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Bacterial protein translocation requires only one copy of the SecY complex in vivo

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The transport of proteins across the plasma membrane in bacteria requires a channel formed from the SecY complex, which cooperates with either a translating ribosome in cotranslational translocation or the SecA ATPase in post-translational translocation. Whether translocation requires oligomers of the SecY complex is an important but controversial issue: it determines channel size, how the permeation of small molecules is prevented, and how the channel interacts with the ribosome and SecA. Here, we probe in vivo the oligomeric state of SecY by cross-linking, using defined co- and post-translational translocation intermediates in intact Escherichia coli cells. We show that nontranslocating SecY associated transiently through different interaction surfaces with other SecY molecules inside the membrane. These interactions were significantly reduced when a translocating polypeptide inserted into the SecY channel co- or post-translationally. Mutations that abolish the interaction between SecY molecules still supported viability of E. coli. These results show that a single SecY molecule is sufficient for protein translocation.

Introduction

In bacteria, most secretory and membrane proteins are transported across or are integrated into the plasma membrane by a process that is similar to protein translocation across the ER membrane in eukaryotes (Driessen and Nouwen, 2008; Park and Rapoport, 2012). The translocation of these proteins is triggered by hydrophobic sequences, either cleavable signal sequences or noncleaved transmembrane (TM) sequences. The polypeptide substrates are translocated across the membrane through a hydrophilic channel formed by a conserved heterotrimeric membrane protein complex, the SecY complex in bacteria and archaea, and the Sec61 complex in eukaryotes. The complex consists of a large α-subunit (SecY or Sec61p) that spans the membrane ten times, and two smaller, single-spanning β- and γ-subunits (called SecG and SecE in bacteria). The channel associates with different partners that provide the driving force for translocation. In bacteria, the SecY channel can either associate with the ribosome to translocate proteins during their synthesis (cotranslational translocation), or it can cooperate with the cytosolic ATPase SecA to transport proteins after completion of their synthesis (post-translational translocation). The exact mechanism of protein translocation is still poorly understood. In particular, it is unclear whether one or more SecY/Sec61 complexes are required for translocation, an issue that impacts on several crucial aspects of translocation.

The question of how many SecY/Sec61 copies form the translocation channel has been controversial. Based on crystal structures of SecY complexes from different bacterial and archaean species, it was proposed that a single copy of the complex forms the translocation channel (Van den Berg et al., 2004; Tsukazaki et al., 2008; Zimmer et al., 2008; Egea and Stroud, 2010). The channel has an hourglass shape (Van den Berg et al., 2004), with an empty cytoplasmic cavity and an extracellular cavity that is filled with a short helix, the plug, which moves out of the way during protein translocation. The constriction of the hourglass is formed by a pore ring of amino acids, which likely surround the polypeptide chain during its passage through the channel (Van den Berg et al., 2004). Translocation through a single SecY copy is supported by disulfide cross-linking experiments with a SecA-dependent translocation substrate, which indicate that both the signal sequence and the following polypeptide segment can be cross-linked to the same SecY molecule (Osborne and Rapoport, 2007). In addition, electron
microscopy structures show that a single copy of Sec61/SecY complex is bound to a ribosome, with the cytoplasmic funnel of the translocation channel located underneath the ribosome tunnel (Ménétret et al., 2007, 2008; Becker et al., 2009; Frauenfeld et al., 2011). Based on the crystal structures, it has been proposed that the channel itself is responsible for maintaining the membrane barrier for small molecules (Van den Berg et al., 2004). Indeed, recent experiments support the view that the resting channel is sealed by both the pore ring and the plug domain; during translocation, the pore ring forms a gasket-like seal around the polypeptide chain, which prevents the permeation of small molecules (Park and Rapoport, 2011).

Other experiments suggest that the channel is formed from oligomers of the SecY/Sec61 complex. For example, fluorescence-quenching experiments indicate a channel diameter of 40–60Å in intact microsomal membranes (Hamman et al., 1997), which is inconsistent with the pore being formed from just one copy of the Sec61 complex. It was argued that these experiments are more reliable than those performed in detergent or with reconstituted SecY molecules (Hamman et al., 1997; Lin et al., 2011). Because of the large pore size, it was proposed that the membrane barrier for small molecules is provided by BiP binding to the luminal end of the channel in the resting state, and by the translating ribosome binding to the cytoplasmic side of the channel during translocation (Hamman et al., 1998). Oligomers of the SecY/Sec61 complex have also been detected in intact membranes by cross-linking (Kaufmann et al., 1999; Schaletzky and Rapoport, 2006), fluorescence energy transfer (Mori et al., 2003; Snapp et al., 2004), and freeze-fracture electron microscopy experiments (Scheuring et al., 2005). However, it is unclear how the SecY/Sec61 molecules are arranged in these oligomers. A two-dimensional structure of the E. coli SecY complex in a lipid bilayer and cross-linking data indicate that two SecY molecules can associate back-to-back, i.e., with the long TM segments of the SecE subunits facing each other (Kaufmann et al., 1999; Breyton et al., 2002; Deville et al., 2011). Recent EM data show a synthetic signal peptide bound to only one of the two back-to-back–associated SecY molecules (Hizlan et al., 2012). Other orientations of the SecY molecules in the oligomers have also been suggested (Das and Oliver, 2011; Dalal et al., 2012). The oligomers detected in membranes cannot be very stable, as detergent-solubilized SecY complexes tend to behave as monomers, except under gentle solubilization conditions (Bessonou et al., 2002).

Even if a single SecY/Sec61 complex is sufficient to form the pore of the channel, this does not necessarily mean that protein translocation can occur with just one copy. For example, it is conceivable that additional Sec61/SecY molecules stabilize the ribosome-channel junction (Schaletzky and Rapoport, 2006; Gumbhart et al., 2009), or that a second SecY molecule prevents the dissociation of SecA from the translocating SecY copy, thereby enhancing the processivity of SecA during translocation of a polypeptide chain (Osborne and Rapoport, 2007; Deville et al., 2011; Dalal et al., 2012). In fact, several results suggest that a dimer may be required for at least SecA-dependent translocation. Using proteoliposomes with reconstituted SecY proteins, it was shown that a defective SecY molecule can be rescued for translocation by linking it covalently with a wild-type SecY copy (Osborne and Rapoport, 2007). Furthermore, liposomes containing a single SecY molecule had a reduced translocation activity compared with vesicles containing dimeric SecY (Deville et al., 2011), and lipid nanodiscs containing only one SecY molecule did not stimulate ATPase activity of SecA, in contrast to nanodiscs containing two SecY copies (Dalal et al., 2012). The coexpression of two different mutant SecYs, each displaying a translocation defect, also resulted in increased translocation activity (Dalal et al., 2012). On the other hand, a recent study using fluorescence-correlation spectroscopy suggested that a single SecY complex molecule is sufficient for SecA-mediated translocation in vitro (Kedrov et al., 2011). However, these experiments were performed at extremely low SecY concentrations, which favor the dissociation of oligomers, and they were complicated by the fact that SecY is reconstituted into proteoliposomes in both orientations. Most importantly, they did not monitor directly the mobility of active SecY channels, as the translocation substrate was unlabeled. A major problem with all these studies is that they are performed at rather artificial conditions.

Here, we have tested whether SecY oligomers are required for protein translocation under physiological conditions. To this end, we have developed new methodology that allowed us to study defined translocation intermediates in intact E. coli cells. We use these methods to demonstrate that a single SecY molecule is sufficient for both co- and post-translational translocation.

## Results

### Interactions between resting SecY channels in the E. coli plasma membrane

We first investigated the oligomeric state of resting SecY channels by treating E. coli cells with the transcription inhibitor rifampicin, which leads to the depletion of translocating polypeptides. Single cysteines were introduced into periplasmic loops of SecY and a bismaleimide was added to intact cells to induce cross-links between two SecY molecules. The cysteines were placed in four of the five periplasmic loops of SecY on the periphery of the channel (Fig. 1 A). Cysteines at positions 297 and 395 were incorporated as part of a small, flexible insert to increase their accessibility to the cross-linking reagent. The mutants and a cysteine-lacking control SecY were expressed from a plasmid under the endogenous promoter and were functional, as they complemented a secY deletion (Fig. S1 A).

We first tested whether the introduced cysteines are accessible to a modification reagent (biotin-PEG₃-maleimide) that has about the same size as the bismaleimide cross-linker. After treatment, modified proteins were detected after incubation with streptavidin by a mobility shift in SDS-PAGE. Streptavidin (SA)-bound SecY bands were visible for all cysteines (Fig. 1 B). Next, we incubated cells with bismaleimide-PEG₃ (BM-PEG₃), a bi-functional cross-linker with an ~17Å linker between the maleimide groups. The reaction was quenched and the samples were subjected to SDS-PAGE and blotting with SecY antibodies. Efficient cross-linking between two SecYs was seen with Cys151 and Cys212 (Fig. 1 C). Cross-linking with Cys297
A single SecY complex suffices for translocation \cite{Das2011}. A model of a front-to-front associated SecY dimer would indeed bring Cys151 of two SecYs close to one another (Fig. S1 C).

To provide further evidence for these two distinct interaction surfaces of SecY, we used disulfide bridge cross-linking. For the front-to-front interaction, we placed single cysteines at different positions in the loop between TM segments 3 and 4 and examined the formation of a disulfide-bridged dimer (Fig. 1 D). A cysteine placed at position 154 gave a prominent cross-link, even without addition of an oxidation reagent (Fig. 1 D). As expected, or 395 was significantly less efficient. Similar results were obtained when BM-PEG was added directly to the bacterial culture, rather than to bacteria resuspended in buffer (Fig. S1 B). Cross-linking between Cys212 residues might have been expected, as this residue is close to the interface of a previously observed back-to-back SecY dimer (Fig. 1 A; Breyton et al., 2002). However, Cys151 is in the loop between TM segments 3 and 4, which lies on the opposite side of SecY (the front; Fig. 1 A). This front-to-front interaction may correspond to a dimer suggested by SecA–SecY cross-linking experiments (Das and Oliver, 2011).
the intensity of the cross-linked product was greatly diminished upon addition of a reducing reagent (β-mercaptoethanol; β-ME). The spontaneous formation of a disulfide bridge suggests that two SecYs must come close to one another through their front surfaces.

To test for disulfide bridge formation between the back surfaces of SecY complexes, we used a SecE mutant with a cysteine at position 106 (Kaufmann et al., 1999). To exclude cross-linking between free SecE(106C) molecules that are not part of the SecY complex (Kaufmann et al., 1999), we generated a fusion protein containing SecE(106C), SecG, and SecY in one polypeptide chain (Fig. 1 E); the C terminus of SecE was linked to the N terminus of SecG with a short linker, and the C terminus of SecG was connected to the N terminus of SecY through an additional, unrelated TM segment. This fusion protein (scSecEGY) was stable and complemented a secY-null mutant (Fig. S1 A). When cells were lysed and treated with the oxidation reagent copper phenanthroline (CuPh3), a prominent disulfide-linked dimer of the fusion protein was observed after blotting with antibodies to either SecY or the N-terminal His-tag (Fig. 1 F). No dimer was seen when the cysteine was lacking or when β-ME was added after cross-linking. Thus, SecY complexes can interact with each other through their back surfaces. When one cysteine was introduced at the front (position 151), and another one at the back (position 212), the addition of the bismaleimide cross-linker led to a ladder of cross-linked SecY products (Fig. S1 D), indicating that the two interaction surfaces in the SecY complex can be used at the same time.

To test the stability of the SecY oligomers, we expressed simultaneously a SecY molecule with a cysteine at either position 151 or 212 from the endogenous promoter, and an additional SecY copy lacking a cysteine (SecY-Cys−) from the inducible arabinose promoter; SecY-Cys− also contained a C-terminal calmodulin-binding peptide (CBP) tag (SecY-Cys−-CBP) to distinguish it from the cysteine-containing SecY copy. If SecY forms stable oligomers, one would expect that the coexpression of the two SecY molecules over an extended time period (1 h) leads to defined assemblies that contain both cysteine-containing and -lacking SecY molecules, and the cross-linking yield should therefore decrease. Upon expression of SecY-Cys−-CBP, the ratio of cysteine-free to cysteine-containing SecY molecules reached ~1.5:1, but the cross-linking efficiency of cysteine-containing SecY molecules was not reduced (Fig. S1, E and F). These data support the notion that the interactions between SecY molecules with both their front and back surfaces are relatively short-lived.

Translocation intermediates can be generated in vivo with just one SecY copy

Next, we tested whether the cotranslational insertion of a polypeptide into the translocation channel requires a SecY oligomer. To this end, we generated a translocation intermediate in vivo, using a previously established substrate (DsbA-SecM, formerly called NC100; Park and Rapoport, 2011). This is a polypeptide of 100 amino acids, containing the signal sequence of DsbA (Fig. 2 A), which targets the substrate to the cotranslational pathway (Scherle et al., 2003). A SecM-stalling sequence at the C terminus causes the ribosome to arrest translation, with the nascent chain associated as peptidyl-tRNA (Nakatogawa and Ito, 2001). DsbA-SecM was synthesized from the inducible arabinose (Ara)-inducible promoter in cells producing SecY at approximately endogenous level using a GUG translational start codon (plasmid pACYC-SecYEG). After addition of the oxidant CuPh3 to the cell culture to induce disulfide bridge formation, the lysate was analyzed by SDS-PAGE and blotting with SecY antibodies. Where indicated, rifampicin (Rif) was added for different time periods. Red arrows and black asterisks indicate cross-links between SecY and substrate or endogenous proteins, respectively. For quantification of three independent experiments, see Fig. 3 C, right panel.
when the cells were treated with rifampicin to clear all translocation sites before addition of the oxidant (lanes 7–10). Also, this cross-linked product was not generated when DsbA-SecM expression remained uninduced, although minor cross-links to endogenous nascent chains were observed instead (lanes 5 and 6). The observed cross-linking yield of 73% is a lower estimate because some SecY channels may be occupied by endogenous substrates even after expression of DsbA-SecM, and disulfide formation is not 100% efficient. The fact that the cross-linking efficiency is substantially higher than 50% argues that only one molecule of SecY is required to accommodate the translocating DsbA-SecM chain.

To perform similar experiments with a post-translational substrate, we developed a new method to generate a translocation intermediate with a SecA-dependent substrate (OmpA-GFP). This polypeptide contains 79 amino acids, including the signal sequence of the post-translational substrate proOmpA, fused to a fast-folding GFP variant (Pédelacq et al., 2006). With this substrate, one expects that the N terminus inserts into the SecY channel and that the folded GFP blocks further translocation through SecA and SecY (Fig. 3 A). To monitor insertion of the polypeptide into the channel, a cysteine was placed immediately after the signal sequence at position 21, and another cysteine into SecY (position 68). Efficient disulfide cross-linking between OmpA-GFP and SecY was observed upon addition of an oxidant to intact cells (Fig. 3 B, lane 2; the appearance of two cross-linked bands is due to incomplete unfolding of GFP in SDS sample buffer). No cross-linking was seen when either the substrate or SecY lacked the cysteine (lanes 6 and 8), when the cysteines were modified with N-ethylmaleimide (NEM) before addition of the oxidant (lane 3), or when the signal sequence was rendered nonfunctional by introducing two arginine residues (lane 10). As expected, the cross-linked product disappeared upon addition of the reducing agent β-ME (lane 4). These data demonstrate that a stable, post-translational translocation intermediate can be generated in vivo. With this substrate and SecY expressed at its endogenous level, ~67% of all SecY molecules could be cross-linked (Fig. 3 C, lane 4; controls as in Fig. 2 B). When the cysteine was placed at position 32 of OmpA-GFP, instead of position 21, the cross-linking efficiency was even higher (74%; see Fig. S2). Given that the cross-linking efficiency is substantially higher than 50%, only one molecule of SecY is required to accommodate the translocating OmpA-GFP chain.

To further investigate whether the majority of translocation sites are occupied with OmpA-GFP, we tested whether the polypeptide substrate can block the permeation of small molecules through an open SecY channel. We have previously shown that SecY lacking its plug domain (ΔP) is permeable to various small molecules, including the modification reagent birnin-maleimide and chloride ions, and that a cotranslationally inserted polypeptide chain can block the permeation of these molecules (Park and Rapoport, 2011). We now asked whether the post-translationally inserted polypeptide OmpA-GFP can do the same. When birnin-maleimide (browning-PEG₄-maleimide) was added to cells expressing SecY(ΔP), various cytosolic proteins, including a prominent protein of 30 kD (p30), were modified as demonstrated by blotting with HRP-conjugated streptavidin (Fig. 3 D, lane 3). The localization of the modified proteins in the cytosol was previously demonstrated by cell fractionation (Park and Rapoport, 2011). Most of the permeability is due to nontranslocating, resting channels, as the addition of rifampicin did not drastically change cytosolic protein modification (lane 4). When OmpA-GFP was expressed under the inducible arabinosine promoter, the extent of modification was reduced to a level similar to that seen with cells expressing wild-type SecY (lane 2 vs. 10). Expression of a signal sequence mutant of OmpA-GFP did not have this effect (lane 8). Similar results were obtained when the permeation of chloride ions was tested after conversion of E. coli cells into spheroplasts (Fig. S3). Thus, most of the SecY channels can be occupied with the post-translational translocation substrate OmpA-GFP.

The oligomeric state of the SecY channel engaged in translocation

We next tested whether the insertion of a polypeptide into the SecY channel changes the oligomeric state of SecY. The cotranslational (DsbA-SecM) or post-translational (OmpA-GFP) substrate was expressed under the arabinosine promoter in cells expressing SecY with a single cysteine at either position 151 (at the front) or 212 (at the back). Cross-linking with the bi-functional reagent BM-PEG₄ showed that both the front-to-front and back-to-back interactions of SecY molecules were drastically reduced (Fig. 4, lane 4 vs. 2, lane 10 vs. 8, lane 16 vs. 14, and lane 22 vs. 20). Thus, it appears that SecY oligomers dissociate into monomers upon insertion of a translocating polypeptide chain. Because both front-to-front and back-to-back dimers dissociate, it seems likely that SecY molecules weakly associate with each other in the plane of the membrane, and that the equilibrium is shifted toward monomers upon insertion of a translocating polypeptide.

To investigate the possibility that a translocating SecY channel might associate with a nontranslocating SecY copy, we performed experiments under conditions where not all channels are occupied with a model substrate. We first tested whether a SecY channel containing the cotranslational substrate DsbA-SecM can be cross-linked back-to-back with a nontranslocating SecY channel. These experiments used the single-chain scSecEGY construct with a cysteine at position 106 of SecE for back-to-back cross-linking, and a cysteine at position 68 of SecY for cross-linking with the substrate. To achieve low occupancy of SecY with substrate, we reduced ribosome-associated nascent chains by expression of MazF, an RNase that cleaves mRNAs at ACA sequences (Zhang et al., 2003). The occupancy was indeed reduced (Fig. 5 A, lane 15). For the experiments, the cells were first treated with 5,5'-dithiobis-(2-nitrobenzoic acid) (DTNB) to induce disulfide bridge formation between SecY and the substrate, and then cell extracts were treated with CuPh₃ to test for cross-linking between SecY molecules. Both cross-links between SecY and DsbA-SecM (lanes 9 and 10, 19 and 20) and between SecY and SecY (lanes 18 and 20) were observed, but no double cross-links containing two SecYs and substrate (lanes 10 and 20). Assuming that substrate binding does not
Figure 3. Saturation of SecY channels with a post-translational translocation intermediate. (A) Scheme of a post-translational translocation intermediate generated with SecA and the substrate OmpA-GFP. The translocating chain contains the signal sequence of OmpA at the N terminus and the “superfolder” GFP at the C terminus. Its insertion into the SecY channel is monitored by disulfide bridge formation between cysteines in the substrate and SecY. (B) The insertion of OmpA-GFP, containing a cysteine at position 21 (21C), into SecY containing a cysteine at position 68 (68C) was tested by disulfide bridge formation after the addition of the oxidant CuPh₃ to intact E. coli cells. Where indicated, the substrate or SecY lacked a cysteine or the cysteines were blocked with N-ethylmaleimide (NEM) before addition of CuPh₃. As a control, a substrate was used with a defective signal sequence (RR-21C). Where indicated, disulfide bridges were reduced by β-mercaptoethanol (β-ME). All samples were analyzed by SDS-PAGE followed by blotting with SecY or GFP antibodies. (C) OmpA-GFP was expressed from the arabinose (Ara)-inducible promoter in cells producing SecY at approximately endogenous level using a GUG translational start codon (plasmid pACYC-SecYEG). After addition of CuPh₃, the lysate was analyzed by SDS-PAGE and blotting with SecY antibodies. Where indicated, rifampicin (Rif) was added for different time periods. Red arrows and black asterisks indicate cross-links between SecY and substrate or endogenous proteins, respectively. (D) Table showing the effects of various treatments on SecY: OmpA-GFP complex formation. The table includes treatments such as Ara, Rif, Biotin-maleimide, and their effects on ΔP (WT) and ΔP (Res). The lanes represent different time points for Rif treatment. The right panel shows quantification of the cross-linking efficiency between SecY and translocation substrates, based on the decrease of non-cross-linked SecY in experiments such as shown in the left panel and Fig. 2 B. Three different experiments were analyzed (mean...
drastically change the distance between the cysteines in the interacting SecY molecules, it appears that substrate does not insert into back-to-back–associated SecY dimers.

Next, we performed similar experiments with the post-translational substrate OmpA-GFP. To increase the percentage of nonoccupied SecY channels, we reduced the expression of OmpA-GFP by changing the translation start codon from AUG to the less efficient GUG codon, and by adding rifampicin for 30 min to clear the SecY channels from most endogenous substrates (Fig. S4). As a result, the cross-linking efficiency of SecY to OmpA-GFP was drastically reduced (Fig. 5 B, lane 15). The cells were first treated with DTNB to induce SecY substrate cross-links, and then with CuPh₃ to test for SecY–SecY back-to-back cross-linking. While single cross-links were prominent (lanes 9, 10, 19, and 20; and lanes 18, 20), double-cross-links containing both two SecYs and substrate were weak (lanes 10 and 20). Thus, it appears that the majority of substrate molecules insert into monomeric SecY.

Next, we tested whether front-to-front–associated SecY molecules can insert a translocation substrate. Here, we exploited the fact that SecYs with a cysteine at position 154 spontaneously form a disulfide-bridged dimer. SecY also contained a cysteine at position 68 to test for the insertion of substrate containing a cysteine following the signal sequence. After inducing the expression of either DsbA-SecM or OmpA-GFP, the oxidant CuPh₃ was added to generate a disulfide bridge between SecY and substrate. With the cotranslational substrate, efficient cross-links between SecY and SecY (Fig. 5 C, lanes 13–16) and between SecY and DsbA-SecM (lanes 4, 8, 12, and 16) were observed, but no double cross-links (lanes 8 and 16). Thus, the cotranslational substrate does not insert into front-to-front–associated SecY dimers. With the post-translational substrate, weak double cross-links were seen (Fig. 5 D, lanes 8 and 16), indicating that the majority of molecules also inserts into monomeric channels.

**Dimerization-defective SecY mutants**

To directly test the role of the back-to-back and front-to-front association of SecY molecules, we generated mutants in which these interactions are disrupted. We first screened for mutations with defective back-to-back association by placing different amino acids at position 106 of SecE, the point of closest contact of two SecY complexes. To this end, we expressed from a plasmid SecY complex containing mutant SecE and SecY with a cysteine at position 212; SecY dimer formation was determined after addition of BM-PEG₃. Placing a bulky or negatively charged residue at position 106 of SecE reduced dimer formation only moderately, but introducing an arginine had a drastic effect, although the levels of SecE and SecY were only slightly reduced (Fig. 6 A). The residual dimer formation likely originates from SecY complexes containing endogenous SecE. Indeed, when the same mutant was expressed in a strain lacking endogenous SecE, no dimer formation was observed (Fig. 6 B). Remarkably, this strain had no detectable growth defect (Fig. 6 C), suggesting that a back-to-back–associated SecY dimer is not required for protein translocation.

To disrupt the front-to-front association of SecY molecules, we introduced arginine residues into TM segment 3 of SecY, which is close to the predicted interaction surface. Based on the crystal structure (Tsukazaki et al., 2008; Zimmer et al., 2008), we placed two arginines at positions where their side chains would point away from the SecY complex. To avoid problems with membrane integration efficiency, we also replaced some of the less hydrophobic amino acids in TM3 with more hydrophobic ones. The resulting SecY mutant (TM3²RR) was totally defective in front-to-front dimerization, as measured by cross-linking of SecY with a cysteine at position 151 after addition of BM-PEG₃ (Fig. 6 D). However, when present as the sole copy, the mutant SecY supported cell growth indistinguishably from the wild-type strain (Fig. 6 E). Thus, a front-to-front–associated SecY dimer is also not essential for protein translocation. A mutant of the SecY complex that carried mutations disrupting both front-to-front and back-to-back associations (SecY(TM3²RR) and SecE(106R)) was also able to complement a strain lacking both SecE and SecY and grew with wild-type kinetics (Fig. S5). Thus, even the simultaneous disruption of both interactions has no deleterious effect on translocation.

One potential caveat to our conclusion is that a small amount of dimers may still be formed in the mutants and might be essential for the viability of cells. To exclude this possibility, we expressed wild-type and mutant SecY at different levels and monitored both dimer formation and cell viability. To express SecY at reduced levels, we used plasmids with different origins and SD). (D) OmpA-GFP with either a wild-type (WT) or defective (RR) signal sequence was expressed under the arabinose (Ara)-inducible promoter in cells producing SecY at approximately endogenous level using a GUG translational start codon. SecY carried either a cysteine at the front [SecY(151C)] or at the back [SecY(212C)]. Cross-linking of SecYs (SecY₁) was tested after addition of bismaleimidePEG₃(BM-PEG₃) to intact cells. Where indicated, cells were treated with rifampicin (Rif) before cross-linking.

![Figure 4: Dissociation of SecY oligomers upon insertion of a translocating chain](image-url)
of replication and different translation start codons for the secY gene. With these constructs, the level of SecY expression could be varied from 127% compared with the endogenous SecY level in wild-type cells all the way down to 5% (Fig. 7 A). As expected, lowering the SecY level decreased the cross-linking efficiency, both for the front-to-front and the back-to-back associations (Fig. 7 B). However, the decrease was less pronounced than expected from a bimolecular cross-linking reaction between randomly colliding SecY complexes, suggesting that the SecY–SecY interactions have a finite lifetime. When tested in a secY-null strain, the reduction of SecY levels to ~60% had no effect on growth (Fig. 7 C; left). A slight growth defect was seen at a level of 43% and a major defect at 23%. Importantly, the results were similar with a SecY mutant that is defective in front-to-front association (Fig. 7 C; middle). A slight difference in viability was seen at very low levels of SecY expression (~25% of wild-type; Fig. 7 C), which is explained by the reduced stability of the SecY mutant (see immunoblots in Fig. 6 D). Similar results were obtained with a SecY complex compromised in back-to-back dimer formation (Fig. 7 C; right). These data indicate that disruption of dimer formation has a negligible effect on cell growth, even when SecY levels are close to the minimum required for cell viability. Thus, a single copy of SecY is sufficient to support protein translocation.

Discussion

Our experiments provide strong evidence that a single SecY complex is sufficient for protein translocation in vivo. This implies that the pore of the translocation channel is formed from just one SecY molecule and that additional copies of SecY are not essential for moving a polypeptide co- or post-translationally through the channel.

Our cross-linking experiments show that SecY complexes can associate with one another in the plane of the membrane by back-to-back and front-to-front associations. A back-to-back interaction of SecY molecules has been observed previously (Kaufmann et al., 1999; Breyton et al., 2002; Dalal et al., 2012),
A single SecY complex suffices for translocation • Park and Rapoport

and a front-to-front association was suggested on the basis of SecA-SecY photo-cross-linking experiments (Das and Oliver, 2011). Our results now show that, at least in the resting state, SecY molecules can interact with both surfaces inside the membrane of intact E. coli cells. In fact, it is possible that surfaces other than the front and back of a SecY complex can also mediate dimerization. Both the front-to-front and back-to-back interactions of SecY complexes appear to be transient, as demonstrated by competition experiments with noncross-linkable SecY molecules. The interactions can be abolished by introducing positive charges into TM segments at the front or back of the SecY complex, likely because these charges lead to repulsion of SecY complexes in the hydrophobic environment of the membrane. Taken together, our experiments argue against a defined oligomeric state of the SecY complex in native membranes and suggest that SecY complexes interact relatively weakly inside the lipid bilayer, although the actual lifetime of the interactions remains to be determined. A weak interaction between SecY complexes is consistent with fluorescence-correlation spectroscopy experiments, which show little dimer formation when SecY is present at low concentrations in liposomes (Kedrov et al., 2011). It also explains why SecY complexes are monomeric upon solubilization in detergent (Bessonneau et al., 2002).

Using new methods to assemble translocation intermediates in vivo, we show that short translocating polypeptides insert into monomeric SecY. With an excess of substrate, almost all SecY complex molecules can be occupied with either a co- or post-translational translocation substrate. These experiments show that even if oligomers formed through interaction surfaces other than the front or back of the SecY complex, such oligomers would not be required for the insertion of a translocation substrate into the channel. Polypeptide insertion occurs into monomeric SecY channels even under conditions where there are plenty of free SecY molecules available. In fact, for a cotranslational substrate, both back-to-back and front-to-front dimers are entirely incompatible with translocation, as shown by the absence of dimer cross-links with SecY containing a translocating polypeptide. For a post-translational substrate, some molecules inserted into dimeric SecY, but most still preferred monomeric SecY. Taken together, these results indicate that the insertion of a polypeptide chain into the SecY channel requires only a single SecY copy. In principle, it is possible that later stages of translocation require additional SecY copies. However, the fact that
SecY mutants with disrupted back-to-back or front-to-front associations grew at the same rate as wild-type cells suggests that oligomers are not essential for the entire translocation process. This conclusion is consistent with recent fluorescence-correlation experiments (Kedrov et al., 2011).

Our results do not exclude the possibility that oligomerization of SecY complexes may facilitate protein translocation. For example, a nontranslocating SecY molecule might contribute to SecA binding to the channel. Such an assumption could explain the previous observations that a defective SecY mutant can be rescued for translocation by its covalent association with a wild-type SecY copy (Osborne and Rapoport, 2007); a weakened interaction of the translocating SecY copy with SecA might be compensated for by additional interactions of a nontranslocating SecY copy with SecA. A similar interpretation could apply to the observation that two defective SecY mutants can form an active complex (Dalal et al., 2012), that SecA has a substrate-stimulated ATPase activity only when interacting with two SecY molecules in lipid nanodiscs (Dalal et al., 2012), and that cross-linked SecY dimers have an increased translocation activity in single-molecule experiments (Deville et al., 2011). In all these cases, a nontranslocating SecY copy might boost the activity of the translocating SecY copy. However, our data indicate that these nontranslocating SecY copies are not essential for translocation.

The fact that cotranslational translocation requires only one SecY copy is consistent with mechanisms derived from electron microscopy data: the ribosome is bound to a single
SecY channel in such a way that a nascent polypeptide can move directly from the ribosome tunnel into the SecY channel (Ménétret et al., 2007, 2008; Becker et al., 2009; Frauenfeld et al., 2011). Our new data, in conjunction with previous results (Park and Rapoport, 2011), also show that the pore residues of a single SecY molecule form a gasket-like seal that prevents the permeation of small molecules during co- and post-translational translocation. Given the structural conservation of the channel, it is likely that in eukaryotes the pore and membrane barrier are also formed from a single copy of the Sec61 complex.

For SecA-mediated translocation, the new results raise the interesting question of how an interaction of SecA with a single SecY molecule can push a polypeptide chain through the membrane. In one model, SecA would be processive, moving an entire polypeptide chain through the SecY channel without dissociating from it. The interaction of SecA with a single SecY molecule is in fact strong in the ATP-bound state, a state that could be visualized in a crystal structure of the complex (Zimmer et al., 2008). However, in the ADP-bound state, SecA has a weaker affinity for SecY (Zimmer et al., 2008), raising the possibility that SecA would dissociate if it did not have additional binding sites with the membrane. It had been assumed that these sites are provided by a nontranslocating SecY copy (Osborne and Rapoport, 2007), but it now appears that this mechanism is not essential.

A major aspect of the work presented here is the development of methodology to generate protein translocation intermediates in vivo. All previous experiments on the mechanism of protein translocation had been done in vitro or had monitored in vivo heterogeneous populations of nascent chains. Our ability to generate both co- and post-translational translocation intermediates together with the structural information that is available for the SecY complex, SecA, and other translocation components, now opens a new era in the field in which detailed mechanistic questions can be asked in a physiological context.

Finally, it should be pointed out that the question addressed in this paper, i.e., the oligomeric state of the SecY complex, is relevant to other membrane proteins for which oligomerization is considered. For example, as in the case of SecY, it has been generally difficult to determine the oligomeric state of G protein–coupled receptors or ion channels (Duffield et al., 2003; Herr et al., 2010; Grage et al., 2011; Kasai et al., 2011; Dixon et al., 2012), and in several cases, it has been controversial whether oligomers are functionally important. Much of the uncertainty comes from the fact that membrane proteins often interact only weakly through hydrophobic surfaces inside the membrane. Thus, the in vivo cross-linking methodology and the manipulation of interaction surfaces, developed by us for SecY, may help to test the role of oligomers in these cases as well.

### Materials and methods

#### Bacterial strains and plasmids

Strains and plasmids used in this study are listed and described in Tables S1 and S2. Standard PCRs and site-directed mutagenesis were performed with KOD polymerase (EMD Millipore) and were verified by sequencing. E. coli strain DH5α was used for all cloning procedures.

E. coli chromosomal secY- and secE-null strains were constructed by standard λRed recombination techniques (Datsenko and Wanner, 2000). In brief, to make a secYnull strain [EP63], EP61 (ΔsecY ΔompT, see Table S1) cells were transformed with λRed recombinase-encoding pKD46 together with pET2-SecYEG, which expresses the wild-type SecYEG complex under a tetracycline-inducible promoter. The pET2-SecYEG plasmid also includes the p15A origin of replication and a kanamycin resistance gene. After induction of λRed recombinase, the cells were electroporated with a PCR product containing a hygromycin B resistance gene, flanked by short sequences homologous to the chromosomal secY locus (the PCR was performed using the forward primer 5′-TCAAGAGCTGCTGGCGGTAATAATCAGGAATTAGTGGGGTAAAGACCCTGAACTC-3′, the reverse primer 5′-GAACCTCATTATTTCCGGATCTCGGCCTCGGCGGCTAGCGAC-3′; and pAG32 as a template). Colonies were selected on LB agar plates containing 50 µg/ml kanamycin, 100 µg/ml hygromycin B, and 100 µg/ml anhydrotetracycline (aTet). Removal of the chromosomal secY gene was verified by PCR. The resulting strain cannot form a colony on plates without aTet, but grows normally when transformed by a plasmid constitutively expressing wild-type SecY (e.g., pACYC-SecYEG). To generate strains deleted in chromosomal secE [Fig. 6, B and C], EP52 (ΔsecY ΔompT::kan secE-CBP::zeo) cells were transformed with pKD46 and pACYC-SecYEG (containing either the wild-type or L106R mutant secE copy). λRed recombinase–induced cells were electroporated with a PCR product containing a streptomycin resistance marker, flanked by short sequences homologous to the chromosomal secE locus (the PCR was performed using the forward primer 5′-GTTTGCGCAGGATTGTTTGGTTTGTAGAAAAATCGAGGAATAAGTAGCAGATGGGTAAAAAGCCTGAACTC-3′, the reverse primer 5′-CAAAACGGGAAAACCGCTGAACGACGTACCAGCGCTTTTTAGGA-GTGGTGGTGTTATGAGGGAAGCGGTGATCGC-3′; and pCDFDuet-1 as a template). Selection was performed on plates containing 40 µg/ml chloramphenicol and 30 µg/ml streptomycin. A secY/ secE-null strain (EP66) was constructed in essentially the same way, starting with the secYnull strain. The deletion of chromosomal secE was verified by PCR.

#### Growth of bacteria

Experiments were performed with the following strains: EP62 (ΔsecY ΔompT::secY-CBP::zeo) for Figs. 1 (B and C), 6 [A and D], 7 [A and B], and S1; B; EP52 (ΔsecY ΔompT::kan secY-CBP::zeo) for Fig. 5 D; EP53 (ΔsecY ΔompT::secY-CBP::zeo Δαt::kan) for Fig. S3; and EP63 (ΔsecY ΔompT::secY-CBP::hph) for Figs. 1 (D–F), 2 B, 3 [B and C], 4, 5, 6, 7 F, 7 C, S1 (A, D–F), S2, and S4. To express SecY complexes, the cells were transformed with pACYC-SecYEG, which expresses all subunits of the SecY complex from a constitutive endogenous promoter (the ptet promoter). When overexpression of a translocation substrate was needed, pBAD-NC100 (for DsbA-SecM) or pBAD-OmpA-GFP was additionally introduced into the cells. When maximum occupancy of translocation sites by DsbA-SecM or OmpA-GFP was intended (Figs. 2 B, 3 [C and D], 4, S2, and S3), the GUG start codon was used for the SecY gene in pACYC-SecYEG containing the indicated SecY cysteine mutants and pBAD-SecYEG encoding cysteine-free SecY with a C-Terminal calmodulin-binding peptide (CBP) tag. E. coli cells were picked from freshly transformed colonies, inoculated into LB medium supplemented with appropriate antibiotics (100 µg/ml ampicillin for pBAD and pRN1 plasmids; 40 µg/ml chloramphenicol for pACYC-SecYEG; and 15 µg/ml chloramphenicol for pSC101 and pBeloBAC plasmids), and grown at 37°C to log phase (OD600nm = 0.4–0.6) before induction and any other manipulations to induce overexpression of DsbA-SecM or OmpA-GFP. The GUG start codon was used for the SecY gene in pACYC-SecYEG containing the indicated SecY cysteine mutants and pBAD-SecYEG encoding cysteine-free SecY with a C-Terminal calmodulin-binding peptide (CBP) tag. E. coli cultures were grown to log phase, and treated with 100 µg/ml rifampicin for 30 min. After harvesting 4 ml of each culture, the cells were resuspended in 1 mL of buffer containing 50 mM Tris-HCl, pH 7.5, 150 mM NaCl, and 1 mM EDTA. After addition of 0.4 mM bioin PEG_maleimide (Thermo Fisher Scientific), the suspension was incubated for 1 h at 4°C. After washing with 20 mM β-mercaptoethanol for 20 min at 4°C, the cells were washed three times with 1 mL of the buffer and then resuspended in 200 µL of a standard washing buffer containing 100 mM Tris-HCl, pH 7.5, 150 mM NaCl, and 1 mM EDTA.

### In vivo biotinylation and streptavidin gel-shifting assays

E. coli cultures were grown to log phase, and treated with 100 µg/ml rifampicin for 30 min. After harvesting 4 ml of each culture, the cells were resuspended in 1.5 ml of buffer containing 50 mM Tris-HCl, pH 7.5, 150 mM NaCl, and 1 mM EDTA. After addition of 0.4 mM bioin PEG-maleimide (Thermo Fisher Scientific), the suspension was incubated for 1 h at 4°C. After washing with 20 mM β-mercaptoethanol for 20 min at 4°C, the cells were washed three times with 1 mL of the buffer and then resuspended in 200 µL of a standard washing buffer containing 100 mM Tris-HCl, pH 7.5, 150 mM NaCl, and 1 mM EDTA.
of buffer containing 50 mM Tris-HCl, pH 7.5, 10 mM β-mercaptoethanol, 1 mM phenylmethylsulfonyl fluoride, 1.5 kU r-lysozyme (EMD Millipore), 16 U/ml Benzonase nuclease (EMD Millipore), and 0.5% Triton X-100. 25 µg streptavidin (GenScript) was added to a 40-µl aliquot of the reaction, and binding was allowed for 1 h at 4°C. The samples were then supplemented with 0.1% SDS, 12.5% glycerol, and bromophenol blue for SDS-PAGE.

Cysteine cross-linking experiments

Cells were grown to log phase and pelleted by brief centrifugation. Where indicated, E. coli cultures were supplemented with 100 µg/ml rifampicin for 30 min at 37°C before harvest. For cross-linking of SecY molecules with a bi-functional cross-linker, the cells were resuspended at the original volume in a buffer containing 50 mM Tris-HCl, pH 7.5, 150 mM NaCl, and 1 mM EDTA. Cross-linking was initiated by addition of 0.4 mM bismaleimide-PEG (The work was supported by a grant from the National Institutes of Health [GM052586]. The authors declare no competing financial interests. T.A. Rapoport is a Howard Hughes Medical Institute investigator.

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References


Online supplemental material

Fig. S1 shows the functionality of SecY mutants and the interaction between resting SecY complexes in vivo. Fig. S2 shows that the majority of SecY complexes can be occupied with the OmpA-GFP substrate. Fig. S3 shows that insertion of OmpA-GFP reduces chloride permeation through the open SecY channel. Fig. S4 shows that the occupation of SecY with OmpA-GFP can be reduced by lowering the expression level. Fig. S5 demonstrates that a SecY mutant defective in front-to-front and back-to-back dimerization is as functional as wild-type SecY. Tables S1 and S2 list the strains and the SecY mutant defective in both front-to-front and back-to-back dimerization.

SDS-PAGE, image acquisition, and densitometry analysis

SDS-PAGE was performed using 4–12% Bis-Tris gels (Invitrogen and Bio-Rad Laboratories) with either MÉS-SDS or MOPS-SDS running buffer (Invitrogen). For each SDS-PAGE experiment, samples from equal numbers (ODD600nm) of cells were loaded on lanes. Rabbit polyclonal antibodies against the C terminus of E. coli SecY were described previously (Cannon et al., 2005). Mouse monoclonal antibodies recognizing an internal segment of E. coli SecY were a gift from Ian Collinson (University of Bristol, England, UK). Mouse monoclonal anti-GFP (clones 7.1 and 13.1), anti-Myc (9E10), and anti-His antibodies (A01186) were obtained from Roche, Sigma-Aldrich, and GenScript, respectively. Rabbit polyclonal anti-trigger factor (TF) antibodies (A01329) were obtained from GenScript. A standard ECL reagent was used to develop immunoblots. All images including immunoblots and agar plates were taken with the CCD-based device LAS-3000 (Fujifilm) using the acquisition software Image Reader LAS-3000 (Fujifilm). The levels of images were adjusted using Adobe Photoshop. Image software (National Institutes of Health, Bethesda, MD) was used for densitometry analysis (using raw 16-bit images).


