A Minimal Tat System from a Gram-positive Organism

A BIFUNCTIONAL TatA SUBUNIT PARTICIPATES IN DISCRETE TatAC AND TatA COMPLEXES

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The Tat system transports folded proteins across bacterial and thylakoid membranes. In Gram-negative organisms, a TatABC substrate-binding complex and separate TatA complex are believed to coalesce to form an active translocon, with all three subunits essential for translocation. Most Gram-positive organisms lack a tatB gene, indicating major differences in organization and possible differences in mode of action. Here, we have studied Tat complexes encoded by the tatAdCd genes of Bacillus subtilis. Expression of tatAdCd in an Escherichia coli tat null mutant results in efficient export of a large, cofactor-dependent substrate, TorA. We show that the tatAd gene complements E. coli mutants lacking either tatAE or tatB, indicating a bifunctional role for this subunit in B. subtilis. Second, we have identified and characterized two distinct Tat complexes that are novel in key respects: a TatAdCd complex of ~230 kDa that is significantly smaller than the analogous E. coli TatABC complex (~370 kDa on BN gels) and a separate TatAd complex. The latter is a discrete entity of ~270 kDa as judged by gel filtration chromatography, very different from the highly heterogeneous E. coli TatA complex that ranges in size from ~50 kDa to over 600 kDa. TatA heterogeneity has been linked to the varying size of Tat substrates being translocated, but the singular nature of the B. subtilis TatA complex suggests that discrete TatAC and TatA complexes may form a single form of translocon.

The Tat (twin arginine translocation) pathway is involved in the transport of proteins across the chloroplast thylakoid membrane and the plasma membranes of a wide range of bacteria (1–6). It differs fundamentally from the other export pathway, the Sec pathway, in its ability to translocate prefolded proteins over the plasma membrane. This process appears not to require energy in the form of ATP hydrolysis but is instead dependent on the presence of the proton motive force across the membrane (1, 7, 8). Substrates for this translocation pathway bear N-terminal signal peptides that contain a highly conserved, characteristic twin-arginine motif in the N-terminal domain of the signal peptide (9–11).

In Escherichia coli and other Gram-negative organisms, the above studies have identified three genes as being essential for Tat-dependent protein translocation: tatA, tatB, and tatC (usually in the form of a tatABC operon). The three tat genes of E. coli encode membrane proteins of 9.6, 18.4, and 28.9 kDa in size, respectively. The TatA and TatB proteins are both predicted to contain a single transmembrane spanning domain, whereas the larger TatC protein is predicted to contain six transmembrane-spanning domains (12). These three proteins have been shown to form two main types of complex within the cytoplasmic membrane of E. coli. The first is a TatABC complex of ~370 kDa (13, 14), which is thought to be involved in substrate recognition and binding; in particular, substrates appear to interact initially with the TatB and TatC subunits (15, 16). The second form of Tat complex appears to contain only TatA molecules, and whereas the E. coli TatABC complex is both discrete and stable, the TatA complexes range in size from less than 100 kDa to over 500 kDa (17, 18). Single-particle electron microscopy reveals the TatA to form ring-like structures of varying diameter (18), prompting suggestions of a role in formation of the translocation pore.

Tat systems in other Gram-negative organisms appear (so far) to conform to a similar pattern, whereas Gram-positive organisms contain very different Tat systems. In virtually every case, with the exception of Streptomyces species (19), these organisms contain only tatAC genes, indicating fundamental differences between the two types of Tat apparatus. Because TatA and TatB proteins share a degree of sequence homology, one possibility is that the TatA proteins in Gram-positive bacteria are bifunctional, performing the functions of both the TatA and TatB proteins of E. coli (20). Alternatively, TatB may perform a function in E. coli that is not required in Gram-positive organisms, or the two types of system may differ in other key respects.

In this report we have set out to characterize in detail a Tat system from a Gram-positive organism, Bacillus subtilis. This is a nonpathogenic, Gram-positive soil bacterium that secretes high levels of extracellular proteins. B. subtilis contains three variants of the tatA gene, denoted tatAd, tatAy, and tatAc, together with two variants of tatC, denoted tatCd and tatCy; it lacks a tatB gene. Recently studies have shown the presence of two distinct translocases, one involving TatAd and TatCd and the other involving TatAy and TatCy. TatAdCd and TatAyCy display differing substrate specificities (21). The secretion of
PhoD, a protein with phosphodiesterase and alkaline phosphatase activity, is completely TatAdCd-dependent (22), and the three genes are part of the _pho_ regulon that is only expressed under phosphate-limiting conditions. No other TatAdCd-dependent proteins have been identified to date. TatAyCy has been shown to form an active translocase for the translocation of YwbN, an iron-dependent DyP-peroxidase (22, 23). The function of the third TatA component, TatAc, remains unknown.

Little is currently known about the organization of the _B. subtilis_ Tat proteins within the membrane. Here, we analyze the organization and nature of the complexes formed by the components of the _B. subtilis_ TatAdCd pathway. We show that these subunits form an active translocase when expressed in an _E. coli_ background, and we furthermore show that TatAd is indeed bifunctional. Finally, we show that the _B. subtilis_ Tat complexes have unexpected properties that suggest a new model for Tat-dependent protein transport, involving a single defined translocon rather than a spectrum of size variants.

**EXPERIMENTAL PROCEDURES**

**Bacterial Strains, Plasmids, and Growth Conditions**—All of the strains and plasmids used are listed in Table 1. _E. coli_ MC4100 (24) was used as the parental strain, and _ΔtatABCDE_ (4) has been described previously. Arabinose-resistant derivatives were used as described previously (13). _E. coli_ was grown aerobically in Luria broth at 37 °C. _E. coli_ was grown anaerobically in Luria broth supplemented with 0.5% glycerol, 0.5% trimethylamine _N_-oxide (TMAO),3 and 1 μM ammonium molybdate. The media were supplemented with ampicillin to a final concentration of 100 μg/ml and arabinose to 0.5 mM when required. _B. subtilis_ was grown in TY (tryptone/yeast extract) medium, consisting of bactotryptone (1%; w/v), Bacto yeast extract (0.5%; w/v), and NaCl (1%; w/v), unless indicated otherwise. The media were supplemented with kanamycin (10 μg/ml), chloramphenicol (5 μg/ml), and/or spectinomycin (100 μg/ml).

**DNA Techniques**—All of the cloning techniques and transformation of _E. coli_ were performed as described by Sambrook et al. (25). All of the enzymes used were from Roche Applied Science or Fermentas Life Sciences. The PCR was performed using Expand DNA polymerase (Roche Applied Science). For arabinose-inducible overproduction of _B. subtilis_ TatAdCd, plasmid pBADCd was constructed as follows. The _tatAdCd_ operon was amplified from _B. subtilis_ 168 chromosomal DNA with primers RTERAdF (5'–GCC GTC TCG CAT GTT TTC AAA CAT TGG AAT ACC GGG CTT G-3') and JJdstrep02 (5'-ATA TTC TAG ATT TTG GGT CCA ACT GTA GCT GGT GCG ACC AAT TCG AAG CGG CCG CCG CTG TTG CTG CC-3'). RTERAdF was designed as such that restriction of the generated _tatAdCd-strep_ PCR-amplified fragment with dovetail enzyme Esp3I would create an NcoI overhang to ensure direct cloning in the vector pBAD24. JJdstrep02 was constructed in such a way that a C-terminal _Strep_-tag II (26) (underlined) would be directly attached to _tatAd_ during the PCR amplification. pBADCd was constructed by ligating an Esp3I- and XbaI-cleaved PCR-amplified fragment of _tatAdCd-strep_ into NcoI- and XbaI-cleaved pBAD24. For isopropyl β-D-thiogalactopyranoside-inducible overproduction of _B. subtilis_ TatAdCd, _tatAdCd-strep_ was cut out of pBADCd with Nhel and XbaI and ligated into Nhel/XbaI-cut pEXT22 to construct pEXT-AdCd.

For arabinose-inducible overproduction of _B. subtilis_ TatAd, plasmid pBAD-His was constructed as follows. The _tatAd_ gene was amplified from _B. subtilis_ 168 chromosomal DNA with primers RTERAdF (5'-GCC GTC TCG CAT GTT TTC AAA CAT TGG AAT ACC GGG CTT G-3') and TatAdhis-Xba-R (5'-GCT CTA GAT CAG TGA TTG TGA TGG TGA TGG CCC GCG TTT TTG TCC TGC-3'). The PCR product was constructed in such a way that a C-terminal _His_6 tag (underlined) would be directly attached to _tatAd_ during the PCR amplification. pBAD-His was constructed by ligating an Esp3I- and XbaI-cleaved PCR-amplified fragment of _tatAd-strep_ into NcoI- and XbaI-cleaved pBAD24.

**Expression and Purification of the TatAdCd Complex**—_E. coli_ Δ_tatABCDE_ cells containing plasmid pBADCd or pBAD-His were grown aerobically to mid-exponential phase with induction of _tatAdCd_ on plasmid pBADCd and _tatAd_ on plasmid pBAD-His using 0.5 mM arabinose. The membranes were isolated as described previously and solubilized in 2% digitonin (13). Solubilized membranes were incubated with 2 μg/ml avidin to block any biotin-containing proteins before application to an equilibrated 2 ml Streptactin affinity column (Institut fur Bioanalytik). The column was washed with eight column volumes of equilibration buffer containing Tris-HCl, pH 8.0, 10% glycerol, 150 mM NaCl, and 0.1% digitonin. Bound protein was eluted from the column in six 1.0 ml fractions.

### TABLE 1

<table>
<thead>
<tr>
<th>Plasmids and strains</th>
<th>Relevant properties</th>
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<tr>
<td><strong>Plasmids</strong></td>
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<tr>
<td>pEXT-AdCd</td>
<td>pEXT22 derivative containing the <em>B. subtilis</em> <em>tatAdCd</em> operon; _Kan'</td>
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<tr>
<td>pBAD-His</td>
<td>pBAD24 derivative containing the <em>B. subtilis</em> <em>tatAd-His</em> gene; _Amp'</td>
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<td><strong>Strains</strong></td>
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<td><em>B. subtilis</em></td>
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**B. subtilis Tat Complexes**

The abbreviations used are: TMAO, trimethylamine _N_-oxide; GFP, green fluorescent protein; BN, blue native.
**B. subtilis Tat Complexes**

using the same buffer as above but containing 3 mM desthiobiotin (Sigma). Elution fractions were pooled and concentrated to 250 µl using Vivaspin-4 centrifugal concentrators (molecular weight cut-off, 10,000; Vivasience). The concentrated sample was loaded onto a Superose-6HR gel filtration column (Amersham Biosciences) and was eluted with the equilibration buffer described above. For complete purification of the TatAdCd complex, the sample of solubilized membrane was subjected to Q-Sepharose chromatography before the Streptactin and Superose-6HR chromatography steps; the method was as described in Ref. 13.

**SDS-PAGE and Western Blotting** — The proteins were separated using SDS-polyacrylamide gel electrophoresis and immunoblotted using specific antibodies to TatAd (kindly provided by T. Nakamura and K. Nakagawa, respectively). Western blotting was performed as described above and solubilized in 50 mM Bis-Tris, pH 7.0, 750 mM 6-aminocaproic acid, and 2% (w/v) digitonin. Solubilized membranes and purified protein were loaded and separated on a polyacrylamide gradient gel (5–13%). The proteins were detected by immunoblotting as described above.

**TMAO Reductase Activity and TorA-GFP Assays** — TMAO reductase activity assay was performed as described previously (13, 29). *E. coli* cells were grown anaerobically until mid-exponential growth phase prior to fractionation into periplasmic, cytoplasmic, and membrane fractions. The cell fractions were loaded and separated on a 10% native polyacrylamide gel that was subsequently assayed for TMAO reductase activity as described previously. For TorA-GFP export assays, a construct comprising the TorA signal peptide linked to GFP (30) was expressed using the pBAD-24 plasmid as previously described (31). For these experiments, TatAdCd was expressed from the compatible pEXT22 vector.

**Microscopy** — Images were recorded with a Leica DMRE microscope equipped with a Leica TCS SP2 confocal unit and an argon laser. The 488-nm laser line was selected, and the images were recorded with a photomultiplier using the Leica confocal software. The samples were visualized with a 63 × oil immersion objective (numerical aperture, 1.4; Leica). The image size is 512 × 512 pixels, and the images were averaged from four successive scans.

**RESULTS**

**Overexpressed TatAdCd Forms an Active Translocation Pathway in E. coli** — We set out to determine whether overexpressed TatAdCd can form an active translocation pathway in *E. coli*, to use a single defined background for comparing Tat systems from Gram-negative and Gram-positive organisms. The tatAdCd genes were expressed in an *E. coli* tat null mutant (ΔtatABCDE), and we conducted a TMAO reductase activity assay as described under “Experimental Procedures.” TMAO reductase (TorA) is a periplasmic protein required for growth of *E. coli* on a minimal TMAO and glycerol medium. It is a known *E. coli* Tat substrate that is frequently used for Tat export assays because its presence can be detected through an assay using methyl-viologen-linked reduction on a native polyacrylamide gel. TatAdCd was overexpressed from plasmid pBAD in ΔABCDE cells under anaerobic conditions, after which the cells were fractionated, and TorA was localized as shown in Fig. 1.

The right-hand sets of lanes in Fig. 1 show control tests in which the wild type *E. coli* strains, MC1061 and MC4100 (from which the ΔABCDE strain was derived) were fractionated into membrane, cytoplasm, and periplasm samples (lanes M, C, and P, respectively). The data show that the TorA activity is localized primarily in the periplasm as expected, with low levels found in the cytoplasm as is often observed (13). In the ΔABCDE strain (denoted Δtat), no periplasmic activity is detected, and TorA is found exclusively in the cytoplasm. Expression of plasmid-borne *E. coli* TatABC in this strain (from the pBAD-ABC vector) restores export activity as expected. The important point is that expression of *B. subtilis* TatAdCd, using the same vector, also leads to efficient export of TorA. Clearly, TatAdCd is able to form an active translocation pathway in the *E. coli* ΔABCDE strain, and this is the first demonstration that a TatAC-type system from a Gram-positive organism can function in a Gram-negative background and export authentic *E. coli* Tat substrates. Moreover, because TatB has been found to be essential for TorA translocation in *E. coli* (32), this strongly suggests that *B. subtilis* TatAd displays both TatA and TatB activity.

**Overexpression of TatAdCd Does Not Fully Complement E. coli ΔABCDE Cells in Tat-dependent Substrate Translocation** — Although repeated tests consistently showed TatAdCd to be capable of efficiently exporting TorA, it was considered important to analyze its ability to also export other substrates. We first tested whether the cells can export a fusion protein comprising the TorA signal peptide linked to GFP. This fusion is exported by the Tat pathway in *E. coli* (30, 31). We expressed TorA-GFP in *E. coli* ΔABCDE cells and coexpressed tatAdCd or *E. coli* tatABC on the compatible pEXT22 plasmid.

**FIGURE 1. Expression of *B. subtilis* TatAdCd in an *E. coli* tat null mutant leads to efficient export of TorA.** The figure shows a native polyacrylamide gel stained for TMAO reductase (TorA) activity. Membrane, cytoplasm, and periplasm samples (M, C, and P, respectively) were prepared and analyzed from two wild type strains of *E. coli* (MC1061 and MC4100 as indicated), from ΔtatABCDE cells (Δtat) and from ΔtatABCDE cells expressing *E. coli* TatABC from plasmid pBAD-ABC, or *B. subtilis* TatAdCd from plasmid pBAD as indicated. The mobility of active TorA is indicated.

<table>
<thead>
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<th>pBAD-ABC</th>
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<th>MC1061</th>
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<td>M</td>
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-TorA
as detailed under “Experimental Procedures.” The cells were fractionated into membrane, cytoplasm, and periplasm fractions, and the data are shown in Fig. 2A. In control tests (Fig. 2A, wild type panel), GFP is found as mature size protein in the periplasm (P) when expressed in wild type cells. Some mature size protein is also found in the cytoplasm, but we have observed this phenomenon before and concluded that it is due to proteolytic clipping of the precursor form (31). The TorA-GFP accumulates exclusively in the cytoplasm when expressed in a tat null mutant (Δtat panel), again mostly as mature size protein. The remaining panels show that the protein is exported if either E. coli TatABC or B. subtilis TatAdCd is coexpressed in a Δtat background. High levels of mature protein are present in the periplasm in both cases, confirming efficient export.

These data were confirmed by confocal microscopy of the cells as shown in Fig. 2B. Clear periplasmic halos of GFP fluorescence are evident when the TorA-GFP is expressed in wild type cells or in cells expressing TatAdCd or E. coli TatABC. In contrast, the fluorescence is purely cytoplasmic when the construct is expressed in ΔtatABCDE cells.

Fig. 2B also illustrates an important point regarding the ability of the TatAdCd system to export other substrates. Two Tat substrates in E. coli, amidase A and C, have been shown to be involved in cytokinesis (33). These substrates are mislocalized in a ΔABCDE deletion strain causing a distorted cell division phenotype; as a result the cells grow in long chain-like filaments (34). The wild type phenotype is clearly restored by complementing the ΔABCDE strain with plasmid-borne TatABC (TatABC image). However, expression of B. subtilis TatAdCd also restores the wild type cell division phenotype (TatAdCd panel), strongly suggesting that the TatAdCd complex of B. subtilis is able to translocate one or both of the amidase A and C proteins.

We also analyzed the translocation of SufI, another authentic Tat substrate, in E. coli ΔtatAE strain, in E. coli ΔABCDE deletion strain complemented with B. subtilis TatAdCd (Fig. 3). The mature size, 50-kDa SufI protein is clearly detected in the periplasm (P) of wild type MC4100 cells with some precursor protein apparent in the cytoplasmic fraction (C). An additional band slightly smaller than mature SufI is also detected in the membrane fraction (M), although the significance of this band is unclear. As expected, deletion of the E. coli Tat machinery resulted in accumulation of SufI in the cytoplasm (Δtat panel). In this case, export could not be restored by expression of TatAdCd of B. subtilis (Δtat/pBAdCd panel), with no SufI detected in the periplasm. We conclude that not all Tat-dependent substrates of E. coli can be translocated by this AC-type translocase.

TatAd Is Bifunctional and Able to Complement Both the ΔtatAE and ΔtatB E. coli Mutants—The absence of a tatB gene in most Gram-positive organisms suggests that the Gram-positive TatA subunits are able to carry out both the TatA and TatB roles involved in Tat systems from Gram-negative organisms (20). This important point has not been addressed experimentally, and we therefore expressed B. subtilis TatAdCd in the E. coli ΔtatAE and ΔtatB strains to test whether it can complement the defects. The results (Fig. 4) show that an exported periplasm when His-tagged TatAd is expressed in either the ΔtatAE or ΔtatB strains, clearly demonstrating that this subunit is able to execute both the TatA and TatB roles. Note that the signal intensity of the periplasmic TorA band appears to be low when TatAd is expressed in the ΔtatAE strain, but this assay is not quantitative, and from other experiments TatAd complements the two strains to an apparently equal
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FIGURE 4. B. subtilis TatAd complements both the ΔtatAE and ΔtatB E. coli mutants. His-tagged TatAd was expressed using the pBAD-His vector (“Experimental Procedures”) in the E. coli ΔtatAE, ΔtatB and ΔtatABCDE mutants as shown. After induction for 3h in the presence of 0.1 mM arabinose, the cells were fractionated into membrane, cytoplasm, and periplasm samples (M, C, and P, respectively), which were analyzed on a native gel that was stained for TorA activity. Similar fractionations were made using ΔtatAE and ΔtatB cells in control experiments.

extent (data not shown). In the control sample, no periplasmic TorA activity is detected when TatAd is expressed in a tat null mutant strain (ΔtatABCDE; the panel is overexposed to detect the cytoplasmic and membrane-bound TorA activity in the P and M lanes). No export of TorA is evident in the ΔtatAE or ΔtatB strains either, because Tat activity is absolutely dependent on the presence of TatB plus either TatA or the TatA homolog, TatE (Ref. 4 and data not shown).

Purification of Overexpressed TatAdCd Reveals the Presence of Two Forms of Tat Complex: TatAdCd and TatAd — To analyze the Tat complexes present after expression of B. subtilis TatAdCd in E. coli, the membranes were solubilized in digitonin, after which the lysate was subjected to Streptactin affinity chromatography utilizing the Strept-tag II on the C terminus of TatCd as described under “Experimental Procedures.” Column fractions were subjected to immunoblotting using specific antibodies to TatAd and the Strept-tag II on TatCd. The data shown in Fig. 5A confirm that essentially all of the TatCd-strep had bound to the column; virtually none was detected in the wash fractions. Most of the TatCd-strep was found in elution fractions 2–4, with a clear peak in fraction 3. A small amount of TatAd copurified with the TatCd-strep strongly suggesting the presence of a TatAdCd complex. However, the vast majority of the TatAd did not coelute with the TatCd-strep and was instead detected in the first three wash fractions. This is reminiscent of similar studies on E. coli TatABC, with the majority of additional “free” TatA likewise detected in the wash fractions as a separate complex (13). The data thus point to the presence of two types of complex, one composed of TatAdCd and another composed only of TatAd.

To determine the composition of the TatCd/TatAd-containing complex, the elution fractions were subjected to gel filtration chromatography using a Superose-6 matrix, and Fig. 5B shows a silver-stained gel of samples from each stage of the overall purification protocol: total membrane starting material, Q-Sepharose chromatography, Streptactin affinity chromatography, and gel filtration chromatography. The final sample shows the presence of only the 25-kDa TatCd subunit. TatAd does not stain well with silver, but its presence was confirmed by immunoblotting (Fig. 5B, left panel). The TatAdCd complex has thus been purified to homogeneity. Note that the TatAd blot of the purified samples is weak compared with the original membrane sample; this reflects the fact that only a very small proportion of the TatAd pool is associated with TatCd.

Highly Discrete TatAdCd and TatAd Complexes — The sizes of the two forms of B. subtilis Tat complex were analyzed using calibrated gel filtration chromatography. Digitonin-solubilized membranes from cells expressing TatAdCd-strep were applied to a calibrated Superose-6 gel filtration column as described under “Experimental Procedures,” and elution fractions were immunoblotted using antibodies against TatAd and TatCd-strep (Fig. 6A). The elution profiles of the TatAdCd and TatAd complexes were quantified by densitometry of the bands, and the graphs are shown in Fig. 6A. We also expressed, solubilized, and fractionated the membrane-bound E. coli TatABC and TatA complexes under exactly the same conditions for comparison, and we analyzed the TatA-type complexes extracted from the cytoplasm (also indicated in Fig. 6B). The data show that TatCd elutes in fractions 20–27, and TatAd elutes in fractions 22–26. Quantification of the intensity of the bands reproducibly shows that TatCd is eluting with a peak in fraction 23 corresponding to a molecular mass of ~350
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Digitonin forms particularly large micelles, so for a more accurate estimation of the size of the TatAd complex, we expressed TatAd alone and solubilized the membranes in either dodecyl maltoside or octyl glucoside prior to fractionation in the same detergent (Fig. 6B, upper graph, white squares or triangles, respectively). In both cases the TatAd complex elutes later than when solubilized in digitonin (black triangles), presumably because of the much smaller micelle size. In both dodecyl maltoside and octyl glucoside, TatAd elutes at a position that corresponds to a mass of 160 kDa, which we assume to be a more accurate reflection of the complex size (although the micelle will still contribute to a degree).

Cytosolic TatAd Is Present as Very Large Aggregates—Although studies on the *E. coli* and thylakoid systems have focused on roles of membrane-bound TatABC proteins, recent studies on the *B. subtilis* TatAdCd system have suggested a completely different mode of action in which the precursor of PhoD is initially recognized by TatAd in the cytosol (27, 35, 36). This would differ dramatically from the *E. coli* and thylakoid systems, where substrates bind to a membrane-bound TatBC dimer (15, 16). Having characterized the size properties of membrane-bound TatAd when expressed in *E. coli*, we therefore tested whether TatAd is also present in the cytosol. This was done after expression of two forms of TatAd, an untagged version of TatAd (using the plasmid pBAdCd as in the above studies) and one with a His6 tag present on the C terminus of TatAd (pBAd-His plasmid). The two forms were expressed using the pBAD24 vector, and the cytosolic fraction was subjected to Superose 6 gel filtration chromatography (Fig. 6B, lower graph). The data show that the untagged TatAd is present as very large multimeric forms. The protein elutes in fraction 14 (white diamonds), which corresponds to an average size of ~2 MDa. Surprisingly, the presence of a His tag causes a huge change of structure, and the protein elutes much later from the column, at a position corresponding to a mass of ~200 kDa (similar to that observed in Ref. 27). These data do raise questions about the significance of the cytosolic TatAd, and this issue is discussed below.

**Blue Native Gel Electrophoresis Shows the Presence of a ~230-kDa TatAdCd Complex**—To analyze the purified TatAdCd and TatAd complexes further, blue native (BN) polyacy-
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![Diagram of Tat complexes](image)

**FIGURE 7.** Blue native gel electrophoresis identifies a discrete TatAdCd complex with an estimated mass of ~230 kDa. Samples of ΔtatABCDE cells expressing E. coli TatABC (lanes Ec) or B. subtilis TatAdCd (lanes Bs), and samples of purified TatAdCd (lane AdCd; see Fig. 5) were subjected to blue native gel electrophoresis as described under “Experimental Procedures.” The gel was immunoblotted with antibodies to the Strep-tag II on the C terminus of TatC/TatCd (A), to E. coli TatA (B), or TatAd (C). Mobilities of molecular mass markers (in kDa) are indicated on the left, and the mobilities of E. coli TatABC and B. subtilis TatAdCd are also indicated.

rylamide gel electrophoresis was utilized according to the method described under “Experimental Procedures” (Fig. 7). Gel filtration chromatography provides a reasonable estimate of complex size, but it is heavily affected by the size of detergent micelles. To circumvent this effect and obtain a more accurate description of the complexes, purified TatAdCd and solubilized membranes expressing TatAdCd were run on a blue native polyacrylamide gel. This gel system has been specifically developed for the analysis of membrane protein complexes because it effectively removes the bias caused by the detergent micelles. Digitonin-solubilized membranes from cells expressing B. subtilis TatAdCd-strep (lanes Bs), E. coli TatABC (lanes Ec), or purified B. subtilis TatAdCd-strep (lanes AdCd) were loaded onto a BN gel. The gels were subjected to Western blotting followed by immunodetection with antibodies against the Strep-tag II (Fig. 7A), E. coli TatA (Fig. 7B), and B. subtilis TatAd (Fig. 7C).

Reproducing earlier findings (17), the E. coli TatABC complex was visualized as a band comigrating with the marker band of 440 kDa using antibodies against the Strep-tag II (Fig. 7A, lane Ec). Previous studies have shown that, after careful calibration of this gel system, the actual size of this complex is ~370 kDa as judged by this technique (28). Analysis of purified B. subtilis TatAdCd complex (prepared as described above) reveals a band that comigrates with the 232-kDa marker. A band of the same size is detected when the same blot is probed with antibodies to TatAd (Fig. 7C), confirming that this band corresponds to a TatAdCd complex of ~230 kDa. A band of similar size is evident in samples of whole membranes taken from cells expressing TatAdCd (lane Bs), although it is less clear, and some smearing is evident. However, because essentially all of the TatAdCd complex binds to the Streptactin affinity matrix, and only the ~230-kDa TatAdCd complex is detected, we are confident that this is the major species of TatAdCd complex present in the membrane.

Fig. 7B clearly shows the “ladder” of differently sized E. coli TatA complexes, but it has not been possible to study the B. subtilis TatAd complex using BN gels. Although the TatAd antibodies clearly detect the purified TatAdCd complex in Fig. 7C (lane AdCd), there is no clear additional band in the whole membrane sample (lane Bs) from cells expressing TatAdCd. It is possible that the TatAd complex is too small for accurate analysis using the BN system under these conditions.

**DISCUSSION**

A wealth of data have emerged from studies on the TatABC and TatA complexes of Gram-negative bacteria (particularly E. coli) as well as the corresponding plant thylakoid complexes (Hcf106-TatC complex and homo-oligomeric Tha4 complexes). In most respects, the E. coli and plant systems appear to operate by broadly similar mechanisms in which two key points are considered to be noteworthy. First, cross-linking data point to the presence of a membrane-bound substrate-binding complex in which TatB and TatC play critical roles (15, 16). A tight association between these components has been confirmed by one study that showed a translational TatB-TatC fusion to be active (13). Second, the available evidence indicates that a TatA (or Tha4) complex assembles and exists as a separate entity and appears to be recruited by the TatABC (or plant Hcf106-TatC complex) only at the point of translocation (37).

In this study we have sought to study Tat complexes from the Gram-positive organism B. subtilis. The absence of tatB genes in the majority of Gram-positive organisms clearly indicates that their Tat systems differ significantly from the E. coli model, and it is important to identify similarities and differences (particularly any mechanistic differences) between the two types of system. In this context, our data are important because they show for the first time that an authentic E. coli Tat substrate, TorA, can be effectively transported by the B. subtilis TatAdCd system. This indicates that there are no system-specific factors in B. subtilis that are required for this system to operate, which could be absent in Gram-negative organisms. This focuses attention on the TatAdCd subunits as the critical components.

The absence of a tatB gene in B. subtilis raises the possibility that TatA is bifunctional in Gram-positive bacteria, fulfilling the roles of both TatA and TatB from Gram-negative organisms (20). This possibility is backed up by the recent demonstration (38) that selective mutations in E. coli TatA can enable it to carry out both TatA and TatB functions. In this report we have provided experimental confirmation of the bifunctional nature of TatAd; this subunit can complement both the ΔtatAE and ΔtatB E. coli mutants. TatA and TatB play completely different roles in the E. coli Tat system (1, 2, 13, 15, 18), which clearly indicates a dual role for TatAd in the B. subtilis TatAC-type mechanism.

When compared with the E. coli Tat complexes, the B. subtilis Tat complexes exhibit important common features but also significant differences. The primary common feature is the presence of two distinct Tat complexes. We have shown that expression of the B. subtilis tatAdCd genes results in the presence of separate membrane-bound TatAdCd and TatAd complexes, and these results are very reminiscent of findings on the E. coli system where separate TatABC and TatA complexes are present at steady state (13, 17, 18).

However, the B. subtilis Tat complexes encoded by tatAdCd differ from their E. coli counterparts in three important
respects. One of these has already been noted: the absence of TatB in the core substrate-binding complex; its position appears to be occupied by TatAd. The second relates to the nature of the TatAdCd complex; like the \textit{E. coli} TatABC complex, the TatAdCd purifies as a highly discrete entity, but our data indicate that the \textit{B. subtilis} TatAdCd complex is significantly smaller than its \textit{E. coli} counterpart: 230 kDa compared with 370 kDa for the \textit{E. coli} complex as estimated previously by BN gels (17). This may have implications for the number and/or organization of the TatC-containing domains, although it should be noted that an individual TatAdCd domain is smaller than an equivalent \textit{E. coli} TatABC domain (--35 kDa compared with 56 kDa, assuming equimolar stoichiometry as observed for TatBC in the \textit{E. coli} complex (13)).

The third and perhaps most significant difference concerns the TatA complexes. The \textit{E. coli} TatA complex exists as a remarkably heterogeneous set of complexes that range in size from ~50 kDa to well over 500 kDa (17, 18), and this heterogeneity can be clearly visualized as a striking ladder of bands on BN gels. In the above studies it was proposed that this heterogeneity could provide the flexibility for this system to assemble active translocons of differing sizes, which would be logical if a wide range of substrates are to be accommodated without compromising membrane integrity. In contrast, the \textit{B. subtilis} complex is highly discrete in nature; there is no evidence for heterogeneity among the complexes isolated. Nevertheless, this combination of TatAdCd and TatAd complexes is able to transport substrates of very differing sizes, such as authentic TorA (85 kDa) and GFP (25 kDa), as well as its original PhoD substrate in \textit{B. subtilis} (62.5 kDa). On the basis of these data, we believe that the active translocon may be a singular unit capable of accommodating substrates that differ dramatically in terms of size and shape. This would, of course, require real flexibility within the active translocation complex. This scenario would raise questions about the functional significance of the \textit{E. coli} TatA heterogeneity but would be consistent with our observation that the TatA size spectrum is identical in cells that are completely unable to export proteins via this pathway (39).

The TatAdCd complex is furthermore surprisingly small; the size exclusion chromatography estimate is ~160 kDa, and the detergent micelle probably accounts for some of this estimate. These data have interesting implications for the translocation mechanism because TatAdCd is capable of exporting TorA, which is one of the larger Tat substrates (85 kDa). If, as proposed, the active Tat translocon is generated by the coalescence of a TatABC and TatA complex, the sizes of the \textit{E. coli} complexes have been deemed to be consistent with this model (for example, an active translocon of up to 1 MDa in size could be generated by fusion of one of the largest TatA complexes with the 370-kDa TatABC complex). It is less clear whether a substate of this size can be transported in a folded state by a translocon comprising a 270-kDa TatAdCd complex and 160-kDa TatAd complex. Therefore, it may be the case that the actual translocation process is more complicated than currently imagined, perhaps involving the recruitment of several TatA or TatAd (or even several TatABC or TatAdCd) complexes in both Gram-negative and Gram-positive bacteria.

Finally, it is useful to consider these data in the light of other studies on Tat systems from Gram-positive organisms. Recent studies on the \textit{B subtilis} TatAdCd system (27, 35, 36) suggest a translocation mechanism that is very different from any current model for the \textit{E. coli} or thylakoid Tat system. These studies showed that TatAd can be detected as cytoplasmic oligomers of ~250 kDa, and these oligomers were shown to be able to bind the precursor form of PhoD, the natural substrate of TatAdCd (a membrane-bound form of TatAd is also present in \textit{B. subtilis}). The authors proposed that cytosolic TatAd acts as a soluble receptor for substrate, after which the membrane-bound TatCd recognizes this cytosolic assembly and assists in its membrane integration. More confusingly still, studies on \textit{Streptomyces lividans} (one of the few Gram-positive organisms containing \textit{tatABC} genes) have shown that both TatA and TatB can be detected in the cytoplasm, and the authors proposed that a cytosolic TatAB complex binds substrates and delivers them to TatC (40). These models are fundamentally different in key respects to current models for the Tat system in Gram-negative bacteria and plant thylakoids, where the Tat components are only active in the membrane (13, 15–18).

Although our aim in this study was to analyze the potentially bifunctional TatAd protein and the complexes formed by TatAdCd expression, our data do have relevance to this ongoing debate about Tat mechanism(s) and whether Tat systems differ so diametrically in Gram-negative and Gram-positive organisms. First, we have shown that the TatAd subunit carries a bifunctional TatAd protein and the complexes formed by TatAdCd (which we have shown to be present) rather than TatAdCd apparatus instead, and it thus seems probable that it interacts with a membrane-bound TatBC-containing complex in \textit{E. coli}. Cross-linking studies with a construct comprising the TatA signal peptide linked to a thylakoid lumen passenger protein (41) have shown that the TatA signal peptide specifically binds to a membrane-bound TatBC heterodimer as previously shown for another Tat precursor protein, SufI (15). We have shown that TatA-GFP is capable of using the \textit{B. subtilis} TatAdCd apparatus instead, and it thus seems probable that it interacts with a membrane-bound TatAdCd complex (which we have shown to be present) rather than following a completely different export pathway involving the binding of a soluble TatAd complex. Nevertheless, these are indirect forms of evidence and different, more direct approaches are required to determine whether TatAd functions in the membrane, the cytoplasm, or both.

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REFERENCES