Fingerloop activates cargo delivery and unloading during cotranslational protein targeting

Aileen R. Ariosa  
*California Institute of Technology*

Stacy S. Duncan  
*Iowa State University*

Oshu Saraogi  
*California Institute of Technology*

Xiaodong Lu  
*Iowa State University*

April Brown  
*Iowa State University*

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Abstract
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Disciplines
Bioinformatics | Computational Biology | Molecular Biology | Veterinary Microbiology and Immunobiology

Comments
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Authors
Aileen R. Ariosa, Stacy S. Duncan, Oshu Saraogi, Xiaodong Lu, April Brown, Gregory J. Phillips, and Shu-Ou Shan

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Fingerloop activates cargo delivery and unloading during cotranslational protein targeting

Aileen R. Ariosa*, Stacy S. Duncanb,*, Ishu Saraogi†, Xiaodong Luba, April Brownb, Gregory J. Phillipsb, and Shu-Ou Shan†

aDivision of Chemistry and Chemical Engineering, California Institute of Technology, Pasadena, CA 91125; bDepartment of Veterinary Microbiology, College of Veterinary Medicine, Veterinary Medical Research Institute, Iowa State University, Ames, IA 50011

ABSTRACT During cotranslational protein targeting by the signal recognition particle (SRP), information about signal sequence binding in the SRP’s M domain must be effectively communicated to its GTPase domain to turn on its interaction with the SRP receptor (SR) and thus deliver the cargo proteins to the membrane. A universally conserved “fingerloop” lines the signal sequence–binding groove of SRP; the precise role of this fingerloop in protein targeting has remained elusive. In this study, we show that the fingerloop plays important roles in SRP function by helping to induce the SRP into a more active conformation that facilitates multiple steps in the pathway, including efficient recruitment of SR, GTPase activation in the SRP–SR complex, and most significantly, the unloading of cargo onto the target membrane. On the basis of these results and recent structural work, we propose that the fingerloop is the first structural element to detect signal sequence binding; this information is relayed to the linker connecting the SRP’s M and G domains and thus activates the SRP and SR for carrying out downstream steps in the pathway.

INTRODUCTION Membrane and secretory proteins, whose syntheses are initiated in the cytosol, must be efficiently localized to their correct cellular destinations to assume their function. The signal recognition particle (SRP) is part of the essential cellular machinery responsible for the cotranslational recognition and delivery of proteins destined to the eukaryotic endoplasmic reticulum (ER) or the bacterial plasma membrane (Walter and Johnson, 1994). As a nascent polypeptide emerges from a translating ribosome, SRP recognizes the ribosome nascent chain complex (termed RNC or the cargo), through interaction with both the ribosome exit site and with N-terminal signal sequences on its substrate protein (Pool et al., 2002; Halic et al., 2004, 2006; Schaffitzel et al., 2006). The cargo is delivered to the membrane via the interaction of SRP with the SRP receptor (SR; called FtsY in bacteria). Subsequently, the RNC is transferred to the protein translocation machinery (Sec61p in eukaryotes or SecYEG in bacteria), where the nascent protein is either translocated across or integrated into the membrane (Gilmore et al., 1982a,b; Keenan et al., 2001).

The composition of the SRP varies across different species, but its functional core is highly conserved and composed of two essential components: the SRP54 protein subunit and the SRP RNA (called Ffh and 4.5S, respectively, in bacteria; Walter and Johnson, 1994). SRP54 (Ffh) contains two structurally and functionally distinct domains connected by an ∼30-amino-acid-long linker: 1) a methionine-rich M domain containing a hydrophobic groove that serves as the signal sequence–binding site and a helix-turn-helix motif that binds the 4.5S RNA (Freymann et al., 1997; Keenan et al., 1998; Batey et al., 2000; Janda et al., 2010); and 2) a special GTPase, NG

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*Present address: Department of Medicine, Division of Infectious Diseases, Vanderbilt University, Nashville, TN 37232.

Address correspondence to: Shu-Ou Shan (sshan@caltech.edu).

Abbreviations used: Amp, ampicillin; BODIPY-F, boron dipyromethene fluorescein; Cm, 7-hydroxycoumaryl ethylglycine; DACM, N-(7-dimethylamino-4-methyl coumarin-3-yl); DTT, dithiothreitol; ER, endoplasmic reticulum; FRET, Förster resonance energy transfer; GppNHp, 5′-guanylylimido-diphosphate; GTP, guanosine-5′-triphosphate; Kan, kanamycin; pPL, preprolactin; RNC, ribosome nascent chain complex; Spc, spectinomycin; SR, SRP receptor; SRP, signal recognition particle; TKR, trypsin-digested, salt-washed ER microsomal membranes.

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domain responsible for interacting with the SR (Egea et al., 2004; Focia et al., 2004) and for contacting the ribosome exit site (Pool et al., 2002; Schaffitzel et al., 2006). The SR, FtsY, also contains an NG domain highly homologous to that in Ffh (Montoya et al., 1997). During protein targeting, the GTP-dependent assembly of a stable complex between the NG domains of Ffh and FtsY mediates the delivery of cargo proteins to the target membrane (Egea et al., 2004; Focia et al., 2004). Subsequent rearrangements in the Ffh•FtsY complex further induce the reciprocal activation of their GTPase activity; this late rearrangement is essential for driving the unloading of cargo to the translocation machinery (Zhang et al., 2008, 2009).

Hydrolysis of GTP then drives the rapid disassembly of the Ffh•FtsY complex, allowing the two proteins to be recycled for additional rounds of targeting (Shan and Walter, 2005).

The SRP RNA is a ubiquitous and indispensable component of the SRP. The Escherichia coli 4.5S RNA contains the universally conserved domain IV of eukaryotic SRP RNA, which forms a hairpin structure capped by a highly conserved GGAA tetraloop (Batey et al., 2000). The SRP RNA binds with picomolar affinity to the SRP54 (or Ffh) M domain in the vicinity of the signal sequence–binding site (Batey et al., 2001). It also regulates the interaction between the Ffh and FtsY GTPases during protein targeting. The tetraloop of the SRP RNA mediates a key electrostatic interaction with FtsY, which accelerates the stable association between the SRP and FtsY GT- Pases by a factor of 200–3000 (Shen et al., 2011). This stimulation occurs only in the presence of RNC bearing correct signal sequences, or stimulatory detergents and signal peptides that partially mimic the effect of RNC, ensuring that the recognition of cargo is tightly coupled to its membrane delivery during protein targeting (Siu et al., 2007; Bradshaw et al., 2009; Zhang et al., 2010; Shen et al., 2011). In addition, the SRP RNA also activates GTP hydrolysis in the SRP•FtsY complex – 10-fold, whereas the cargo negatively regulates this GTPase activation (Peluso et al., 2001; Zhang et al., 2010). Thus there is extensive molecular communication between the cargo, the SRP RNA, and the GTPases throughout different stages of protein targeting. However, the precise molecular mechanism that allows information to be propagated from the signal sequence–binding site in the M domain to the SRP RNA and the GTPases remains to be defined.

Flanking the signal sequence–binding site is an evolutionarily conserved flexible region, the fingerloop, which forms a “flip” over the hydrophobic binding groove. In the absence of a signal sequence, the M domain can adopt a “closed” conformation in which the fingerloop inserts several of its hydrophobic residues into the signal sequence–binding site; it has been proposed that this conformation stabilizes the hydrophobic signal sequence–binding pocket in the free SRP (Rosendal et al., 2003). The fingerloop has also been crystallized in an “open” conformation, in which it folds back from the signal sequence–binding pocket (Keenan et al., 1998). In a recent crystal structure of the M domain in complex with a signal peptide, a few residues of the fingerloop directly interact with the hydrophobic signal peptide (Janda et al., 2010). These observations have led to the suggestion that the fingerloop forms a flexible “lid” that closes down on the signal sequence–binding groove upon cargo binding to the SRP, providing additional hydrophobic contacts with the hydrophobic signal peptide (Keenan et al., 1998, 2001; Rosendal et al., 2003). In addition, the flexibility of the fingerloop, along with the abundance of methionine residues in the M domain, is thought to provide an adaptable binding site that accommodates a variety of signal sequences (Keenan et al., 2001; Bernstein, 1998; Koch et al., 2003; Halic and Beckmann, 2005). Nevertheless, no direct experiments assessing the contribution of the fingerloop in signal sequence binding have been available, and the role of this highly conserved loop in SRP function has remained unclear.

Given its proximity to the signal sequence–binding site, the fingerloop is in an ideal position to sense information about signal sequences; the conformational plasticity of the fingerloop also makes it a good candidate for transmitting this information to the GTPases. In support of this notion, a previous study reported that mutations in the fingerloop disrupt the ability of the SRP RNA to stimulate Ffh•Fts complex assembly (Bradshaw and Walter, 2007; Hainzl et al., 2011). However, these defects could also be explained by the inability of the fingerloop mutants to bind signal sequences. In this work, we defined the roles of the SRP fingerloop on individual molecular steps during the protein-targeting reaction. Our results showed that the fingerloop is not strictly required for high-affinity signal sequence binding, but rather, it helps mediate conformational changes in response to signal sequence binding that propagates to the remainder of Ffh and the 4.5S RNA, thus activating the SRP and FtsY GTPases and facilitating the delivery and unloading of cargo to the translocon.

**RESULTS**

The fingerloop domain is essential for Ffh function

To characterize the fingerloop (FL) of Ffh in vivo, we first constructed strain SLD108 to facilitate complementation tests (see Materials and Methods). SLD108 is not viable at 42°C, because the sole functional copy of ffh is expressed from a temperature-sensitive plasmid, pFfhTspc (Table 1). Growth can be restored at 42°C if the strain is also transformed with a plasmid expressing a functional copy of ffh, pBADffhN6x, which expresses ffh under control of the araBAD operator and promoter. To determine the importance of the fingerloop for Ffh function, we also constructed the ffhΔFL allele by deleting a 60-base pair region that encodes the fingerloop (Figure 1A; Zheng and Gierasch, 1997) on pBADffhN6x (see Materials and Methods).

In cells carrying pBADffhN6x, we observed growth at both the permissive temperature of 30°C, as well as at 42°C, the nonpermissive temperature for pFfhTspc replication (Figure 1B). We observed, conveniently, that arabinose was not necessary for this plasmid to complement ffh::kan1 when grown at 42°C, due to leaky expression from the araBAD promoter at the elevated temperature (Figure 1B). Colonies that appeared at 42°C were retested and confirmed to be spectinomycin sensitive (Spc?), indicating loss of the pFfhTspc plasmid. Moreover, the Spc+ transformants were only able to grow at 30°C when provided with 0.01% l-arabinose (unpublished data). In contrast to the wild-type control, expression of ffhΔFL failed to complement ffh::kan1 in SLD108 (Figure 1B). Consistent with this result, none of the cells recovered from the heavy portion of the streak were Spc+ nor were they able to grow at 30°C.

The fingerloop is often unstructured in crystallographic and biochemical studies of the SRP (Zheng and Gierasch, 1997; Cleverley et al., 2001; Doudna and Batey, 2004; Janda et al., 2010). As an alternative approach to identify key features in the fingerloop, we compared the amino acid sequences of this loop from 109 distinct species representing all three domains of life, using multiple sequence alignment (Thompson et al., 1994). These analyses identified two amino acid pairs, Leu350/Met351 and Pro355/Gly356 from E. coli, that are highly conserved (Figure 1A). To assess the importance of these residues, we generated mutant alleles in which each of these residues was replaced by alanine (Spc+). When expressed in SLD108, the ffhLM→AA allele complemented only slightly better than ffhΔFL, while expression of ffhPG→AA complemented as well as ffh+ (Figure 1B). Expression levels of all Ffh constructs were consistent across the board (Supplemental Figure S1).
Fingerloop is important for SRP-mediated protein targeting

To directly test the effect of the fingerloop mutations on cotranslational protein targeting, we used a well-established in vitro assay that examines the ability of purified SRP and FtsY to target a model SRP substrate, preprolactin (pPL), to ER microsomal membranes (Powers and Walter, 1997; Shan et al., 2007). The efficiency of targeting and translocation can be quantified based on cleavage of pPL signal sequence upon its successful incorporation into the membrane (Figure 2A). Wild-type SRP efficiently targeted pPL, reaching a translocation efficiency of greater than 60% at saturating FtsY concentrations (Figure 2, A and B). Deletion of the fingerloop significantly reduced the targeting efficiency, with only ~30% successful targeting and translocation at saturating FtsY concentrations (Figure 2, A and B). Further, a much higher FtsY concentration was required to reach saturation for the targeting reaction mediated by SRP(ΔFL). The LM→AA mutant also displayed impaired targeting of pPL, but the defect is milder than that of mutant SRP(ΔFL) (Figure 2, A and B).

Qualitatively, these results agreed with the in vivo observations, and together they provide direct evidence that the conserved fingerloop plays an important role in cotranslational protein targeting. We note that several factors could contribute to the stronger phenotype of fingerloop mutants in vivo than in vitro. The in vitro assay represents a single round of targeting and translocation, whereas the defects of SRP mutations can accumulate over multiple rounds of targeting in vivo. In addition, the slower translation rate in vitro than in vivo gives the SRP and FtsY a longer window of time to complete the targeting reaction, such that defects in their assembly (see below: The fingerloop facilitates signal sequence-induced stimulation of SRP•FtsY complex assembly) could be masked. Finally, SRP is limiting in vivo and competes among a much larger number of translating ribosomes than in translation extracts; mutational effects on SRP•RNC binding (see below: The fingerloop is not strictly required for high-affinity cargo binding by the SRP) are therefore easily masked in the in vitro targeting assay but could contribute more significantly in vivo.

The fingerloop is not strictly required for high-affinity cargo binding by the SRP

To test whether compromised binding affinity for signal sequences accounts for the defects of fingerloop mutants in protein targeting, we compared the binding affinities of the wild-type and mutant

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Table 1: Bacterial strains and plasmids.

<table>
<thead>
<tr>
<th>Strain or plasmid</th>
<th>Relevant genotype or description</th>
<th>Source or reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>NEB5α</td>
<td>( \text{fhuA2Δ(argF-lacZ)U169 phoA glnV44 80 Δ(lacZ)M15 gyrA96 recA1 relA1 endA1 thi-1 hsdR17 (general cloning host)} )</td>
<td>New England Biolabs</td>
</tr>
<tr>
<td>ECF529</td>
<td>( \text{ΔaraBAD, ΔrhaBAD, ΔaraFGH, ΔaraE, rnm88(CTC-AGA)-lac} )</td>
<td>Bowers et al., 2004</td>
</tr>
<tr>
<td>XLU102</td>
<td>ECF529, ( \text{Δbla::frt} )</td>
<td>This study</td>
</tr>
<tr>
<td>SLD108</td>
<td>XLU102, ( \text{ffh::kan1, pFfhTSpc} )</td>
<td>This study</td>
</tr>
</tbody>
</table>

Plasmids

- pFfhTSpc: pSC101ts, \( \text{ffh}^+, \text{spc}^\text{(Spc)} \)
- pBAD\text{ffh}6x: araC, \( \text{ffh}^+, \text{bla}^\text{(AmpR)} \), ColE1 (vector for expressing \( \text{ffh} \) under \( \text{P}_{\text{araBAD}} \) control)
- pBAD\text{ffh}N6x: pBAD\text{ffh}6x (NheI)
- pBAD\text{ffh}N6xΔFL: pBAD\text{ffh}N6x with fingerloop deleted
- pBAD\text{ffh}N6xLM-\text{AA}: pBAD\text{ffh}N6x with \( \text{LM} \rightarrow \text{AA} \) mutation
- pBAD\text{ffh}N6xPG-\text{AA}: pBAD\text{ffh}N6x with \( \text{PG} \rightarrow \text{AA} \) mutation

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FIGURE 1: Phenotypes of \( \text{ffh} \) fingerloop mutants. (A) The amino acid sequence of the fingerloop domain of Ffh deleted in the \( \text{ffh}Δ\text{FL} \) allele. Positions of amino acids of the \( \text{E. coli} \) Ffh protein are shown. The underlined amino acids were converted to alanine in the \( \text{ffh}Δ\text{FL} \) and \( \text{ffhPG}→\text{AA} \) alleles. (B) Plasmids expressing \( \text{ffh}Δ\text{FL} \), \( \text{ffhPG}→\text{AA} \), \( \text{ffhLM}→\text{AA} \), and \( \text{ffh}^+ \) alleles were transformed into the temperature-sensitive strain SLD108 and cultured at 30°C (top) or 42°C (bottom) as shown. (C) SLD108 transformants expressing each of the four \( \text{ffh} \) alleles were spotted onto LB+Amp+/-arabinose plates at the dilutions shown at the top and incubated at 42°C overnight.

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SRPs for RNCs bearing the nascent chain of FtsQ, a bona fide SRP substrate (RNC_{FtsQ}; Zhang et al., 2010). RNCs bearing the nascent chain of firefly luciferase (RNC_{Luc}), which contains no signal sequences, served as a control for the ability of SRP to bind ribosomes translating incorrect substrate proteins. SRP was labeled with fluorescein at Cys-421 near the signal sequence–binding groove, and SRP-RNC binding was monitored as a change in the fluorescence anisotropy of Ffh (C421)-fluorescein (Zhang et al., 2010). Equilibrium titrations based on this anisotropy signal showed that wild-type SRP binds to RNC_{FtsQ} and RNC_{Luc} with equilibrium dissociation constants (K_d) of 1.7 and 128 nM, respectively (Figure 3, A and B, filled circles), reflecting a 10-fold contribution of the signal sequence to cargo binding. Unexpectedly, both the ΔFL and LM→AA mutants of SRP were able to bind tightly to RNC_{FtsQ}, with less than threefold change in the value of K_d (Figure 3, A, open symbols, and C). The binding affinity of SRP for RNC_{Luc} was also not substantially affected by the fingerloop mutations (Figure 3, B, open symbols, and C).

To directly monitor signal sequence interactions with the Ffh M domain, the binding of wild-type and mutant SRPs to the RNC were measured using a fluorescent nonnatural amino acid, 7-hydroxycoumaryl ethylglycine (Cm), incorporated near an engineered signal sequence into its binding groove (Saraogi et al., 2009). Förster resonance energy transfer (FRET) between Cm-labeled RNC_{AARL} and boron dipyromethene fluorescein (BODIPY-FL) labeled at residue 421 of Ffh M domain reports directly on the docking of the signal sequence into its binding groove (Saraogi et al., 2011). This assay allowed us to measure, in real time, the association and dissociation rate constants of cargo-SRP binding (Figure 3, D and E, respectively). The results showed that mutants SRP(ΔFL) and SRP(LM→AA) bind and dissociate from RNC_{AARL} with rate constants that differ by no more than threefold from wild-type SRP (Figure 3F). The values of K_d calculated from these rate constants is only twofold weaker with mutant SRP(ΔFL) and sixfold weaker with mutant SRP(LM→AA) (Figure 3F). These results support conclusions from the anisotropy assay; together they indicate that the fingerloop is not strictly necessary for high-affinity signal sequence binding by the SRP. The modest effects of the fingerloop mutants on SRP-RNC binding could contribute, in part, to the phenotype of fingerloop mutants in vivo. Nevertheless, it would be easily masked in the in vitro targeting reaction, in which the concentration of SRP is >50-fold above the K_d values, even with SRP(LM→AA). Thus the observed defects of fingerloop mutants in the in vitro targeting assay could not be attributed to their reduced ability to bind the RNC and instead must arise from subsequent steps in the SRP pathway.

The fingerloop facilitates signal sequence–induced stimulation of SRP•FtsY complex assembly

To efficiently deliver its substrate proteins to the membrane, SRP must rapidly assemble a stable complex with its receptor FtsY. However, to ensure fidelity of protein targeting, complex assembly between free SRP and FtsY is extremely slow but is substantially accelerated by correct cargoes (Zhang et al., 2010) and, to a lesser extent, by signal peptides or the detergent Nikkol, which mimics the effect of signal peptides (Bradshaw et al., 2009). We therefore asked whether efficient SRP•FtsY complex assembly in response to cargo is affected by deletion or mutation of the fingerloop. To this end, we measured the rate constants for formation of the 5'-guanylylimidodiphosphate (GppNHP)-stabilized complex between SRP and FtsY, using either FRET between N-(7-dimethylamino-4-methylcoumarin-3-yl) (DACM)-labeled SRP(C235) and BODIPY-FL–labeled FtsY(C487) or acrylodan-labeled SRP(C235), which specifically changes fluorescence upon guanosine-5'-triphosphate (GTP)-dependent formation of the stable complex (Zhang et al., 2008, 2009). We determined complex assembly rate constants under three conditions: 1) without any stimulant; 2) in the presence of the signal-peptide mimic Nikkol; and 3) in the presence of RNC_{FtsQ}. In the latter cases, SRP was pre-incubated with saturating concentrations of Nikkol or RNC based on the information from previous studies (Bradshaw et al., 2009; Zhang et al., 2010) and above to ensure that >98% of SRP was loaded with cargo or the signal peptide mimic, so that effects of the fingerloop mutations on cargo/signal sequence–binding affinities were bypassed.

In the absence of any stimulant, complex assembly for wild-type SRP and the fingerloop mutants were slow and differed by no more than threefold, ranging from 250–610 μM−1·s−1 (Figure 4, A and C). Consistent with previous results (Bradshaw and Walter, 2007; Bradshaw et al., 2009), stable SRP•FtsY complex assembly was accelerated 50-fold with wild-type SRP in the presence of Nikkol, but this stimulation was abolished with the ΔFL and LM→AA mutations (Figures S2 and 4C). These data support the suggestion that the fingerloop helps mediate the signal peptide–induced stimulation of complex assembly (Bradshaw and Walter, 2007).

As previously demonstrated, RNC_{FtsQ} exerts a larger stimulatory effect on the SRP•FtsY complex assembly than signal peptides or Nikkol, accelerating their complex assembly more than 10^3-fold (Figure 4, B and C; Bradshaw et al., 2009; Zhang et al., 2009; Shen et al., 2011). Intriguingly, RNC_{FtsQ} also provided significant stimulation for the mutants SRP(FL) and SRP(LM→AA), increasing their complex assembly rate constants by 360- and 620-fold, respectively (Figure 4, B and C). In contrast to the observations in the presence of Nikkol, the mutants SRP(ΔFL) and SRP(LM→AA) exhibited only 10- and 2.5-fold slower complex assembly kinetics in the presence of RNC_{FtsQ}, respectively. Thus the additional presence of the ribosome in a complete cargo partially rescued the defects of the fingerloop mutants in mediating efficient SRP•FtsY complex assembly in response to a signal peptide mimic.
GTP-dependent assembly of stable SRP-FtsY complex comprises two steps: the formation of a transient early intermediate followed by a GTP-dependent rearrangement of this intermediate to a stable closed complex (Zhang et al., 2008, 2009). Using established fluorescence assays and conditions (see Materials and Methods), we further dissected which of these steps was affected by the fingerloop mutations. In the presence of cargo, the early intermediate formed by the SRP(AFL) and SRP(LM→AA) mutants were two- to threefold weaker compared with the early intermediate formed by wild-type SRP (Figure S3 and Table 2). In addition, this intermediate rearranged to the closed complex two- to fourfold slower with mutant SRP(AFL) and SRP(LM→AA) than with wild-type SRP (Figure S4 and Table 2). Thus the combination of defects in stabilizing the early intermediate and in mediating the early→closed rearrangement accounted for the overall defect of fingerloop mutants in assembling the stable SRP•FtsY complex.

The fingerloop is important for GTPase activation and cargo unloading

Although the fingerloop mutants exhibited defects in cargo-induced stimulation of SRP•FtsY assembly, in the presence of RNC these defects were modest and insufficient to account for their observed defects in cotranslational protein targeting, especially with the ΔFL mutant. We therefore asked whether additional downstream steps in the SRP pathway were also impaired by these mutations. Previous work has shown that after a stable SRP•FtsY complex is assembled, GTPase activation in this complex is crucial for the successful unloading of cargo from the SRP to the translocation machinery on the target membrane (Shan et al., 2007). We therefore asked whether the fingerloop mutations impaired the ability of the SRP•FtsY complex to activate its GTPase sites.

To this end, we monitored the reciprocally stimulated GTPase reaction between SRP and FtsY (Peluso et al., 2001). In this assay, the observed reaction rates at subsaturating FtsY concentrations are rate-limited and reflect the assembly of the SRP•FtsY complex, whereas the rate constant at saturating FtsY concentrations (kcat) reports on the GTP hydrolysis rate once a stable complex is formed (Figures 5 and S5). The complex formed by the wild-type SRP hydrolyzed GTP efficiently, with a kcat of 100 min⁻¹ (Figures 5 and S5). For both fingerloop mutants, the observed GTPase rates at subsaturating FtsY concentrations were much slower (Figure S5, A and B, kcat/Km reports on the kinetic defects in complex assembly in the presence of the signal peptide mimic Nikkol (Figures S2 and 4C). However, once a stable GTPase complex was formed at saturating FtsY concentrations, mutant SRP(LM→AA) exhibited minimal effects in activated GTP hydrolysis, whereas mutant SRP(AFL) had a significantly reduced GTPase rate (Figures 5 and S5, kcat/Km), indicating an additional defect of this mutant in ongoing GTPase activation.

Mutant SRPs and FtsYs that specifically block GTPase activation block protein targeting at late stages, when the unloading and transfer of the cargo need to occur (Shan et al., 2007). We therefore asked whether the fingerloop also plays an important role in the timely and efficient transfer of cargo to translocation sites on the target membrane. To address this question, we modified our targeting assay to more specifically isolate this cargo-unloading step (Figure 6A). We generated [35S]methionine-labeled, stalled RNC. The lines are quadratic fits of data to Eq. 1 in Materials and Methods described in Akopian, and Shan, unpublished data. (F) Summary of the association and dissociation rate constants (koff, kcat) of wild-type SRP, SRP(AFL) and SRP(LM→AA) (ΔAA), mutant Ffh(LM→AA) for binding RNC1A9L, as described in Materials and Methods. The results with wt SRP (dotted line) are from Saraogi, Akopian, and Shan, unpublished data. (F) Summary of the association and dissociation rate constants (koff and kcat, respectively) of wild-type SRP, SRP(AFL), and SRP(LM→AA) for binding RNC. The Kd values were calculated according to Kd = kcat/koff.

FIGURE 3: Fingerloop mutants did not exhibit significant defects in cargo binding. (A and B) Equilibrium titrations to measure the binding of wild-type Ffh (●), mutant Ffh(ΔFL) (○), and mutant Ffh(LM→AA) (□) to RNCs bearing the nascent chain from FtsQ (A) or luciferase (B). The lines are quadratic fits of data to Eq. 1 in Materials and Methods. (C) Summary of the binding affinities from (A) and (B). (D and E) FRET was used to monitor the association (D) and dissociation (E) of wild-type SRP, SRP(ΔFL) (●), and SRP(LM→AA) (□) for binding RNC. The results with wt SRP (dotted line) are from Saraogi, Akopian, and Shan, unpublished data.
RNCs bearing the pPL86 nascent chain (RNC\textsubscript{pPL86}) via in vitro translation. RNC\textsubscript{pPL86} was incubated with saturating SRP (wild-type or \Delta FL), FtsY, and GTP for sufficient time to allow the formation of a stable RNC\textsubscript{pPL86}\cdot SRP\cdot FtsY complex, such that the kinetic defect of mutant SRP(\Delta FL) in complex assembly was bypassed. Microsomes were then added to trigger the transfer of RNC\textsubscript{pPL86} from the targeting complex to translocation sites on the ER membrane, which was monitored at different time points by sedimentation (Figure 6A). This experiment showed that the targeting complex formed by wild-type SRP was able to unload RNC\textsubscript{pPL86} to the membrane, and the unloading reaction was complete as early as 15 s (Figure 6B, white bars). In contrast, cargo transfer proceeded much more slowly with mutant SRP(\Delta FL), and even after 2 min, <20% of RNC\textsubscript{pPL86} stably engaged with the microsomal membrane (Figure 6B, black bars). These results directly demonstrated that the fingerloop plays an important role in the cargo handover event at the last stage of the protein-targeting reaction.

### TABLE 2: Effects of fingerloop mutations on the equilibrium stability of the early complex in the presence of RNC\textsubscript{FtsQ} (K\textsubscript{d,early}) and on the rate constants for rearrangement of the cargo-SRP\cdot FtsY early complex to the stable closed complex (k\textsubscript{rearrange}).

<table>
<thead>
<tr>
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<th>SRP</th>
<th>\Delta FL</th>
<th>LM\textsubscript{\rightarrow}AA</th>
</tr>
</thead>
<tbody>
<tr>
<td>K\textsubscript{d,early} (nM)</td>
<td>86 (1)</td>
<td>175 (2)</td>
<td>236 (4)</td>
</tr>
<tr>
<td>k\textsubscript{rearrange} (s\textsuperscript{-1})</td>
<td>0.6 (1)</td>
<td>0.18 (0.3)</td>
<td>0.3 (0.5)</td>
</tr>
</tbody>
</table>

The rate and equilibrium constants are derived from the data in Figures S3 and S4. The values in parenthesis are relative to that of wild-type SRP.

The fingerloop is crucial for SRP RNA–mediated stimulatory effects

The effects of the fingerloop mutants, especially Ffh(\Delta FL), in the GTPase assay above were reminiscent of the effects of removing the SRP RNA (Peluso et al., 2000, 2001; Shen et al., 2011), which accelerates complex assembly between SRP and FtsY and promotes their subsequent GTPase activation. This raises the possibility that the defects of the fingerloop mutants were caused by defective function of the SRP RNA. To test whether this is the case, we measured the GTPase activity for wild-type and mutant Ffh in the absence of the SRP RNA. Under these conditions, both Ffh(\Delta FL) and Ffh(LM\textsubscript{\rightarrow}AA) exhibited k\textsubscript{cat} and k\textsubscript{cat}/K\textsubscript{m} values similar to those of wild-type Ffh (Figure 7, A and D), indicating that the intrinsic ability of Ffh to form a complex with FtsY and to hydrolyze GTP are unaffected by the fingerloop mutations. Thus the defects of the fingerloop mutants in complex assembly and GTPase activation described above likely arise from the inability of the SRP RNA to exert its stimulatory effect on the GTPase interactions.

To provide additional evidence for this notion, we tested another unique signature of the action of SRP RNA: its ability to accelerate the disassembly, as well as the assembly, of the Ffh\cdot FtsY complex without perturbing the proteins.

### DISCUSSION

Cotranslational protein targeting by SRP is essential for maintaining the proper localization of proteins in all cells. During this process, recognition of the signal sequence on the translating ribosome must be tightly coupled to its rapid delivery to the target membrane and efficient unloading onto the translocation machinery. This coupling requires that the GTPase domains in the SRP and FtsY actively communicate with spatial and temporal cues from the cargo and the target membrane. In this work, we showed that the universally conserved SRP fingerloop helps convey the information about signal sequence in the M domain of SRP to its NG domain; this facilitates multiple stages of the targeting reaction, including recruitment of...
the SR, subsequent activation of the GTPases, and the handover of cargo to the translocation machinery in the membrane.

The fingerloop flanks the signal sequence–binding site, forming a flexible flap that could close down on the signal sequence–binding groove upon cargo binding to the SRP (Keenan et al., 1998; Rosendal et al., 2003; Janda et al., 2010; Hainzl et al., 2011). Further, the structural plasticity of the fingerloop, together with the richness of methionine residues in the M domain, has been proposed to provide the conformational flexibility necessary for the SRP to bind diverse signal sequences (Bernstein, 1998; Keenan et al., 1998). Given this, it was surprising to find that mutation or even deletion of the entire fingerloop still resulted in subnanomolar binding affinities of SRP for its substrates. One possible explanation is that the fingerloop exerts a similar effect on both sides of the binding equilibrium: the free Ffh and Ffh bound to the signal sequence. Crystallographic studies showed that in the absence of signal sequences, the fingerloop could insert into the hydrophobic signal sequence–binding groove to stabilize the free Ffh (Figure 8A, SRP; Rosendal et al., 2003). Upon cargo recognition, the interaction of the fingerloop with the binding groove is replaced by interaction with the signal peptide (Figure 8A, RNC•SRP), thereby giving rise to an apparent “isoenergetic” effect on cargo binding affinity. Nevertheless, the results here strongly suggest the fingerloop helps ensure a proper mode of signal-sequence docking in the M domain that is required to induce important conformational changes in the SRP, as manifested by the defects of these mutants in subsequent steps of protein targeting. The observation that the LM→AA mutant binds the RNC more weakly than the ΔFL mutant but is nevertheless more efficient in mediating protein targeting and supporting cell growth further highlights the importance of these downstream steps.

A major effect of fingerloop mutations is that the SRP and FtsY GTases lose their ability to respond to the signal peptide mimic Nikkol and efficiently assemble a complex with one another. How does the fingerloop exert this effect? Several observations here and from previous work offered a few clues. The fingerloop mutations phenocopied the effects of deleting the SRP RNA on SRP•FtsY assembly, suggesting they abolished the ability of this RNA to accelerate this process. The conserved tetraloop of the SRP RNA provides a tethering interaction that holds FtsY near the SRP GTase to facilitate their initial encounter (Siu et al., 2007; Shen and Shan, 2010). In this mechanism, the SRP’s NG domain must be properly positioned close to the RNA tetraloop; this likely requires a reorientation of the relative position of the M and NG domains from that in the free SRP, which appears to be triggered by the cargo and less effectively by the signal peptide or the signal peptide mimic Nikkol (Figure 8A, step 1; Halic et al., 2006; Bradshaw et al., 2009; Zhang et al., 2009, 2010; Estrozi et al., 2011; Hainzl et al., 2011; Shen et al., 2011). We therefore deem it most likely that the SRP fingerloop helps the SRP to undergo this structural rearrangement in response to signal sequence binding, inducing it into a more active conformation for FtsY recruitment.

This hypothesis is further supported by the observation that mutation of the SRP fingerloop has a much less deleterious effect when the SRP is bound to a complete cargo, RNC•FtsQ, than to the less effective signal peptide mimic Nikkol. This intriguing relationship between the SRP fingerloop and the RNC is akin to “synthetic lethality” effects, which suggests that the fingerloop and the RNC play overlapping and redundant roles in inducing a more active conformation of SRP for complex assembly (Figure 8B). The RNC, by interacting with both the M and N domains of the SRP, is highly effective in bringing the SRP’s NG domain into close proximity to the RNA tetraloop. Thus, in the presence of RNC, the SRP is predominantly in the active conformation (Figure 8B, black line). This redundancy would compensate for the destabilizing effect of the fingerloop mutations, partially masking their deleterious effect (Figure 8B, ΔΔGFL < ΔΔG Nikkol). In contrast, Nikkol is less effective at inducing SRP molecules into the “active” structure (Figure 8B, red line; Shen et al., 2011). Although mutation of the fingerloop exerts the same destabilizing effect on the active conformation, the full extent of this effect is manifested (Figure 8B, ΔΔGFL < ΔΔG Nikkol), as there is no redundancy to buffer the deleterious effect of these mutations.

Once the early RNC•SRP•FtsY complex is formed (Figure 8A, step 2; Zhang et al., 2008, 2009; Estrozi et al., 2011), it undergoes additional conformational changes that are essential for subsequent steps of the pathway and ultimately lead to unloading of the cargo (Figure 8A, step 3; Shan et al., 2007; Ataide et al., 2011) and activation of GTP hydrolysis (Shan et al., 2007; Siu et al., 2007; Zhang et al., 2009). The SRP RNA also facilitates GTase activation (Peluso et al., 2001; Ataide et al., 2011), and recent work further...
Materials and Methods

Measurement of the disassembly of the SRP (E)

Summary of the rate constants obtained from (B) and (C). The equilibrium stability (by Ffh

FIGURE 7: Effects of fingerloop mutants on complex assembly and GTPase activation are linked to the SRP RNA. (A) Reciprocally stimulated GTPase reaction in the absence of SRP RNA for wild-type Ffh (●) and mutants Ffh(LM→AA) (●) and Ffh(ΔFL) (●). The lines are fits of data to Eq. 3 in Materials and Methods. Measurement of the disassembly of the SRP+FtsY complex formed by Ffh(ΔFL) (B) and Ffh(LM→AA) (C). The lines are single exponential fits of the data, which gave the dissociation rate constants. (D) Summary of the $k_{\text{cat}}$ and $K_m$ values from the data in (A). (E) Summary of the rate constants obtained from (B) and (C). The equilibrium stability ($K_d$) of the SRP+FtsY closed complex (wild-type and mutants) were calculated according to $K_d = k_{\text{off}}/k_{\text{on}}$, based on rates obtained in (B) and (C) and Figures 4C and S2.

suggested a potential model for this stimulatory effect: at late stages of the GTPase rearrangements, the Ffh+FtsY NG domain complex could detach from SRP RNA tetraloop and, instead, interact with the 5’, 3’-distal end of the SRP RNA, where GTP hydrolysis can be stimulated (Figure 8A, step 3; Ataide et al., 2011). In this structure, the NG domain complex would be removed from the signal sequence–binding site and the ribosome exit site, which could represent a conformation more conducive to the release of cargo. Regardless of the model, our observations here that deletion of the fingerloop abolishes SRP RNA–dependent GTPase activation and also impairs the unloading of cargo strongly suggest that the fingerloop is also intimately involved in late conformational rearrangements of SRP that complete the protein-targeting cycle (Figure 8A, step 3).

Together, the results presented here demonstrate that the SRP fingerloop contributes to multiple steps in the targeting reaction beyond initial signal sequence binding, including the recruitment of the SR, subsequent GTPase activation, and cargo unloading. In light of the recent structural work, it is intriguing to note that all of these molecular steps require global reorganization of the relative position of the M and NG domains of the SRP, during which the linker connecting its G and M domains undergoes major restructuring (Figure 8A). Because of its proximity to the signal sequence–binding site, we speculate that the fingerloop is the first structural element that senses signal sequences and changes conformation. Through the remainder of the M domain linker, thus inducing more global rearrangements of the SRP in both the early and late stages of the protein-targeting reaction.

MATERIALS AND METHODS

Materials

The strains and plasmids used in this study are shown in Table 1. All antibiotics and other chemicals were obtained from Sigma-Aldrich (St. Louis, MO). Restriction enzymes used for cloning were obtained from New England Biolabs (Ipswich, MA) and Fermentas Life Sciences (Glen Burnie, MD). Oligonucleotide primers were synthesized by Integrated DNA Technologies (Coralville, IA). Antibiotics were used at the following concentrations: ampicillin (Amp), 100 μg/ml; kanamycin (Kan), 30 μg/ml; spectinomycin (Spc), 100 μg/ml. Ffh, FtsY, and 4.5S RNA were expressed and purified using established protocols (Peluso et al., 2001). Single cysteine mutations were constructed using the QuikChange mutagenesis protocol (Stratagene, Agilent, Santa Clara, CA) and were purified using the same procedures as wild-type protein. The fluorescent dyes fluorescein, BODIPY-FL, DACM, and acrylodan were purchased from Invitrogen (Carlsbad, CA). RNCs were prepared and purified as previously described (Schaffitzel and Ban, 2007; Saracogi et al., 2011). Single cysteine mutants of Ffh and FtsY were labeled using maleimide chemistry and purified as previously described (Zhang et al., 2008). Labeling efficiency was usually >95%.

Plasmid constructions

All plasmids are derivatives of pBADffh6x, a plasmid that expresses an allele of ffh that expresses a hexahistidine epitope tag at the carboxy terminus of Ffh (Table 1). This plasmid was made by PCR amplification of ffh from E. coli genomic DNA using primers ffhNS (ACCATGGTTGTAAATTTAACCGATCGTTTGCG) and ffhC-AS (TCAATGGTGATGGTGATGACCGGTACG). The primers were designed to introduce an NcoI restriction site (shown in bold in primer ffhNS-F) to the PCR product. The amplification product was introduced to pBAD-topo (Invitrogen), such that the 3’ end of ffh was fused in-frame with a hexahistidine coding sequence. The resulting plasmid was subsequently digested with Ncol and religated yielding pBADffh6x.

This plasmid was further modified using site-directed mutagenesis to introduce an Nhel restriction site at the start of the fingerloop coding region, yielding pBADffhN6x. No amino acid substitutions resulted from this change. The fingerloop region of Ffh, corresponding to amino acids 350–369 (Figure 1A), was deleted in plasmid pBADffhN6xΔFL. This plasmid was made by PCR amplification of ffh using primers ffhNhel-FL.S (ATGGCTAGCAAAAGTGCTGGTGCGTAT- GGAAGCC) and ffhNhe-FL.A (CCCCAGGCTTCCCTGGTCC). The
A model for the role of SRP fingerloop (brown) in relaying the information of signal sequence binding to the GTPases and enabling multiple stages of SRP+FtsY interactions during protein targeting is shown in (A). Step 1, the presence of a signal sequence in the M domain is propagated to the NG domain (both in light blue, connected by the flexible linker in dark blue) by the fingerloop, priming the SRP for binding its receptor, FtsY (green), near the SRP RNAs tetraloop end (orange). In step 2, FtsY associates with SRP to form the [RNC•SRP•FtsY]early intermediate. During step 3, [RNC•SRP•FtsY]early rearranges to activate GTP hydrolysis and facilitate the transfer of the RNC to the translocation machinery. Structures or structural models for each complex (PDB IDs [from top to bottom]: 1QZW, 2128, and 2KXV; Rosendal et al., 2003; Halic et al., 2006; Estrozi et al., 2011) are shown adjacent to the respective SRP/FtsY diagrams. (B) Free-energy profile explaining the different observed effects of fingerloop in the presence of the signal sequence mimic Nikkol (red) or the RNC (black). In both cases, removal of the fingerloop (dashed line) disfavored the conformational change of SRP to an active conformation ($\Delta \Delta G$) more conducive to complex assembly with FtsY. In the presence of Nikkol, this conformational change is unfavorable, even with wild-type SRP; thus the effect of the fingerloop is fully manifested ($\Delta \Delta G = \Delta \Delta G^{\text{Nikkol}}$). In contrast, when bound to the RNC, the SRP is preorganized into the active conformation; thus, although removal of the fingerloop exerts the same destabilizing effect, the full extent of its defect is masked in the observed complex assembly rates ($\Delta \Delta G^{\text{RNC}} < \Delta \Delta G$).

FIGURE 8: A model for the role of SRP fingerloop (brown) in relaying the information of signal sequence binding to the GTPases and enabling multiple stages of SRP+FtsY interactions during protein targeting is shown in (A). Step 1, the presence of a signal sequence in the M domain is propagated to the NG domain (both in light blue, connected by the flexible linker in dark blue) by the fingerloop, priming the SRP for binding its receptor, FtsY (green), near the SRP RNAs tetraloop end (orange). In step 2, FtsY associates with SRP to form the [RNC•SRP•FtsY]early intermediate. During step 3, [RNC•SRP•FtsY]early rearranges to activate GTP hydrolysis and facilitate the transfer of the RNC to the translocation machinery. Structures or structural models for each complex (PDB IDs [from top to bottom]: 1QZW, 2128, and 2KXV; Rosendal et al., 2003; Halic et al., 2006; Estrozi et al., 2011) are shown adjacent to the respective SRP/FtsY diagrams. (B) Free-energy profile explaining the different observed effects of fingerloop in the presence of the signal sequence mimic Nikkol (red) or the RNC (black). In both cases, removal of the fingerloop (dashed line) disfavored the conformational change of SRP to an active conformation ($\Delta \Delta G$) more conducive to complex assembly with FtsY. In the presence of Nikkol, this conformational change is unfavorable, even with wild-type SRP; thus the effect of the fingerloop is fully manifested ($\Delta \Delta G = \Delta \Delta G^{\text{Nikkol}}$). In contrast, when bound to the RNC, the SRP is preorganized into the active conformation; thus, although removal of the fingerloop exerts the same destabilizing effect, the full extent of its defect is masked in the observed complex assembly rates ($\Delta \Delta G^{\text{RNC}} < \Delta \Delta G$).

Strain constructions

To characterize function of the fingerloop mutants in vivo, we constructed SLD108. This strain is deleted for genes whose products are necessary for arabinose transport (araFGH, araE) and utilization (araBAD). In addition, SLD108 expresses a mutant LacY permease that allows homogenous uptake of arabinose throughout the population, such that the heterogeneity of gene expression of genes under araC control is eliminated (Morgan-Kiss et al., 2002). For construction of SLD108, ECF529 (Bowers et al., 2004) was first modified by lambda Red homologous recombination to inactivate bla (Ampβ) encoded on the chromosome of this strain and replacing it with a Kanγ gene cassette. For this, primers bla-KD4.S (ATGAGTATCTCA-CATTTCGGTGTCGCCCTTATTCCCTTTTGTGCAGCTTgcgcttgaggtct- gagcctgtc) and bla-KD4.AS (TTACCAATGCTTAATCAGTGAG-CATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTtgtgtaggct- agagctgcttc) were used to amplify a PCR product using pKD4 as a template (Datsenko and Wanner, 2000). Sequences in uppercase designate the portions of the primers with homology to bla, and sequences in lowercase are homologous to pKD4 (Datsenko and Wanner, 2000). The gel-purified PCR product was electroporated into ECF529 transformed with pSIM5, as previously described (Datta et al., 2006), and Kanγ, Ampβ recombinants were identified.

The Kanγ cassette was subsequently deleted using Flp-mediated site-specific recombination, as previously described (Datsenko and Wanner, 2000). For complete construction of SLD108, the resulting Kanγ (sensitive) strain was subsequently transformed with pFfhTspc expressing ffh+ from a temperature-sensitive replicon (Phillips, 1999) and imparting Spcγ (spectinomycin resistant), and the ffh::kan1 allele (Phillips and Silhavy, 1992) was introduced by P1 transduction, as previously described (Peterson and Phillips, 2008).

For complementation tests, plasmids expressing the different fhh alleles were transformed into SLD108. Ampγ colonies were re-streaked on LB+Amp agar plates and incubated at 30°C and 42°C.
Where indicated, dilutions of saturated cultures were spotted onto LB+Amp plates containing 0%, 0.01%, and 0.02% of l-arabinose and incubated overnight at 42°C.

Fluorescence measurements

Fluorescence measurements were carried out on a FluoroLog-3-22 spectrofluorometer (Jobin-Yvon, Edison, NJ) in assay buffer (50 mM KHEPES, pH 7.5, 150 mM KOAc, 10 mM Mg(OAc)₂, 2 mM dithiothreitol (DTT); 10% glycerol, with or without 0.01% Nikkoli). The buffer also contained 100–200 μM GppNHp, a nonhydrolyzable GTP analogue. All reactions were carried out at 25°C, unless otherwise stated.

The binding affinities of SRP for RNCs or ribosomes were determined using two methods. In the first approach, fluorescence anisotropy measurements were carried out with 5–10 nM of fluorescein-labeled (C421) and various concentrations of RNC<sub>FtsY</sub> or RNC<sub>Luc</sub>. Observed anisotropy values (A) are fitted to Eq. 1,

\[
A = A_0 + (A_1 - A_0) \frac{[SRP] + [RNC] + K_D - \sqrt{([SRP] + [RNC])^2 - 4[SRP][RNC]}}{2[SRP]}
\]

where \(A_0\) is the anisotropy value of free SRP, \(A_1\) is the anisotropy value when SRP is bound to cargo, and \(K_D\) is the equilibrium dissociation constant of SRP for the RNC (Zhang et al., 2010). In a second approach, the binding of SRP to the RNC was determined using FRET between 7-hydroxycoumarin–labeled RNC and BODIPY-D-transfected SRP (Saraogi et al., 2011). Time courses for SRP-RNC assembly (\(k_{on}\)) and disassembly (\(k_{off}\)) were determined using either a FluoroLog-3-22 spectrofluorometer (Jobin-Yvon) or an SF-2004 stopped-flow apparatus (KinTek, Pittsford, NY). For determining SRP-RNC assembly rates, 20 nM RNC<sub>1A9L</sub> was mixed in which the early intermediate. The time course of fluorescence change was fitted to single-exponential functions to give the rearrangement rate constants. For experiments concerning SRP or Ffh loaded with different RNCs, concentrations 50- to 100-fold above their respective \(K_D\) for Ffh were used to ensure > 90% occupancy of SRP by the cargo.

GTPase assay

All GTPase assays were performed at 25°C in assay buffer (50 mM KHEPES, pH 7.5, 150 mM KOAc, 10 mM Mg(OAc)₂, 2 mM DTT; 10% glycerol) with or without 0.01% Nikkoli. GTP hydrolysis reactions were followed and analyzed as previously described (Peluso et al., 2001). In general, reciprocally stimulated GTPase reactions between SRP and FtsY were determined in reactions containing 100–500 nM wild-type or mutant Ffh, 200–1000 nM 4.5S RNA (where applicable), 100 μM GTP, doped with γ<sup>32</sup>P-GTP (MP Biomedicals, Solon, OH), and various concentrations of FtsY. The concentration dependence of the observed rate constant (\(k_{obs}\)) was fitted to Eq. 3, in which \(k_{cat}\) is the rate constant at saturating FtsY concentrations and \(K_m\) is the concentration of FtsY that gives half the maximal rate:

\[
k_{obs} = k_{cat} \frac{[FtsY]}{[FtsY] + K_m}
\]

Translocation assay

The protein-targeting efficiency of wild-type Ffh and mutants ΔFL and LM–Aα was determined by a cotranslational translocation assay using pPL as a substrate, as described previously (Shan et al., 2007). Reactions were carried out using 333 nM SRP, various concentrations of FtsY, and 2 eq of trypsin-digested, salt-washed ER microsomal membranes (TKRM).

Cargo-unloading assay

The targeting of RNC<sub>pPL86</sub> was performed with slight modifications of the procedures used by Wilson et al. (1988). Stalled RNCs bearing pPL86 were generated by in vitro translation using wheat germ translation extract (Promega Corporation, Madison, WI) in the presence of [35S]methionine (PM Biomedical). The stalled RNC<sub>pPL86</sub> was incubated with saturating SRP or SRP(ΔFL). FtsY, and GTP (to final concentrations of 250 nM, 1 μM, and 3 mM, respectively) for 30 min at room temperature to ensure that the ternary complex, RNC<sub>pPL86</sub>-SRP-SRP(ΔFL)•FtsY, was formed. Cargo unloading was initiated by addition of 2 eq of TKRM at 25°C. The reaction was stopped at different time points (15, 30, 60, 90, and 120 s) by flash-freezing with liquid nitrogen. The samples were thawed on ice and immediately layered onto a sucrose cushion (0.5 M sucrose, 50 mM KHEPES, pH 7.5, 150 mM KOAc, 10 mM Mg(OAc)₂, and 2 mM DTT). Membrane-bound RNCs were sedimented by centrifugation at 55,000 rpm at 4°C for 3 min (TLA100, Optima TLX Ultracentrifuge; Beckman Coulter, Brea, CA). The reaction was analyzed by 15% SDS–PAGE and autoradiography.

ACKNOWLEDGMENTS

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supported by NIH grant R01 GM069628. A.R.A. was supported by NIH/NRSA training grant 5T32GM07616 and by the Betty and Gordon Moore Foundation.

REFERENCES


SUPPLEMENTARY INFORMATION

Fingerloop activates cargo delivery and unloading during co-translational protein targeting

Aileen R. Ariosa*, Stacy S. Duncan†‡, Ishu Saraogi*, Xiaodong Lu†, April Brown†, Gregory J. Phillips†, and Shu-ou Shan*§

*Division of Chemistry and Chemical Engineering, California Institute of Technology, Pasadena, CA 91125
†Department of Veterinary Microbiology, College of Veterinary Medicine, Veterinary Medical Research Institute (VMRI), Iowa State University, Ames, IA 50011
‡Present Address: Department of Medicine, Division of Infectious Diseases, Vanderbilt University, Nashville, TN 37232
§Corresponding author. E-mail: sshan@caltech.edu
**Figure S1.** Expression of *ffh* alleles analyzed by SDS-PAGE. Proteins were resolved and detected as described in Materials and Methods. Lanes 1-2: *ffh*PG→AA; 3-4: *ffh*ΔFL; 5-6: *ffh*+, 7-8: *ffh*LM→AA. Lanes 1, 3, 5, 7: + L-arabinose; 2, 4, 6, 8: – L-arabinose. Molecular weight standards are shown on the left, the relative positions of which were identified using a corresponding SDS-PAGE gel stained with Coomassie Brilliant Blue.
**Figure S2.** The effects of fingerloop mutants on SRP-FtsY complex assembly. Measurements of SRP-FtsY complex assembly kinetics of wild-type SRP (●), mutant SRP(ΔFL) (○) and mutant SRP(LM→AA) (◇) in the presence of Nikkol.

**Figure S3.** Effects of the fingerloop on the equilibrium stability of the early complex in the presence of RNC_{FtsQ}.
Figure S4. Rate constants for formation of the stable complex starting from a preformed RNC•SRP•FtsY early complex using either (A) SRP(ΔFL) or (B) SRP(LM→AA).
Figure S5. Deletion of the fingerloop results in inefficient GTPase activation. (A) The reciprocally stimulated GTPase reaction between SRP and FtsY were determined for wild-type SRP (●) and mutants SRP(LM→AA) (◇) and SRP(ΔFL) (○). The data were fit to Eq. 3 in the Methods. (B) Summary of the $k_{\text{cat}}$ and $K_m$ values from the data in part A.

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<th>SRP</th>
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