SecYEG activates GTPases to drive the completion of cotranslational protein targeting

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Signal recognition particle (SRP) and its receptor (SR) comprise a highly conserved cellular machine that cotranslationally targets proteins to a protein-conducting channel, the bacterial SecYEG or eukaryotic Sec61p complex, at the target membrane. Whether SecYEG is a passive recipient of the translating ribosome or actively regulates this targeting machinery remains unclear. Here we show that SecYEG drives conformational changes in the cargo-loaded SRP–SR targeting complex that activate it for GTP hydrolysis and for handover of the translating ribosome. These results provide the first evidence that SecYEG actively drives the efficient delivery and unloading of translating ribosomes at the target membrane.

Introduction

Correct cellular localization of proteins is essential for the proper functioning of all cells. A conserved protein-conducting channel, SecYEG in bacteria or Sec61p in eukaryotes, is the point of convergence of post- and cotranslational protein targeting pathways and mediates the translocation or integration of newly synthesized proteins (Cross et al., 2009; du Plessis et al., 2011). In bacteria, the major posttranslational pathway is mediated by the chaperone SecB and the SecYEG-interacting ATPase SecA, which deliver fully synthesized proteins to the periplasm (Hartl et al., 1990; Zhou and Xu, 2003; Driessen and Nouwen, 2008). The cotranslational route is mediated by signal recognition particle (SRP) and its receptor (SR), which target ribosome-nascent chain complexes (RNCs) to SecYEG (Walter and Johnson, 1994; Cross et al., 2009).

Extensive work on the Sec pathway showed that SecYEG and preproteins stimulate SecA’s ATPase activity and activate it to drive the translocation of preproteins into the periplasm (Duong, 2003; Karamanou et al., 2007; Gold et al., 2010; Deville et al., 2011; Kedrov et al., 2011; Dalal et al., 2012). Whether SecYEG also regulates the activity of SRP and SR to drive cotranslational protein targeting is unknown. The SecY subunit of SecYEG forms a stable complex with the translating ribosome by interacting with the ribosomal exit site and the signal sequence of the nascent protein (Van den Berg et al., 2004; Cannon et al., 2005; Frauenfeld et al., 2011). It is unclear, however, whether SecYEG simply binds RNCs released from SRP or actively regulates the activity of the RNC–SRP–SR targeting complex.

The functional core of SRP is the SRP54 GTPase (Ffh in bacteria) bound to the 4.5 S RNA (Poritz et al., 1990). The bacterial SR, FtsY, has a GTPase domain highly homologous to that in Ffh (Montoya et al., 1997a). During targeting, SRP and FtsY form a heterodimer in which both proteins undergo a series of conformational changes, including the early, closed, and activated states, that culminate in reciprocal GTPase activation (Fig. 1 A; Egea et al., 2004; Shan et al., 2004, 2009; Zhang et al., 2009). To ensure efficient and faithful delivery of cargo proteins to the target membrane, these rearrangements are regulated by RNC (Zhang et al., 2009) and phospholipids (Lam et al., 2009). RNC stabilizes the early intermediate but disfavors its rearrangement to the subsequent states. This generates a highly stable early targeting complex in which RNC is predicted to bind SRP with picomolar affinity and GTP hydrolysis is delayed (Zhang et al., 2009). Rearrangement of this complex to the closed/activated states, however, is required for the unloading of RNC (Shan et al., 2007; Zhang et al., 2009) and activation of GTP hydrolysis. In part, these rearrangements could be driven by anionic phospholipids, which stabilize the

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Results and discussion

SecYEG destabilizes the early targeting complex

We previously showed that RNCs stabilize the SRP–FtsY GTPase complex in the early conformational state, disfavor its rearrangement to subsequent conformations, and delay GTPase activation (Zhang et al., 2008, 2009). These effects prevent abortive reactions and are beneficial at early stages of the pathway. However, they pose a barrier to the cargo unloading and GTPase activation required at later stages of the pathway. To test whether SecYEG can help drive these late events, we purified SecYEG (Fig. S2 A) and first showed that it is active in RNC binding (Fig. S2 B). Furthermore, when reconstituted into proteoliposomes, SecYEG was active in SecA-dependent translocation of proOmpA (Fig. S2 C) and cotranslational translocation of a modified alkaline phosphatase bearing an SRP-dependent signal sequence derived from DsbA (Fig. S2 D). We focused on SecYEG solubilized in dodecyl-β-maltopyranoside (DDM) in this work, as it is fully functional in interaction with RNC, mediates proper insertion of the signal sequence (Mothes et al., 1998; Fig. S2B), and activates SecA (Duong, 2003; Gold et al., 2010; Deville et al., 2011). Further, because liposomes also exert stimulatory effects on the basal activity of FtsY and accelerate formation of the SRP–FtsY complex (Lam et al., 2010), the use of SecYEG in DDM allows us to distinguish its effects from those of phospholipids.

We asked whether and how SecYEG regulates the conformation of the SRP and FtsY GTPases in the RNC–SRP–FtsY complex. We first tested the early intermediate, which is stabilized ~10-fold by RNCs bearing highly hydrophobic signal sequences such as IA9L (Zhang et al., 2009). As this intermediate can form with or without GTP but its subsequent rearrangement is strictly GTP dependent, it can be isolated by leaving out GTP analogues (Zhang et al., 2008; Fig. 1 A). Foster resonance energy transfer (FRET) between coumarin-labeled SRP Cys235 and BODIPY-FL–labeled FtsY Cys487 was used to monitor formation of this intermediate (Zhang et al., 2008). Equilibrium titrations showed that SecYEG destabilized the RNC–SRP–FtsY early intermediate at least 15-fold, whereas DDM had no effect (Fig. 1, B and F). The destabilizing effect of SecYEG increases linearly with its concentration (Fig. 1 C), which indicates strong antagonism between SecYEG and the early complex. Importantly, SecYEG also lowered the FRET end point (Fig. 1, B and F), which suggests that it alters the conformation of the GTPases in the early complex.

We next asked whether SecYEG affects the subsequent states in the GTPase complex (Fig. 1 A). To test this, we used an environmentally sensitive dye, acrylodan, conjugated to SRP Cys235. In the presence of a nonhydrolyzable GTP analogue, 5′-guanylylimido-diphosphate (GppNHP), acrylodan at this position specifically changes fluorescence upon formation of the closed/activated complex (Zhang et al., 2009). Equilibrium titrations using this assay gave similar $K_d$ values in the absence and presence of SecYEG (Fig. 1, D and F). As the $K_d$ value of this complex is >20-fold below the concentration of SRP needed for reliable titrations, a possible effect of SecYEG

closed/activated states of FtsY (Lam et al., 2010). Membranes, however, are insufficient to drive the release of RNC (Song et al., 2000) or reverse the RNC-induced delay of GTP hydrolysis (Fig. S1). What drives these late events during the targeting reaction is unknown.

Here we show that SecYEG drives late conformational changes of the targeting complex and reactivates GTP hydrolysis. Our results demonstrate an active role of SecYEG in cotranslational protein targeting and suggest a concerted mechanism for handover of RNC from the targeting to the translocation machinery.
on its stability might have escaped detection. To more specifically monitor the activated complex, we used acrylodan-labeled FtsY Cys356, which specifically detects movements of catalytic loops required for GTPase activation (Zhang et al., 2009). This assay revealed a two- to fourfold stabilization of the activated complex by SecYEG (Fig. 1, E and F). Together, these results demonstrate that SecYEG drives conformational changes of the targeting complex by destabilizing the early intermediate and modestly favoring the activated complex (see Fig. 5 A).

**SecYEG reactivates GTP hydrolysis by the targeting complex**

If SecYEG drives GTPase rearrangements to the activated state, it would reverse the RNC-induced delay of GTPase activation and reconvert GTP hydrolysis. To test this hypothesis, we determined the effect of SecYEG on the GTP hydrolysis rate of the SRP–FtsY complex of SecYEG (kcat). As observed previously, RNC delays GTPase activation, reducing the kcat value from 80 min⁻¹ to 22 min⁻¹. SecYEG restored the kcat value to 66 min⁻¹, approaching that of the SRP–FtsY complex alone (Fig. 2 A). This stimulatory effect of SecYEG was saturable, with an apparent Kd value of ~2 µM (Fig. 2 B), which could represent the affinity of SecYEG for the targeting complex. The stimulation was not an artifact of DDM, as DDM concentrations up to 0.22% did not affect GTP hydrolysis from the RNC–SRP–FtsY complex (Fig. 2 C). In comparison, the concentration of DDM in the assay was <0.14%, as determined by a phenol-sulfuric acid reaction (Dubois et al., 1956). Indeed, even 0.02% DDM had an inhibitory effect on the stimulated GTPase activity in the absence of RNC (Fig. 2 D), which suggests that the actual GTPase stimulation by SecYEG may be even greater than observed here.

As SecYEG was reported to interact with FtsY (Angelini et al., 2006; Kuhn et al., 2011), we asked if SecYEG affects the basal GTPase activity of FtsY. Reactions were performed in the presence of 4 µM FtsY, 100 µM GTP, and the indicated concentrations of SecYEG. (f) In the absence of RNC, SecYEG does not significantly affect GTP hydrolysis from the SRP–FtsY complex. The data were fit to Eq. 3 and gave kcat values of 60 and 51 min⁻¹ in the absence (closed) and presence (open) of 12 µM SecYEG, respectively. The data in A, B, D, E, and F are the average of two experiments ± SD (error bars).
SecYEG forms a quaternary complex with RNC, SRP, and FtsY at steady-state, in which GTP hydrolysis is activated. To distinguish between these possibilities, we analyzed the effect of SecYEG on the kinetics of formation of the closed SRP–FtsY complex. RNC dramatically accelerates the assembly of this complex (Zhang et al., 2009), providing a robust diagnostic for whether it is bound to SRP (Fig. 3 A, red and green). If SecYEG did not remove RNC from SRP, then the kinetics of closed complex formation in the presence of SecYEG would remain rapid. Consistent with this prediction, in the presence of SecYEG and RNC, the rate of closed complex assembly was similar to that with RNC-bound SRP and much faster than with free SRP (Fig. 3 A). SecYEG itself does not affect complex assembly between SRP and FtsY (Fig. S3), and thus is not responsible for the fast assembly kinetics observed in Fig. 3 A. Further, in the presence of both SecYEG and RNC, the early → closed rearrangement of the SRP–FtsY complex occurred at the same rate, within error, as that with the RNC-loaded SRP, and was significantly slower than with free SRP (Fig. 3 A). SecYEG itself does not affect complex assembly between SRP and FtsY (Fig. S3), and thus is not responsible for the fast assembly kinetics observed in Fig. 3 A. Further, in the presence of both SecYEG and RNC, the early → closed rearrangement of the SRP–FtsY complex occurred at the same rate, within error, as that with the RNC-loaded SRP, and was significantly slower than with free SRP (Fig. 3 A and B). We further tested the ability of mtSecYEG to destabilize the early intermediate and found that, relative to wtSecYEG, this activity was significantly impaired (Fig. 4, C and D). Thus, the conserved basic residues in the cytosolic loops of SecYEG are essential for its ability to drive conformational changes in the targeting complex and to reactivate GTP hydrolysis. These results also support the specificity of the stimulatory effects observed with SecYEG and suggest that the action of its cytosolic loops occurs before RNC docking, when the targeting machinery first contacts SecYEG.

SecYEG could use its basic cytosolic loops to contact either the ribosome (Ménétret et al., 2007; Becker et al., 2009) or the A domain of FtsY (Kuhn et al., 2011). To distinguish between these possibilities, we removed the N-terminal 196 residues comprising the A domain of FtsY, generating mutant FtsY-NG (Parlitz et al., 2007). FtsY-NG could mediate the formation of the RNC-stabilized early intermediate with SRP with a Kₐ value similar to that of the complex formed by full-length FtsY (Fig. 4, E and F). SecYEG destabilized the early intermediate formed by FtsY-NG to the same extent, within error, as that formed by full-length FtsY (Fig. 4, E and F). These results are in agreement with the poor conservation of the A domain in bacteria (Eitan and Bibi, 2004) and its dispensability in vivo (Eitan and Bibi, 2004; Parlitz et al., 2007). Our results here...
the stabilizing effect of RNC on the early complex (Lam et al., 2010) and reactivate the GTPases in the RNC–SRP–FtsY complex (Fig. S1). Association with SecYEG is required to overcome these “stalling” effects of RNC. Together, phospholipids and SecYEG drive the rearrangement of the targeting complex to the activated conformation, which enables the transfer of RNC to SecYEG and activates GTP hydrolysis, thus completing the targeting cycle. As shown in Fig. 3, SecYEG likely exerts these effects by forming a transient quaternary intermediate with the targeting complex, in which it displaces the SRP GTPase from the ribosomal exit site (Fig. 5 B; Halic et al., 2006). As the early complex is stabilized by interaction with the SRP RNA tetraloop (Shen and Shan, 2010), which is optimal only when the SRP NG domain interacts with L23, displacement of the GTPase complex from the ribosome exit site would also explain the destabilizing effect of SecYEG on the early complex. The questions of the fate of the signal sequence in the quaternary intermediate, what drives its transfer to SecYEG, and whether SecYEG interacts with FtsY’s GTPase domain (Angelini et al., 2005, 2006; Kuhn et al., 2011) during these events invite future investigations.

show that the A domain is not essential for the ability of SecYEG to drive conformational changes in the targeting complex. Instead, the basic cytosolic loops in SecYEG likely interact with the ribosomal protein L23 at the nascent polypeptide exit site (Ménétret et al., 2007; Becker et al., 2009), thus exerting its stimulatory effects.

Collectively, the results here provide the first evidence that SecYEG actively modulates the conformation of the targeting complex to drive completion of the cotranslational protein targeting reaction. Combined with previous work (Song et al., 2000; Gold et al., 2010; Lam et al., 2010; Braig et al., 2011), these results suggest that SecYEG and anionic phospholipids serve overlapping yet distinct functions in mediating the delivery of the targeting complex to sites of translocation. The targeting complex preferentially localizes to regions of the membrane enriched in anionic phospholipids (Fishov and Woldringh, 1999; Vanounou et al., 2003; Erez et al., 2010; Lam et al., 2010), with which SecYEG may also preferentially associate (Campo et al., 2004; Shiomi et al., 2006; Gold et al., 2010). Although phospholipids can induce rearrangements in FtsY to favor the closed/activated states (Lam et al., 2010), they are insufficient to overcome the stabilizing effect of RNC on the early complex (Lam et al., 2010) and reactivate the GTPases in the RNC–SRP–FtsY complex (Fig. S1). Association with SecYEG is required to overcome these “stalling” effects of RNC. Together, phospholipids and SecYEG drive the rearrangement of the targeting complex to the activated conformation, which enables the transfer of RNC to SecYEG and activates GTP hydrolysis, thus completing the targeting cycle. As shown in Fig. 3, SecYEG likely exerts these effects by forming a transient quaternary intermediate with the targeting complex, in which it displaces the SRP GTPase from the ribosomal exit site (Fig. 5 B; Halic et al., 2006). As the early complex is stabilized by interaction with the SRP RNA tetraloop (Shen and Shan, 2010), which is optimal only when the SRP NG domain interacts with L23, displacement of the GTPase complex from the ribosome exit site would also explain the destabilizing effect of SecYEG on the early complex. The questions of the fate of the signal sequence in the quaternary intermediate, what drives its transfer to SecYEG, and whether SecYEG interacts with FtsY’s GTPase domain (Angelini et al., 2005, 2006; Kuhn et al., 2011) during these events invite future investigations.
Materials and methods

Materials

Full-length FtsY, FtsY-NG, Ffh, and 4.5 S RNA were expressed and purified as described previously (Montoya et al., 1997b; Peluso et al., 2001). Single cysteine mutants of FtsY and Ffh were labeled with fluorescent dyes, 7-diethylamino-4-methylcoumarin-3-yl maleimide (DACM), the maleimide derivative of BodipyFL, or acrylodan (Invitrogen) as described previously (Zhang et al., 2008). Site-specific labeling of FtsY and Ffh with fluorescent dyes was performed as described in Zhang et al. (2008, 2009). Single cysteine mutants were generated based on pEK20 using the QuikChange mutagenesis protocol (Agilent Technologies). SecYEG was expressed in MRE600 cells. mRNA containing a truncated mature region of PhoA with 1A9L signal sequence and SecM stalling sequence was translated at 37°C for 25 min. Stalled RNCs were bound to a Strep-Tactin Sepharose column (IBA), eluted with desthiobiotin (Sigma-Aldrich), pelleted, and redissolved in the assay buffer. For GTPase assays, monosomes were purified using a 10–50% continuous sucrose gradient and ultracentrifugation at 23,000 rpm 4°C for 15 h (SW-32 rotor; Beckman Coulter). The monosome fraction was pelleted at 55,000 rpm 4°C for 15 h (TLA-55 rotor; Beckman Coulter) and dissolved in assay buffer.

Preparation of RNC

RNCs were generated and purified as described previously (Schaffitzel and Ban, 2007; Zhang et al., 2009), using in vitro translation in a membrane-free extract from E. coli MRE600 cells. mRNA containing a truncated mature region of PhoA with 1A9L signal sequence and SecM stalling sequence was translated at 37°C for 25 min. Stalled RNCs were bound to a Strep-Tactin Sepharose column (IBA), eluted with desthiobiotin (Sigma-Aldrich), pelleted, and redissolved in the assay buffer. For GTPase assays, monosomes were purified using a 10–50% continuous sucrose gradient and ultracentrifugation at 23,000 rpm 4°C for 15 h (SW-32 rotor; Beckman Coulter). The monosome fraction was pelleted at 55,000 rpm 4°C for 15 h (TLA-55 rotor; Beckman Coulter) and dissolved in assay buffer.

Expression and purification of SecYEG

SecYEG containing N-terminally His6-tagged SecY was expressed from plasmid pEK20 (du Plessis et al., 2009), a gift from A. Driessen (University of Groningen, Groningen, Netherlands). SecY charge reversal mutants were generated based on pEK20 using the QuikChange mutagenesis protocol (Agilent Technologies). SecYEG was expressed in BL21 (DE3) cells and purified using previously described protocols (Van den Berg et al., 2004; Dalal and Duong, 2010) with modifications. All steps were performed at 4°C. Cells were lysed by sonication in KS300G buffer (50 mM K Hepes, pH 7.5, 300 mM NaCl, and 10% glycerol). After removal of intact cells (12,000 g, 20 min), membranes were collected by ultracentrifugation at 42,000 rpm for 45 min (Ti45; Beckman Coulter) and extracted for 1 h in KS100G buffer (50 mM K Hepes, pH 7.5, 100 mM NaCl, and 10% glycerol) containing 1% DDM per 10 mg/ml total protein. The suspension was clarified by ultracentrifugation at 42,000 rpm for 32 min (Ti70 rotor; Beckman Coulter). The supernatant was purified by cation exchange on SP-Sepharose Fast Flow resin (GE Healthcare; 12 ml per 6 liters of cells) in KS100G/0.02% DDM, and eluted using a gradient of 100–1,000 mM NaCl. Elution fractions containing SecYEG were further purified by affinity chromatography on Ni-NTA Agarose (Qiagen; 2 ml of resin per 6 liters of cells). Protein was loaded and washed with KS300G/0.02% DDM/20 mM imidazole, and eluted with KS300G/0.02% DDM/300 mM imidazole. Purified SecYEG was dialyzed against 50 mM K Hepes, pH 7.5, 150 mM KAOac, 10% glycerol, 2 mM DTT, and 0.02% DDM for 12 h. The concentration of SecYEG was determined using absorbance at 280 nm and an extinction coefficient of 71,000 M⁻¹ cm⁻¹ (Kedrov et al., 2011).

Figure 5. **SecYEG drives conformational changes in the RNC-SRP-FtsY complex.** (A) Free energy profile for the FtsY–SRP interaction in the absence (black) and presence (red) of SecYEG. The red arrows denote the effect of SecYEG. Activation energies were calculated from the rate constants using ΔG° = −RT ln(K/κ), where R = 1.987 cal K⁻¹ mol⁻¹, h = 1.58 × 10⁻¹⁶ kcal K⁻¹mol⁻¹, kₐ = 3.3 × 10⁻⁰⁷ kcal K⁻¹mol⁻¹, and T = 298 K. The relative free energies were calculated from the equilibrium stability of the complexes using ΔG = −RT ln(K), where K is the equilibrium constant. A standard state of 1 µM was used. T denotes GTP and D denotes GDP. (B) Model for the role of SecYEG in driving GTPase rearrangements in the targeting complex and completing cotranslational protein targeting. The M domain of Ffh is also shown. The question mark denotes questions regarding the fate of the signal sequence and the interaction of SecYEG with FtsY in the quaternary complex.
The single and double charge reversal mutants of SecYEG were purified as the wild-type SecYEG. The triple charge reversal mutant of SecYEG was purified by two rounds of immobilized metal affinity chromatography using Ni-Sepharose resin (GE Healthcare), following the procedure similar to that described for wild-type SecYEG except that 40 mM imidazole was used during binding and washing, and a 50–500-nM imidazole gradient was used during elution.

Fluorescence measurements

Fluorescence assays were performed as described previously (Zhang et al., 2008, 2009; Lam et al., 2010). All measurements were performed at room temperature in assay buffer [50 mM KPi, pH 7.5, 150 mM KOAc, 10 mM Mg(OAc)2, 2 mM DTT, and 0.01% (w/v) Nikkol] supplemented with 0.02% DDM when necessary. Stability of the early complex was determined using FRET between DACM-labeled SRP Cys235 and BODIPY-fluorescein-labeled FtsY Cys487. Equilibrium titrations were performed with 40 nM SRP, 110 nM RNC where applicable, and 100 µM GDP, with FtsY as a titrant. The data were fit to Eq. 1:

\[
F_{\text{obsd}} = \frac{F_1 \times [\text{SRP}] + [\text{FtsY}] + k_d - \sqrt{F_1 \times [\text{SRP}] + [\text{FtsY}] + k_d^2}}{2 \times [\text{SRP}][\text{FtsY}]},
\]

where \( F_{\text{obsd}} \) is the observed FRET, \( F_1 \) is the maximum FRET value at saturating FtsY concentrations, and \( k_d \) is the equilibrium dissociation constant of the early complex. Scattering due to SecYEG was subtracted before calculating the FRET values.

The stability of the closed/activated complex was determined using acrylodan-labeled SRP Cys235, with FtsY as the titrant. The stability of the activated complex was determined using acrylodan-labeled FtsY Cys356, with SRP as the titrant. Reactions were supplemented with 0.02% DDM. The data were fit to a quadratic equation similar to Eq. 1. When fluorescent FtsY was used, the denominator in Eq. 1 was replaced with 2 \( [\text{FtsY}] \).

The assembly kinetics of the closed complex from free SRP and FtsY was determined in the presence of GppNHp using FRET between DACM-labeled SRP Cys235 and BODIPY-fluorescein-labeled FtsY Cys487, on a Fluorolog 3–22 (Horiba Jobin Yvon) as described previously (Zhang et al., 2009). The rate constant for association of SRP and FtsY \( k_{\text{on}} \) in the absence and presence of SecYEG was determined by measuring the observed rate of association \( k_{\text{on,obsd}} \) at various FtsY concentrations as described previously (Zhang et al., 2009). The FtsY concentration dependence of \( k_{\text{on,obsd}} \) was fit to the equation \( k_{\text{on,obsd}} = k_{\text{on}}[\text{FtsY}] + k_{\text{on}} \), in which \( k_{\text{on}} \) is the rate constant for complex assembly and \( k_{\text{on}} \) is the rate constant for complex disassembly.

The rate of early \( \rightarrow \) closed rearrangement was determined by preforming the early complex with 50 nM acrylodan-labeled SRP C325, 100 nM RNC, and 5 µM FtsY in the absence or presence of SecYEG. Rearrangement to the closed complex was initiated by addition of 200 µM GppNHp and monitored as an increase in acrylodan fluorescence on a stopped-flow apparatus (KinTek). The data were fit to Eq. 2:

\[
F_{\text{obsd}} = F_0 + (F_{\text{max}} - F_0)(1 - e^{-kt}),
\]

in which \( F_0 \) and \( F_{\text{obsd}} \) are the initial and final fluorescence values, respectively, \( F_{\text{obsd}} \) is the observed fluorescence, and \( k \) is the rearrangement rate constant.


translation assay

GTP hydrolysis reactions were performed in assay buffer, and were performed and analyzed as described previously (Peluso et al., 2001). Stimulated GTP hydrolysis of SRP with FtsY was determined using 40 nM SRP, 100 nM RNC where applicable, and increasing concentrations of FtsY as indicated. Wherever applicable, 8–12 µM SecYEG was added last and incubated with the reaction mixture for 10 min before initiation of reaction. The data were fit to Eq. 3:

\[
k_{\text{obsd}} = k_{\text{cat}} \times \frac{[\text{FtsY}]}{K_m + [\text{FtsY}]},
\]

in which \( k_{\text{obsd}} \) is the observed rate constant, \( k_{\text{cat}} \) is the rate constant at saturating FtsY, and \( K_m \) is the concentration of FtsY required to reach the half-maximal rate.

Dose-dependent effects of SecYEG on GTP hydrolysis were measured using a preincubated mixture of 40 nM SRP, 100 nM RNC, and 3 or 8 µM of FtsY, to which an increasing concentration of SecYEG was added before initiation of reaction. The data were fit to an equation analogous to Eq. 3, except that \([\text{FtsY}]\) is replaced with \([\text{SecYEG}]\), \( k_{\text{cat}} \) is replaced with \( k_{\text{cat,YEG}} \), and \( K_m \) is replaced with \( K_m,YEG \).

Co-sedimentation assay

Interaction of SecYEG with RNC was determined using a cosedimentation assay as described previously (Ménétret et al., 2007; Frauenfeld et al., 2003) with modifications. Before use, liposome suspension was activated in a bath sonicator until clear, and diluted with 0.5% Triton X-100 to 4 mg/ml. 200 µg of SecYEG [0.2 mg/ml in 10 mM Tris-HCl, pH 8.0, 10% glycerol, 0.1% DDM, and 100 mM KCl] was mixed with 4 mg of liposomes and incubated for 30 min at 4°C with gentle tumbling. 200 µg of Biobeads SM-2 (Bio-Rad Laboratories), equilibrated in buffer A [50 mM Tris-HCl, pH 8.0, 50 mM KCl, and 1 mM DTT], was incubated with the SecYEG/liposome mixture with gentle stirring for 2 h at 4°C. The beads were removed by centrifugation at 500 g. The procedure was repeated with 200 µg of Biobeads and 4 h of incubation in the second round, and 400 µg of Biobeads and overnight incubation in the third round. SecYEG proteoliposomes were collected by ultracentrifugation at 100,000 rpm for 30 min (TLA-100.3; Beckman Coulter) and dissolved in buffer A containing 10% glycerol. The concentration of SecYEG in proteoliposomes was determined using Coomassie staining on SDS-PAGE along with SecYEG standards of known concentration.

Posttranslational translocation

Activity of SecYEG reconstituted into proteoliposomes was determined by examining SecA-dependent translocation of [35S]-labeled proOmpA and assayed using protection against Proteinase K, as described previously (Cunningham et al., 1989; van der Does et al., 1998, 2003). In brief, in vitro translation of proOmpA was performed in a wheat germ extract (Promega) in the presence of [35S]methionine at 26°C for 30 min and stopped by transferring to ice. Translocation of the substrate into SecYEG proteoliposomes was performed in the presence of SecA and an ATP-regenerating system at 37°C for 15 min and stopped by transferring the reaction to ice. Half of the reaction was treated with 0.02 mg/ml of Proteinase K on ice for 15 min in the absence or presence of 1% Triton X-100 and quenched with PMSF. Both reactions with and without PK treatment were precipitated with TCA, resolved on a denaturing gel, and quantified using autoradiography.

Cotranslational translocation assay

The coupled transcription/translation system used for cotranslational targeting assays has been described previously (Saraogi et al., 2011). The signal sequence of PhoA was replaced with that of the SRP-dependent substrate DsbA and used as a model substrate. The coupled transcription/translation reaction containing [35S]methionine was supplemented with 5 mM GTP, 1 µM SRP, 1 µM FtsY, and either E. coli-derived inner membrane vesicles (IMVs) or SecYEG proteoliposomes, and performed at 37°C for 30 min. The final concentration of SecYEG in the reaction was 2.2 µM. The reactions were quenched on ice, treated with 0.9 mg/ml of Proteinase K for 15 min on ice in the absence or presence of 1% Triton X-100, and quenched with PMSF. The reaction was TCA precipitated and quantified as for the posttranslational targeting reactions.

Online supplemental material

Fig. S1 shows that phospholipids do not reactivate GTP hydrolysis from the targeting complex in the presence of RNC. Fig. S2 describes purification of wild-type and mutant SecYEG, interaction of SecYEG with RNC, and in vitro targeting assays. Fig. S3 shows that SecYEG does not affect kinetics of the closed complex formation. Online supplemental material is available at http://www.jcb.org/cgi/content/full/jcb.201208045/DC1.

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Figure S1. **Liposomes do not reactivate GTPase activity of the RNC–SRP–FtsY targeting complex.** The effect of increasing lipid concentration on the rate of GTP hydrolysis ($k_{\text{cat}}$ values) was measured using 50 nM SRP, 10 µM FtsY, and saturating GTP in the absence (open circles) and presence (closed circles) of 100 nM RNC1A9L. Representative data from two experiments are shown.
Figure S2. Purification and activity of SecYEG. (A) Wild-type (wt) and the triple charge reversal mutant (mt) SecYEG were expressed and purified as described in Materials and methods and resolved on a 15% SDS gel. SecY and SecE-His₆–tagged constructs were used to ensure that the affinity tag does not contribute to ribosome binding. The first panel shows wtSecYEG and mtSecYEG resolved on a denaturing gel. In the second panel, both wtSecYEG and mtSecYEG are tagged at SecY. Charge reversal of basic residues slightly reduces the mobility of SecY. (B) Co-sedimentation assay examining the binding of wtSecYEG and mtSecYEG to RNC, performed as described in the Materials and methods. L denotes the load before centrifugation and P denotes the pellet. (C) SecYEG proteoliposomes mediate SecA-catalyzed translocation of proOmpA. The concentrations of SecYEG in proteoliposomes are indicated above the gel. K denotes Proteinase K. –, equivalent amount of proOmpA before Proteinase K treatment. Where indicated, 1% Triton X-100 was added before treatment with Proteinase K. Gels from two independent experiments are shown. (D) SecYEG proteoliposomes mediate cotranslation translocation of DsbA-PhoA substrate. Combined transcription/translation/translocation of DsbA-PhoA was performed in the presence of either E. coli inner membrane vesicles (IMVs), SecYEG proteoliposomes (3.7 µM), or empty liposomes. The reactions were treated with Proteinase K in the absence and presence of 1% Triton X-100 to assess the extent of translocation. 5% of the translation reaction was loaded as a reference. Representative data from two replicate experiments are shown.

Figure S3. SecYEG does not affect SRP–FtsY complex assembly kinetics in the absence of RNC. Observed complex formation rate constants are determined as described in Materials and methods. Linear fits of the data gave $k_{on}$ values of $3.85 \times 10^4$ M⁻¹s⁻¹ and $3.28 \times 10^4$ M⁻¹s⁻¹ in the absence and presence of SecYEG, respectively. Representative data from two independent experiments are shown.