Subunit dynamics in *Escherichia coli* preprotein translocase  
(SeY/SecE/SecA band 1/subunit exchange/epitope tag)

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**ABSTRACT**  
SecY, SecE, and band 1 copurify as the SecY/E integral membrane domain of *Escherichia coli* preprotein translocase. To measure the *in vivo* association of these polypeptides and assay possible exchange, plasmid-borne secY and secE genes were placed under control of the ara regulator and fused to DNA encoding the influenza hemagglutinin epitope. Cells were incubated with [35S]methionine, grown for a "chase" period, and then induced with arabinose to express epitope-tagged, nonradioactive SecY and SecE. Both the wild-type and epitope-tagged polypeptides assembled into functional, heterotetrmeric SecY/E complex. However, immunoprecipitation with antibody to the epitope tag did not cross-precipitate radiolabeled SecY or SecE. Thus, these subunits normally associate stably *in vivo*.

Protein secretion in *Escherichia coli* has been investigated by both biochemical and genetic techniques (1–3). Studies of temperature-sensitive sec mutants (4, 5) and suppressor prl mutants (6) identified the genes essential for secretion. Biochemical studies revealed that several of the encoded proteins form subunits of preprotein translocase, a membrane enzyme which catalyzes the movement of precursor proteins across the cytoplasmic membrane (7). The enzyme consists of an integral membrane domain, termed SecY/E, and a peripheral membrane domain, the SecA protein. SecY/E consists of three subunits: SecY, SecE, and band 1 (7). Both SecY and SecE have been identified by biochemical and genetic techniques as being required for translocation. Band 1 copurifies with SecY and SecE in detergent extracts and can be immunoprecipitated with SecY and SecE by antibodies to the amino terminus of SecY (7, 8). The purified trimeric complex can be reconstituted into liposomes that, in the presence of SecA and ATP, translocate precursor proteins.

Despite the isolation of a complex containing SecY and SecE, some studies have suggested that SecY and SecE may not remain stably associated. Elegant genetic studies involving suppressor-directed inactivation and sec titration techniques suggest that the SecY and SecE proteins reversibly assemble in the membrane (9, 10). These studies are based on strains containing protein localization mutants (prl) in the SecY or SecE protein together with a leader sequence mutation in a fusion protein (LamB–LacZ). When the mutant fusion protein is expressed, it is recognized by the prl mutant protein and "jams" the translocase. The cells stop growing unless the wild-type prl allele, whose protein product does not recognize the mutant leader sequence, is also expressed. To explain these observations, it was postulated that the preprotein translocase subunits associate reversibly as part of the catalytic cycle of translocation. The suggestion that SecY, SecE, and band 1 may not always remain stably associated has also come from biochemical studies. Under certain conditions, these proteins can be isolated separately. When co-constituted into proteoliposomes, they can function together to support translocation (11). Each of these studies has raised the question of whether SecY, SecE, and band 1 are normally stably associated *in vivo*.

To test this association, we have prepared genes encoding epitope-labeled SecY and SecE. We now report that the SecY and SecE proteins are stably associated. Exchange of these subunits is not detectable, even after a generation of growth in which hundreds of translocation events have occurred at each export site. Under certain conditions, when SecE is epitope-labeled, there is extensive and selective exchange of band 1.

**MATERIALS AND METHODS**  
**Plasmid Constructions.** The *E. coli* secY gene in plasmid pKY6 (5) was amplified by the polymerase chain reaction (PCR) with primer derived from the amino terminus (5'-ACGGAACTTACCATGATCCATACGTGTTCTCAGTTAATGCGGCGGATCTTTTGAAGCTTGAAAG-3') fused with an influenza hemagglutinin (HA) epitope (12, 13). This also introduced an EcoRI site for cloning. The epitope protein sequence, Tyr-Pro-Tyr-Asp-Val-Pro-Asp-Tyr-Ala, was fused to the SecY sequence through a Gly-Gly-Pro motif to aid in displaying the epitope from the SecY protein (12). The oligonucleotide primer from the carboxyl terminus (5'-GGCGTGACCTATTACCGGCGTAGCCTTTTAC-3') introduced a SalI site. After amplification by Pfu polymerase (Stratagene), the DNA fragment was digested with SalI and EcoRI and ligated into pUC19 (14). The *E. coli* secE gene in the plasmid pBAD2 (gift of J. Beckwith, Harvard Medical School) was amplified by PCR, introducing a SalI site before the amino terminus (5'-GGCGTGACAGGTTGTGATGAGCGGAATACCGGAA-3') and a HindIII site after the carboxyl terminus (5'-CAGAAGCTTTCTAGACGCGCAGCTG-3'). Both the pUC19 derivative encoding HA epitope-labeled SecY (pHA-SecY) and the amplified secE fragment were digested with SalI and HindIII and the two fragments containing the sec genes were ligated into pBAD22 (to give pHA-SecY/SecE) and transformed into *E. coli* JM109 (14). The same cloning strategy was used to create epitope-labeled secE followed by wild-type secY in pBAD22. The oligonucleotide primers for epitope-tagged secE were 5'-ACGGAAATTCAGGATGATCAGGCGGCGTAGCCTTTTAC-3' for the amino terminus and 5'-GGCGTGACAGGTTGTGATGAGCGGAATACCGGAA-3' for the carboxyl terminus. The oligonucleotide primers for the secY gene were

Abbreviation: HA, hemagglutinin.

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5'-GGCGCTGACGAGAATAGATGCAATGGCCTAAA-
CAACGGCAGATA-3' for the amino terminus and 5'-
GCCAAGCTTATCCGGTAGCTTTC-3' for the
carboxyl terminus. In both final plasmids, the epitope-labeled gene possessed AGGAG as the Shine–Dalgarno sequence and the wild-type genes were amplified to include their respective Shine–Dalgarno sequences. The plasmid-borne genes were fully functional, as assayed by complementation of temperature-sensitive strains.

**Bacterial Growth.** Bacteria were grown overnight in LB medium (15) with ampicillin at 37°C and diluted to an OD<sub>600</sub> of 0.05 into 50 ml of M9 medium with thiamin (10 μg/ml), ampicillin (50 μg/ml), amino acids (40 μg/ml, without methionine), and 0.2% (wt/vol) glucose. For the subunit-exchange experiments, 2 mM (74 μg/ml) of EXPRES<sup>SS</sup> protein labeling mix (NEN/DuPont) was added to a 50-ml culture (OD<sub>600</sub> of 0.2) for 30 min at 37°C. The cells were centrifuged for 5 min at 3000 × g at 20°C and then were suspended in 50 ml of M9 medium containing thiamin, ampicillin, amino acids, and 0.2% (wt/vol) fructose. Methionine (50 μg/ml) was added to the cells grown to an OD<sub>600</sub> of 0.8. Arabinose (1%, wt/vol) and, where indicated with strain R0205, maltose (0.4%) were added and growth continued for 3 h. The cells were harvested by centrifugation (at 5000 × g at 30°C) suspended in 50 mM Tris Cl, pH 7.5/10% sucrose, frozen dropwise in liquid nitrogen, and stored at −70°C.

**Membrane Preparation.** Membranes were prepared for immunoprecipitation by a modification of the method of Kaback (16). An aliquot of cells was thawed and EDTA (10 mM) and lysozyme (0.3 mg/ml) were added. After 8 min at 23°C, ice-cold water was added (>40 volumes) and the samples were mixed vigorously. Samples were centrifuged for 5 min at 3000 × g at 4°C to remove broken cells and the resulting supernatants were centrifuged for 20 min at 40,000 × g at 4°C. Pellets were suspended in 5 ml of 50 mM Tris Cl, pH 7.5/10 mM EDTA. Nucleic acids were digested by addition of 20 mM MgCl<sub>2</sub> and DNase and RNase (each at 5 μg/ml) for 5 min at 37°C. Membranes were sedimented for 20 min at 40,000 × g and suspended in 0.6 ml of 50 mM Tris Cl, pH 7.5/10 mM EDTA. Aliquots were assayed for radioactivity and protein (17). Typically 5 × 10<sup>10</sup> cpm of 43<sup>S</sup>-labeled membranes was used for each immunoprecipitation.

**Immunoprecipitations and Immunoblots.** For nondenaturing immunoprecipitations, membranes were solubilized (18) by incubation on ice for 15 min with 1.25% (wt/vol) octyl β-d-glucoside in 10 mM Tris Cl, pH 8.0/25% (vol/vol) glycerol containing <i>E. coli</i> phospholipids (Avanti Polar Lipids) at 3.4 mg/ml. Samples were centrifuged for 15 min at 16,000 × g, and the supernatants were added to 300 μl of immunoprecipitation (IP) buffer (50 mM M9 medium, pH 8.0/150 mM NaCl/1.25% octyl β-d-glucoside, 40% glycerol with <i>E. coli</i> phospholipids at 1.5 mg/ml). Antibodies were added to 100 μl of a 10% (vol/vol) suspension of protein A-Sepharose CL-4B (Pharmacia) in 2% (wt/vol) bovine serum albumin, incubated for 1 hr at 4°C with constant mixing, collected by brief centrifugation, suspended in an equal volume of IP buffer, and again collected by centrifugation. Beads were suspended in membrane extracts, the incubation was continued for 1 hr, and complexes were harvested by centrifugation (for 2 min at 4°C). The beads were twice resuspended and centrifuged, each with 1 ml of IP buffer. Proteins were eluted with 25 μl of 4% (wt/vol) SDS/160 mM M9 medium, pH 6.8/200 mM 2-mercaptoethanol/20% (vol/vol) glycerol/0.02% (wt/vol) bromophenol blue and incubated for 10 min at 37°C. The beads were removed (microcentrifuge, 2 min) and the supernatants were electrophoresed in high-Tris SDS/polyacrylamide gels (7) and analyzed by fluorography. For immunoblots, samples were transferred from SDS/polyacrylamide gels to poly(vinylidene difluoride) membranes at 200 mA for 1 hr with an Idea Scientific (Corvallis, OR) apparatus. Membranes were incubated for 12 hr with a 1:500 dilution of antiserum, developed by the ECL Western detection system (Amersham), and quantified by densitometry.

**Antibody Preparation.** Antibody was prepared to the SecE peptides ATVAFARETVKRYWPQETC. Antiserum to the amino terminus of SecY has been described (19, 20). Typically, 25 μl of heat-inactivated antiserum was used per immunoprecipitation. Monoclonal antibody 12CA5 and ascites preparation were as described (12). Ascites proteins were precipitated with ammonium sulfate at 50% saturation and dialyzed versus phosphate-buffered saline. Typically 2 μl of this concentrated antibody solution (16 mg/ml) was used per immunoprecipitation.

**RESULTS**

To test whether SecY and SecE were stably associated in vivo, we fused an epitope of influenza HA to either SecY or SecE. This epitope tagging method has been used by several investigators to purify multisubunit protein complexes (12, 21). The epitope was introduced at the amino terminus of either SecY or SecE, with the wild-type gene for the other Sec protein also encoded on the same plasmid under ara control. Epitope-tagged SecY and SecE were each fully functional in rescuing growth of strains with conditional lethal mutations in the <i>secY</i> or <i>secE</i> genes. <i>E. coli</i> C107 has a temperature-sensitive SecY (22). When either the epitope-tagged or the wild-type <i>secY</i> gene was present on a plasmid (Fig. 1A, sectors II and III, respectively), cells grew at 42°C. The background vector or a <i>secE</i>-containing plasmid did not complement (sectors I and IV). <i>E. coli</i> AF29 has a cold-sensitive mutation in <i>secE</i> (23). When a wild-type or epitope-
tagged secE gene was present (Fig. 1B, sectors II and III, respectively), the defect was complemented.

**Labeling Epitope-Tagged SecY/E.** To examine the epitope-tagged Sec proteins in vivo, we metabolically labeled cells for 30 min with a mixture of 35S-labeled methionine and cysteine after induction of the plasmid-borne genes. Previous work showed that a complex of wild-type SecY, SecE, and band 1 can be isolated from detergent extracts (7). SecY undergoes an endoproteolytic event in these extracts (without loss of translocation activity; ref. 7), and the presence of the epitope tag affects the mobility of the Sec proteins in SDS/ polyacrylamide gels. Immunoprecipitates with the HA antibody of membrane extracts from cells with the plasmid pHASEC/SecE therefore contained the HA-tagged SecY amino-terminal fragment, the SecY carboxyl-terminal fragment, band 1, and SecE (Fig. 2, lane 2). When this same extract was immunoprecipitated with antibody to the native SecY amino terminus, the amino-terminal fragments of both wild-type SecY and the HA-derivatized SecY were recovered, as well as the SecY carboxyl-terminal fragment, band 1, and SecE (lane 1). These data show that comparable amounts of tagged and wild-type SecY were being made and that both wild-type SecY and HA-derivatized SecY assemble into the SecY/E ternary complex. Furthermore, the absence of wild-type SecYN(N) fragment in the anti-HA immunoprecipitates (lane 2) suggests that there is only one SecY subunit per SecY/E protein. Similar results were obtained with nonadenated immunoprecipitates of membrane extracts from cells labeled while synthesizing HA-derivatized SecE (lanes 3 and 4). HA-derivatized SecE assembled into the SecY/E complex (lane 4), which did not have wild-type SecE, suggesting that SecY/E has only one SecE subunit.

**Immunoprecipitation with antibodies to SecY.** To assay subunit exchange between old and new SecY/E complexes, bacteria containing the plasmid for epitope-tagged SecY and wild-type SecE were labeled with [35S]methionine/[35S]cysteine for 30 min under noninducing conditions in the early logarithmic phase of growth. During this labeling period, chromosomally encoded SecY and SecE were synthesized but little epitope-tagged SecY was expressed. The labeled amino acids were removed and excess unlabeled amino acids were added. After continued growth, the culture was divided and expression of unlabelled, epitope-tagged SecY and wild-type SecE was induced in one portion with arabinose. Cells were harvested, membrane extracts were prepared, and SecY/E was immunoprecipitated by antibody to either the amino terminus of SecY or to the influenza HA epitope. Samples were analyzed by SDS/PAGE and fluorography. If there was free exchange of SecY and SecE subunits between enzyme complexes, then the unlabelled, epitope-tagged SecY should have been associated with radioactive SecE. This was not the case. 35S-labeled SecY, SecE, and band 1 were readily detected in a complex by immunoprecipitation with antibodies to the SecY amino terminus (Fig. 3, lanes 3 and 7). For the culture where, after 35S-free chase period, arabinose was added to induce expression of the epitope-tagged SecY and SecE, the immunoprecipitate with anti-HA antiserum (lane 8) was similar to that seen without arabinose induction (lane 6). Since SecE has only three methionines, greater sensitivity is afforded by the plasmid construction in which SecE is epitope-tagged. When the experiment was repeated with epitope-tagged SecE, no labeled SecY was detected in the anti-epitope immunoprecipitates (Fig. 3, lane 4). Radioactive SecY was present and stably associated in SecY/E complexes (lanes 1 and 3) but did not exchange to become associated with the epitope-tagged SecE protein. The only radioactive subunit seen coimmunoprecipitating with the tagged SecE was band 1 (lane 4); the significance of this observation is unclear. We conclude that the SecY and SecE subunits are stably associated in vivo and do not freely exchange.

**Subunit Dynamics in an Export Mutant Strain.** Bicker-Brady and Silhavy (10) have suggested that SecY and SecE might dissociate and reassociate as part of their catalytic cycle, whereas our studies suggest that they remain associated. To determine whether this reflects a strain difference,
DISCUSSION

Several previous studies have indicated that SecY, SecE, and band 1 are associated. They copurify as a complex which can be reconstituted into proteoliposomes for translocation (7). Furthermore, antibody to the amino terminus of SecY can, under non-denaturating conditions, cross-immunoprecipitate SecE and band 1 from detergent extracts. This complex is labile in detergent solution and, during incubation, the cross-immunoprecipitation is lost at the same rate as the ability to be reconstituted for translocation (8). Association has also been inferred from the stabilization of overproduced SecY by concomitant overproduction of SecE (24, 25).

Two lines of experimentation have called the association of SecY and SecE into serious question. One is the isolation of SecY, SecE, and P12, a low molecular weight protein (with properties similar to band 1), as separate polypeptides which can be reconstituted together to form translocation-competent proteoliposomes (11). Though these data are most simply explained as a reconstitution of active SecY/E from its subunits, they serve to raise the question of whether the association seen in detergent extracts is an in vitro artifact. A second line of experiments is the elegant studies of Bieker-Brady and Silhavy (9, 10), using techniques of secretion-directed inactivation and SecE degradation. In these experiments, cell growth was blocked by the jamming of translocation sites during the synthesis of LamB-LacZ fusion proteins. Mutations in the leader sequence of the LamB moiety of these fusions relieved the lethality, presumably because the protein was no longer recognized for export. Lethality could, however, be restored by the selective introduction of suppressor prl alleles in the SecA, SecY, or SecE genes. These studies suggest that the proteins encoded by sec genes can be separately titrated and that they assemble in a specific order during each catalytic cycle of translocation. While we have not reconciled these studies with those reported here, the molecular structure of the “jammed” intermediates and the effects of this jamming on translocase are not known.

Our studies establish that SecY, SecE, and band 1 are stably associated with one another in vivo, as apparent subunit exchange would be seen if the association had first occurred in the detergent extracts. This association is stable during growth times which correspond to hundreds of catalytic turnovers. Induction of fusion protein in suppressor strains does not promote general subunit exchange (Fig. 4). We do, however, see apparent exchange of band 1 into a complex with HA-tagged SecE. The significance of this finding must await further studies of band 1. The recent finding that band 1 and protein P12 are identical (K. Douville, M. R. L., L. Brundage, K.-I. Nishiyama, H. Tokuda, S. Mizushima, and W. T. W., unpublished work) will make this possible.

Other multiprotein systems exhibit subunit exchange (26–31). However, only a few oligomeric membrane proteins have been examined for the dynamics of their subunit association (32, 33). We are not aware of other studies of the in vivo exchange rates of subunits between assembled heterooligomeric enzyme molecules. Epitope tagging provides a means to explore subunit exchange in living cells.

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