{TAG40}{5\cdot1-108}Met4-HindIII | This work |
pDSW204    | IPTG-regulated promoter, Amp* | 39 |
pJC10      | pBAD33-fsQ | 39 |
pCR45-pCR50 | pDSW204-fsQ* araD | This work |
pBLM100    | bla lexA4′-km-rele | 32 |
pALM148    | bla lexA4′-km-rele | 32 |

3 min. The flowthrough (100 μl) was stored at -20°C, and the beads were washed four times with 500 μl of buffer I with 0.1% DDM and then resuspended in 80 μl of 1× SDS-PAGE sample buffer and incubated at 95°C for 5 min. Five μl of each sample was analyzed by SDS-PAGE and Western blotting. Blots were probed with anti-Flag (monoclonal; Sigma) or anti-FtsL or anti-FtsB (polyclonal; laboratory collection) antibody.

RESULTS AND DISCUSSION

Construction of FtsQ TMS mutants and their ability to complement a temperature-sensitive ftsQ1 mutant. In order to study the role of the FtsQ TMS, we introduced several mutations that would alter the hydrophobicity and charge of the TMS (leucine replaced by arginine) or that are predicted to disrupt the structure of the α-helical TMS (valine replaced by proline), as proline is known to introduce a kink into an α-helix (Fig. 1). Single replacements L29R and L32R were made, and both were combined to further decrease the hydrophobicity and increase the charge of the TMS. Also, the single replacement V38P was made, and this mutation was combined with the L29/32R double mutation to generate the L29/32R;V38P triple mutant. Importantly, all mutants were predicted to still form a TMS when analyzed by the topology prediction program TMHMM2.0 (24).

First, the functionality of the mutants was assayed. Wild-type FtsQ and the FtsQ mutants were introduced into the pBAD24 plasmid, resulting in FtsQ expression under the control of arabinose (18). The plasmids were introduced into the temperature-sensitive ftsQ1 strain MJC129 and tested for their capability to restore growth at the nonpermissive temperature in the presence of arabinose, on a plate as well as in liquid culture. A control experiment with the original domain swap construct FFO (19) confirmed that FFO complements ftsQ1(Ts) both on plates and in liquid under our experimental conditions (Fig. 2). All single-residue replacements supported good growth in liquid as well as on plates, indicating that these FtsQ mutants are functional. The triple mutant L29/32R;V38P failed to complement the ftsQ1(Ts) strain, both on plates and in liquid culture, indicating that this mutant is not functional. Finally, the L29/32R double mutant failed to complement in liquid culture but did show growth, albeit reduced, on plates. The partial complementation on plates is probably caused by elevated FtsQL29/32R levels throughout the membrane (see below), which results in sufficient FtsQ at the cell division site to support division. When tested in the ftsQ depletion background used for co-IP studies (see below), FtsQ L29/32R gave rise to formation of wrinkled colonies, again indicative of defective FtsQ (17), whereas the single mutants fully complemented and the triple mutant did not complement at all (not shown). We conclude that the L29/32R mutant is partially defective.

The L29/32R;V38P triple mutant is not correctly assembled into the membrane. Defects in FtsQ function due to a change in the TMS can have several causes. FtsQ is a target for the signal recognition particle pathway (36), which ensures correct targeting of FtsQ to the Sec translocon, where it is cotranslationally translocated (reviewed in reference 26). Defective targeting could result in folding and aggregation of FtsQ in the cytoplasm, which would render the protein translocation incompetent. Also, a change in the TMS could affect the interaction of FtsQ with the Sec translocon and associated proteins such as YidC, resulting in incorrect membrane insertion and translocation. Furthermore, defects could be caused by the inability of FtsQ to localize to the cell division site or the inability to recruit downstream proteins.

To analyze whether the FtsQ TMS mutants were still tar-
geted to the Sec translocon, we made use of a site-specific cross-linking assay developed in our laboratory. Previously, we established that FtsQ nascent chains with a length of 108 amino acid residues and a photoactivatable cross-linker coupled to a Phe residue incorporated at position 40 (108FtsQ) are efficiently cross-linked to both SecY and YidC when the nascent chains are synthesized in the presence of E. coli inverted membrane vesicles (IMVs) (33, 37). Nascent chains of all FtsQ TMS mutants were synthesized, incubated with IMVs, and photo-cross-linked (Fig. 3). Carbonate extraction was used to separate soluble and peripherally associated membrane proteins from IMVs, and the IMP fraction was analyzed for the presence of cross-linked adducts to FtsQ nascent chains. The amount of cross-linked adduct was corrected for the amount of labeled nascent chain present in the reaction and compared with wild-type FtsQ. All constructs except the triple L29/32R; V38P mutant were found to be efficiently cross-linked to both SecY and YidC (Fig. 3A), with a notable increase in cross-linking efficiency for the V38P single mutant and a slight decrease in efficiency for the L29/32R double mutant. This result indicates that the triple mutant is severely affected in targeting to the membrane but that in all other cases the FtsQ TMS (which contains the photoactivatable cross-linker) is targeted to the translocon and presumably inserted into the membrane.

To study the correct translocation of the full-length FtsQ mutant constructs, we made use of a proteinase accessibility assay. When E. coli cells expressing wild-type FtsQ are converted to spheroplasts and subsequently incubated with proteinase K, the large periplasmic domain of FtsQ is degraded and FtsQ can no longer be recovered from the spheroplasts by IP (38). Proteinase accessibility can therefore be used to monitor the translocation of the periplasmic domain. All FtsQ TMS mutants were expressed from pBAD24 in the presence of [35S]methionine before converting the cells to spheroplasts and proteinase K treatment. Subsequently, FtsQ was recovered by IP, as well as the outer membrane protein OmpA and the cytoplasmic protein trigger factor (TF), which served as controls for spheroplast formation and integrity, respectively. The only FtsQ mutant that could be recovered from proteinase-treated spheroplasts was the triple mutant L29/32R;V38P, indicating that this mutant is not translocated across the membrane (Fig. 3B). This is in accordance with the defect in targeting of this mutant to the translocon (see above). All other mutants could be recovered from untreated spheroplasts but were accessible to proteinase K, indicating translocation of the proteins. Importantly, all controls showed efficient spheroplast formation (proteinase accessibility of OmpA) and good spheroplast integrity (proteinase inaccessibility of TF) (Fig. 3B). A slight difference in motility on SDS-PAGE was observed for all mutants except L29R, but it is not uncommon for TMS mutations to change protein mobility (33). Also, we observed that the L29R single mutant was expressed at lower levels in repeated experiments. The reason for the reduced expression level is not known, but it seems that the plasmid used in this assay is the same that restored viability to the ftsQ1(fps) mutant, we conclude that the L29R mutant is expressed to sufficient levels.

The L29/32R double mutant does not efficiently localize to the cell division site. The functional deficiency of the L29/32R double mutant is not caused by a defect in membrane insertion and translocation, as shown above. Therefore, we tested the capability of the mutant proteins to localize to the cell division site, a prerequisite for FtsQ function. GFP fusions to FtsQ were constructed in exactly the same way as an already existing.
and tested GFP fusion to the wild-type protein. GFP-FtsQ is expressed from plasmid, from an attenuated P_{trc} promoter that is not completely shut down in the absence of inducer (1). Strains carrying GFP fusions to either wild-type or mutant FtsQ were grown at steady state in the absence of inducer to allow expression of detectable but low-level amounts of GFP-FtsQ. As expected, all single mutants localized to the cell division site, corresponding with their observed functionality (Fig. 4). In contrast, the L29/32R double mutant localized to the membrane but in a diffuse pattern without clear enrichment at cell division sites (Fig. 4). This failure to efficiently localize to the division site explains why the double mutant is not fully functional, but it may contain sufficient FtsQ at the division site at high levels of protein expression. Finally, the triple mutant, which was found to be incapable of correct membrane insertion and translocation, localized in a diffuse cytosolic pattern, in accordance with its failure to integrate into the membrane.

The FtsQ TMS does not seem to interact with the TMS of other division proteins. We wanted to test whether the FtsQ TMS can directly interact with the TMS of other bitopic membrane proteins involved in cell division, as the loss of such an interaction could explain the FtsQ L29/32R phenotype. The TMSs of FtsQ, FtsI, FtsB, FtsL, and FtsQ L29/32R were assayed for their capacities to form either homo- or heterooligomers using the GALLEX system, which allows the detection of transmembrane helix-helix interactions in the E. coli membrane (32). None of the TMSs was found to interact (data available at http://www.bio.vu.nl/vakgroepen/molmic/publications.html). So, the FtsQ TMS does not interact with TMSs of proteins with which it is known to interact, like FtsB and FtsL, at least not to the extent that the interaction can be detected by the GALLEX assay.

The L29/32R double mutant interacts with FtsB and FtsL. Cell division proteins FtsB and FtsL are dependent on each other and on FtsQ for localization to the cell division site (4). FtsQ, FtsB, and FtsL form a protein complex in the membrane, but strikingly, this complex can be assembled independently of the localization of FtsQ to the cell division site (3). As our FtsQ L29/32R double mutant was defective for localization, we wanted to test whether this mutant still bound FtsB and FtsL. A C-terminal Flag$_3$ tag was added to wild-type as well as the mutant FtsQ proteins to facilitate immunoprecipitation of FtsQ. A complementation experiment with the FtsQ$_{flag3}$ variants indicated that FtsQ$_{flag3}$ is fully functional (not shown). FtsQ$_{flag3}$ was immunoprecipitated from DDM-solubilized membranes, and the precipitates were screened for the presence of FtsB and FtsL. FtsB and FtsL were both efficiently precipitated with wild-type FtsQ or mutant FtsQ, but the FtsQ L29/32R;V38P triple mutant did not efficiently precipitate FtsB and FtsL (Fig. 5). FtsB and FtsL were not detected in a mock experiment using solubilized membranes from cells that did not express FtsQ$_{flag3}$ (lane 1), indicating that the precipitation is dependent on the presence of a Flag$_3$-tagged variant of FtsQ. We conclude that the FtsQ L29/32R mutant can still interact with FtsB and FtsL, despite having lost the ability to localize to the division site. Surprisingly, the FtsQ L29/32R;V38P mutant was detected in solubilized membranes even though the protein is poorly targeted to and not functionally inserted in the membrane (see above). We attribute the detection of the triple mutant, and low amounts of precipitated FtsB and FtsL (lane 6), to the formation of insoluble aggregates by FtsQ L29/32R;V38P that precipitate with the membrane fraction. Subsequently, partial solubilization of the aggregates facilitates aspecific interaction of the triple mutant with FtsB and FtsL. Indeed, we found that of the FtsQ L29/32R;V38P associated with the membrane fraction, only ~50% could be solubilized with 1% DDM, whereas all other FtsQ variants were solubilized efficiently (not shown).

Concluding remarks. In this study we provide evidence for a contributory role of the FtsQ TMS in targeting to the site of...
cell division. Original domain swap experiments suggested that both the cytoplasmic domain and the TMS of FtsQ are not essential for FtsQ function, as they can be replaced by nonhomologous sequences (7, 19). However, a closer inspection of these results shows that they may, in fact, be consistent with a role for the FtsQ TMS in FtsQ function, as the swap constructs are not fully efficient in complementation and localization. More recent reports (13, 17) also have hinted at a role for the FtsQ TMS that extends beyond its functioning as an inert membrane anchor. Our results provide support for this role. It is of course striking that the replacement of the FtsQ TMS with the unrelated TMS of MalF still allows FtsQ localization and function, whereas the double mutant described in this paper has lost the capability to efficiently localize to the division site. The defects observed in the L29/32R double mutant and L29/32R;V38P triple mutant must be caused by an additive effect of the combined single mutations, as none of the single mutants was defective in growth and localization. The L29/32R double mutant was shown to be capable of membrane insertion and complex formation with FtsB and FtsL. Therefore, a likely explanation for the localization defect is that the interaction of FtsQ L29/32R with an upstream division protein, most likely FtsK, is lost or altered. The FtsQ TMS consists of 25 amino acid residues, which is rather long. An attractive hypothesis is that the introduction of two positive charges in the α-helix, close to the cytoplasmic face of the lipid bilayer, causes the helix to reorient in such a way that the charges are closer to the anionic lipid headgroups rather than embedded in the membrane. This reorientation could cause a change in the tilt of the TMS or pull FtsQ slightly more into the membrane. Both structural changes could affect the interaction with FtsK, if the FtsQ-FtsK interaction site is located in the cytoplasmic and/or TMS domain of FtsQ. A change in TMS tilt or pulling FtsQ into the membrane could also alter the structure or accessibility of the periplasmic domain. This could affect the interaction with FtsK (or some other protein) when the two proteins interact via the membrane-proximal regions in their periplasmic domains. As FtsB and FtsL still interact with the FtsQ double mutant, we expect that the more-membrane-distal regions of the FtsQ periplasmic domain are still correctly folded and positioned. Alternatively, the introduction of two positive charges in the FtsQ TMS could repel the TMS of an interacting protein (like FtsK), thereby disrupting other interactions between the two proteins. The MalF TMS, like the wild-type FtsQ TMS, is completely noncharged and would therefore not have the same repulsion effect. Our observations are consistent with the increasing evidence that cell division proteins contact each other through multiple interactions using multiple domains (17). Finally, the introduction of the positive charges could disturb the interaction of the helix with a specialized lipid domain at the division site. The presence of lipid domains enriched in negatively charged nonbilayer lipids at the site of cell division has been observed in E. coli and B. subtilis (27), and this specific lipid composition could play a role in the recruitment of membrane proteins. We will test these hypotheses in future studies. The set of experiments presented in this paper allows a detailed characterization of FtsQ biogenesis, from targeting to the Sec translocon to localization at the division site, and has great potential for the characterization of the biogenesis of other membrane proteins.

ACKNOWLEDGMENTS

We thank Corin ten Hagen-Jongman, Jorrit Boekel, Maija Tusia, Pieter Smit, and Wouter Jong for technical assistance. We thank Dirk Schneider (University of Freiburg, Germany) for the kind gift of GALLEX strains and plasmids.

D.J.S. is funded by a VENI fellowship from the Research Council for Earth and Life Sciences from The Netherlands Organization for Scientific Research. C.R. holds a Marie Curie Outgoing International Fellowship. G.J.H. was funded by EU grant QLRT-1999-30082. T.D.B. is funded by VENIawingsimpuls grant 016.001.024 of The Netherlands Organization for Scientific Research.

REFERENCES

Penicillin-binding protein PBP2 of *Escherichia coli* localizes preferentially in the lateral wall and at mid-cell in comparison with the old cell pole. Mol. Microbiol. 47:539–547.


