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Jessica A. Sexton  
*Washington University School of Medicine in St. Louis*

Jerome S. Pinkner  
*Washington University School of Medicine in St. Louis*

Robyn Roth  
*Washington University School of Medicine in St. Louis*

John E. Heuser  
*Washington University School of Medicine in St. Louis*

Scott J. Hultgren  
*Washington University School of Medicine in St. Louis*

*See next page for additional authors*

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Jessica A. Sexton, Jerome S. Pinkner, Robyn Roth, John E. Heuser, Scott J. Hultgren, and Joseph P. Vogel

Department of Molecular Microbiology and Department of Cell Biology and Physiology, Washington University, St. Louis, Missouri 63110

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The ability of *Legionella pneumophila* to grow and cause disease in the host is completely dependent on a type IV secretion system known as the Dot/Icm complex. This membrane-spanning apparatus translocates effector molecules into host cells in a process that is poorly understood but that is known to require the putative ATPase DotB. One possible role for DotB is suggested by its similarity to the PilT family of proteins, which mediate pilus retraction. To better understand the molecular behavior of DotB, we have purified the protein and shown that it forms stable homohexameric rings and hydrolyzes ATP with a specific activity of 6.4 nmol of ATP/min/mg of protein. ATPase activity is critical to the function of DotB, as alteration of the conserved Walker box lysine residue resulted in a mutant protein, DotB K162Q, which failed to bind or hydrolyze ATP and which could not complement a ΔdotB strain for intracellular growth in macrophages. Consistent with the ability of DotB to interact with itself, the dotB K162Q allele exhibited transdominance over wild-type dotB, providing the first example of such a mutation in *L. pneumophila*. Finally, the DotB K162Q mutant protein had a significantly enhanced membrane localization in *L. pneumophila* compared to wild-type DotB, suggesting a relationship between nucleotide binding and membrane association. These results are consistent with a model in which DotB cycles between the cytoplasm and the Dot/Icm complex at the membrane, where it hydrolyzes nucleotides to provide energy to the complex.

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*L. pneumophila*, an intracellular bacterial pathogen, causes Legionnaires’ disease by replicating inside alveolar macrophages (13). This ability is dependent on a set of genes called *dot* or *icm*, which encode a specialized type IV secretion system (32, 37). The type IV secretion system family is composed of both classical plasmid transfer systems and a related protein export apparatus used by a wide range of pathogens to export toxins (reviewed in reference 4). For *L. pneumophila*, the Dot/Icm complex is believed to translocate numerous effector molecules into host cells in order to modify the endocytic pathway. Thus far, two translocated proteins, LidA and RalF, have been identified (6, 19). RalF is an ADP-ribosylating factor that functions to recruit the macrophage protein ARF1 to *L. pneumophila*-containing phagosomes, while the function of LidA remains unknown. Because neither of these is absolutely required for *L. pneumophila* intracellular growth, additional Dot/Icm-secreted proteins are believed to exist (6).

The Dot/Icm apparatus is a macromolecular complex that comprises a large number of membrane proteins and several proteins predicted to have cytoplasmic localization. One such cytoplasmic protein, DotB, contains conserved nucleotide binding domains present in many ATPases, as well as domains specific to ATPases found in bacterial type II and type IV secretion systems (23, 27, 39). Though DotB is known to be a critical component of the Dot/Icm complex (37, 38), its molecular function is not yet clear. BLAST searches reveal that DotB is most similar to several uncharacterized putative ATPases found in other type IVB secretion systems including a *Coxiella burnetii* DotB homologue (BLAST score, e\(^{-133}\)) and the TraJ protein of plasmid R64 (BLAST score, e\(^{-41}\)). DotB also has limited similarity to the type IVA secretion ATPases HP0525 of *Helicobacter pylori* (BLAST score, e\(^{-7}\)) and VirB11 of *Agrobacterium tumefaciens* (BLAST score, e\(^{-7}\)). Finally, DotB has extensive similarity to the PilT family of proteins (BLAST score, e\(^{-38}\)) found in bacterial type II secretion systems. PilT proteins are ATPases that mediate the retraction of adhesive pili, a process essential to bacterial twitching motility and natural transformation (10, 18, 34).

Since PilT proteins are components of type II secretion systems, which are evolutionarily quite divergent from type IV secretion systems (22), the similarity between DotB and PilT is surprising. Pilus retraction is well documented both in type II secretion systems (e.g., type IV pili) and in the conjugal type IV secretion systems (20). However, in the latter case, the mechanism of this retraction is completely unknown; no pilus retraction factors or PilT-like proteins have yet been identified. Now, *L. pneumophila*, *C. burnetii*, and plasmid R64 DNA sequences have revealed the existence of three PilT homologues in the type IVB secretion systems. Whether these proteins function as the type IVA secretion ATPases are thought to, as assembly and export chaperones for their respective secretion complexes (14–16), or whether they might mediate retraction of pili elaborated by type IV secretion complexes remains to be determined.

The families of type II and type IV secretion ATPases perform a wide range of functions including assembly of transmembrane complexes, pilus assembly, pilus retraction, and
Strain Lp02 (thyA hsdR rpsL) is a derivative of the L. pneumophila supplemented with 100 μg thymidine/ml as needed. Lp02 and Lp02 derivatives were cultured on CYE or AYE extract agar (CYE) or in ACES-buffered yeast extract broth (AYE) as described previously (7, 9). Lp02 and Lp02 derivatives were cultured on CYE or AYE supplemented with 100 μg of thymidine/ml as needed. Escherichia coli strains C600 and XL1-Blue were cultured in Luria-Bertani broth containing ampicillin at 100 μg/ml for maintenance of plasmid selection.

**Strain and plasmid construction.** The suicide plasmid pJB920, used to create the ΔdotB strain JV918, was constructed by PCR amplification of 500-bp regions flanking the ΔdotB open reading frame (ORF) from Lp02 chromosomal DNA with primers engineered to have SalI/BamHI or EcoRI restriction sites. The resulting fragments were cut with SalI/BamHI or BamHI/EcoRI, cloned in a three-piece ligation into the SalI/NorI sites of the suicide vector pSR47S (17), and confirmed by sequencing. Next, pJB920 was transformed into Lp02, where it integrated via homologous recombination into the chromosome, generating a ΔdotB/ΔdotB merodiploid. The merodiploid was resolved by counterselection based on sucrose sensitivity, and the resulting colonies were screened for the absence of dotB via PCR, thus generating strain JV918.

The suicide plasmid pJB92911, used to create the Flag-DotB strain JV3079, was constructed as follows. Regions of 500 bp immediately upstream and downstream of the dotB start codon were amplified by PCR from Lp02 chromosomal DNA with primers engineered to have SalI/BamHI or EcoRI restriction sites. The resulting fragments were cut with SalI/BamHI or BamHI/EcoRI, cloned in a three-piece ligation into the SalI/NorI sites of the suicide vector pSR47S (17), and confirmed by sequencing. Next, oligonucleotides encoding the Flag epitope (DYKDDDDK) were inserted into the Flag-DotB strain JV3079, which contains only Flag-DotB.

**Materials and Methods**

**Bacterial strains, plasmids, and media.** Bacterial strains are listed in Table 1. Strain Lp02 ( thyA hsdR rpsL ) is a derivative of the L. pneumophila serogroup 1 clinical isolate Philadelphia-1 (2). All L. pneumophila strains were cultured on ACES [N-(2-acetamido)-2-aminoethanesulfonic acid]-buffered charcoal yeast extract agar (CYE) or in ACES-buffered yeast extract broth (AYE) as described previously (7, 9). Lp02 and Lp02 derivatives were cultured on CYE or AYE supplemented with 100 μg of thymidine/ml as needed. Escherichia coli strains C600 and XL1-Blue were cultured in Luria-Bertani broth containing ampicillin at 100 μg/ml for maintenance of plasmid selection.

**Strain and plasmid properties.** Strain or plasmid Relevant properties Reference or source

### Table 1. Bacterial strains and plasmids

<table>
<thead>
<tr>
<th>Strain or plasmid</th>
<th>Relevant properties</th>
<th>Reference or source</th>
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<td>CDC*</td>
</tr>
<tr>
<td>Philadelphia-1</td>
<td>(McrA::Flag coding sequence fused to dotB)</td>
<td>This study</td>
</tr>
<tr>
<td>JV918</td>
<td>Lp02 ΔdotB</td>
<td>This study</td>
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<td>JV3079</td>
<td>Lp02 ΔdotB:Flag coding sequence fused to dotB</td>
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<td>E. coli</td>
<td>C600</td>
<td>Stratagene</td>
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<tr>
<td>XL1-Blue</td>
<td>e14 (McrA- supE44 thi-1 thr-1 leuB6 lacZ17 Iota21 recA1 endA1 gyrA96 thi-1 hadR17 supE44 relA1 lac [F' proAB lacZAM15 Tn10(Tet')])</td>
<td>Stratagene</td>
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* CDC, Centers for Disease Control and Prevention (Atlanta, Ga.).
DotB tyrosine 162 with a glutamine. These primers were designed by using the Primer Generator program (http://www.med.jhu.edu/medcenter/primer/primer.cgi) and resulted in PCR products with altered dotB sequences, creating the K162Q mutation as well as a novel Aval site. 5'-3' PCR products were digested with Aval (Pharmacia) and Aval linked to the BamHI site of pJB1540 and cloned into the BamHI site of pJB1540, and confirmed by sequencing. Primers were as follows: dotB, 5'-CCGCGGTCGACGTTAAGTTGATCTGCTATGG and 3'-CCCGGTCGACGATTGATTTGGATATCTTTGG (boldface letters indicate start or stop codons, and restriction sites are underlined); K162Q (dotB internal), 5'-CCCGGTCGACGATATTGACATGTTAGTCG and 3'-CCCGGTCGACGCGTGAGGCTCGTGAATTC (boldface letters indicate a three-nucleotide deletion from the dotB sequence, and restriction sites are underlined).

The expression vectors for His-tagged versions of DotB and DotB K162Q that were used for protein purification were engineered with plasmid pJB1540, a derivative of the Qagen (Valencia, Calif.) expression vector pQE30. Plasmid pJB1540 encodes a thrombin cleavage site downstream of the sequence encoding the six-His tag and was constructed by cloning overlapping oligonucleotides containing a thrombin cleavage site and BamHI cohesive ends into the BamHI site of pQE30, destroying the upstream BamHI site. The wild-type dotB and dotB(K162Q) ORFs (minus the ATG start codons) were amplified with pJB1540 and pJB1386 plasmid DNA with primers containing BamHI or SalI restriction sites at their 5' prime ends. The resulting PCR product was digested with BamHI, SalI, and cloned into the BamHI/SalI sites of pJB1540, and confirmed by sequencing. This resulted in the constructs pJB1572 (wt) and pJB2442 (K162Q mutant). Coding sequences for His-tagged versions of wild-type and mutant DotB were subcloned from pJB1572 and pJB2442 into the RSF1010 vector pRb908 for expression in L. pneumophila. These constructs were designated pJB1192 and pJB2444, respectively.

Intracellular growth assays. The human monocytic cell line U937 was passaged, and cells were differentiated with phorbol 12-myristate 13-acetate (Sigma) as described previously (21). L. pneumophila strains were used to be infection of U937 cells were grown to exponential phase, back-diluted into media containing 2.8 mM isopropyl-thiogalactoside (IPTG) with 1 mM ATP, 10 mM MgCl2, 4 mM EnzChek fluorescent nucleotide (Molecular Probes), and buffer was exchanged with PD-10 column (Amersham Biosciences) equilibrated in buffer B. Proteins were eluted with a 45-ml linear gradient from 20 to 220 mM KPO4 and 0 to 500 mM NaCl in buffer B. DotB eluted at approximately 350 mM KPO4-150 mM NaCl. Fractions containing DotB were pooled, and buffer was exchanged with a PD-10 column (Ambersham Biosciences) into buffer B (20 mM KPO4, pH 7.6, 10 mM NaCl, 1% glycerol, 0.01% Brij 35) with 10 mM imidazole, and protein was eluted off the resin in cold buffer A with 100 mM imidazole. Elution fractions were pooled, total protein content was determined by the Bio-Rad protein assay (based on the method of Bradford), and total activity was determined by the Bio-Rad protein assay (based on the method of Bradford), and total activity was determined by the Bio-Rad protein assay (based on the method of Bradford), and total activity was determined by the Bio-Rad protein assay (based on the method of Bradford).

Antibody generation and affinity purification. Purified His-DotB was injected into rabbits (Cocalico, Inc.) for generation of a polyclonal DotB antibody, which was subsequently affinity purified as follows. Purified His-DotB (2 mg) was separated via sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and transferred to a polyvinylidene fluoride membrane (Millipore), and the His-DotB protein band was cut away from the rest of the membrane. The resulting membrane strip was incubated with 1.5 ml of polyclonal serum diluted with pJB2442) was performed in exactly the same fashion, and preparations were fractioned by SDS-PAGE and Western blotting. The polyclonal DotB K162Q (expressed in C600 and 3°C). The sample was concentrated to a final volume of 400 μl with Ultrafree 4 filter columns with a 10-kDa molecular mass cutoff (Millipore). Concentrated DotB was then applied in a single injection to a 25-ml Superoxime 12 column (Ambersham Biosciences) equilibrated in buffer D. DotB eluted in single peak at a total elution volume of 9.8 ml. Fractions containing DotB were pooled, and brought to a final concentration of 2 mg/ml. This procedure yielded, on average, 38 mg of highly purified DotB (quantitated 97% pure; AlphaLager software). Purification of DotB K162Q (expressed in C600 and 3°C) was performed in exactly the same fashion, and preparations were equally pure.

ATPase and ATP binding assays. ATP hydrolysis reactions were performed with the EnzChek phosphate assay kit (Molecular Probes). Each reaction mixture contained 3 to 24 μM purified protein (molarity was calculated for monomeric DotB) in buffer D with 1 mM ATP, 10 mM MgCl2, 4 mM EnzChek substrate (2-amino-6-mercapto-7-methylpurine riboside [MESG]), and 0.1 U of EnzChek enzyme (purine nucleoside phosphorylase [PNP]). In the presence of inorganic phosphate MESG is converted via PNP to ribose 1-phosphate and 2-amino-6-mercapto-7-methylpurine. This results in an absorbance shift from 330 to 360 nm, thus creating a spectrophotometric readout for the concentration of inorganic phosphate in each reaction. Reactions were performed in 100-μl volumes in 96-well plates and were allowed to proceed for 30 min at 25°C, at which point the absorbance was determined with a VERSAmax plate reader (Molecular Devices). Total phosphate concentrations were determined by comparing sample absorbances to those of a phosphate standard curve.

For ATP binding reactions, 20 μg of purified protein was mock preincubated or preincubated with 10 mM ATP for 1 h at 4°C and then added to 400 μl reaction mixtures containing 20 mM MES (morpholinoethanesulfonic acid; pH 7.0), 40 μl of ATP- or AMP-agarose (Sigma), and 100 μg of BSA (Sigma). Samples were incubated for 30 min at 4°C with 10 μl of 1 mg/ml of L. pneumophila lysate in buffer E (50 mM Tris-HCl, 150 mM NaCl, 20 mM EDTA, 5% nonfat dry milk, 0.5% Triton X-100, 100 μM N-ethylmaleimide, 100 μM phenylmethylsulfonyl fluoride, 10 μl of L. pneumophila cells. Competing ATP was added to a final concentration of 10 μM. Reaction mixtures were incubated at 4°C for 6 h with mixing, and nucleotide-
To test this, bacterial cells used for U937 infections were sub-
lysine-to-glutamine change should be structurally conservative.
The DotB K162Q protein was not stable, despite the fact that a
deletion strain JV918, intracellular growth was identical to that
of the

FIG. 1. Complementation of a dotB mutant for intracellular growth and transdominance of DotB K162Q in wild-type L. pneumophila. (A) Intracellular growth in U937 monocytes. L. pneumophila ΔdotB strain JV918 containing empty vector pJB908 (triangles), the DotB complementing clone pJB1153 (hatched squares), and the DotB K162Q clone pJB1568 (diamonds) was assayed for growth in U937 cells over time. In addition, L. pneumophila wild-type strain Lp02 containing empty vector pJB908 (open squares), the DotB complementing clone pJB1153 (open diamonds), and the DotB K162Q clone pJB1568 (circles) was also assayed for growth in U937 cells. (B) Strains used in panel A were examined by Western blotting for relative DotB levels at the time of infection. Lane 1, Lp02(pJB908); lane 2, Lp02(pJB1153); lane 3, Lp02(pJB1568); lane 4, JV918(pJB908); lane 5, JV918(pJB1153); lane 6, JV918(pJB1568). The molecular masses of relevant markers (in kilodaltons) are on the left. Large arrowhead, DotB or DotB K162Q band; small arrowhead, cross-reacting band that serves to confirm overall sample equivalence.

RESULTS

The K162 residue is essential to DotB function. To determine whether the predicted ATPase activity of DotB might be important for its function, a mutation in the DotB Walker A box was engineered, changing the highly conserved lysine to a glutamine. When the DotB K162Q mutant protein was expressed from the Ppac promoter in the L. pneumophila dotB deletion strain JV918, intracellular growth was identical to that of the dotB deletion strain containing the empty expression vector, indicating that the Walker box mutant was not able to function in L. pneumophila (Fig. 1A). One possibility was that the DotB K162Q protein was not stable, despite the fact that a lysine-to-glutamine change should be structurally conservative. To test this, bacterial cells used for U937 infections were subjected to analysis by Western blotting with affinity-purified DotB antibody. Though apparently not as stable as wild-type DotB (Fig. 1B, compare lanes 6 and 5), DotB K162Q was found to be present in greater abundance than chromosomally encoded DotB in the wild-type strain Lp02 (Fig. 1B, compare lanes 6 and 1). Based on this observation, we concluded that the lack of functionality of DotB K162Q could not be attributed to an insufficient amount of protein.

In addition to being nonfunctional in a ΔdotB strain, DotB K162Q was found to inhibit the intracellular growth of the wild-type L. pneumophila strain Lp02 about 100-fold (Fig. 1A). This inhibition was not simply due to the increased level of DotB protein in the cells, as the overexpression of wild-type DotB did not affect Lp02 intracellular multiplication (Fig. 1A). Therefore, the Walker box mutant protein is not functional on its own and the mutation, when expressed in high copy number, is dominant negative in nature.

DotB is an ATPase. Based on the presence of several conserved nucleotide binding and hydrolysis domains within DotB sequence and on the requirement of the DotB Walker A box residue K162 for function (Fig. 1A), we predicted that DotB protein would exhibit ATP-hydrolyzing activity. To test this prediction, we engineered an N-terminal hexahistidine fusion that was expressed in E. coli and purified by Ni2+ affinity, ion-exchange, hydroxyapatite, and gel filtration chromatography (Fig. 2A). Targeted protease digestion was used to remove the His tag (Fig. 2A, compare lanes 3 and 4), leaving G-S-DotB (a glycine and a serine fused to DotB amino acid residues 2 to 377). The major protein band (42 kDa) was recognized by a
polyclonal DotB antibody (data not shown). On average, 5-liter cultures yielded 3 to 4 mg of purified DotB, and the protein preparation was estimated to be approximately 97% pure.

To assay ATPase activity of DotB, we employed a colorimetric assay that measures the presence of inorganic phosphate in solution (EnzChek; Molecular Probes). When free phosphate is present, it is used as a reagent in a chemical reaction that generates a product with maximum absorbance at 360 nm. Thus, the liberation of Pi by an ATPase, such as our positive control apyrase, can be quantitated by comparing $A_{360}$ to that of a phosphate standard curve. When this simple end point assay was performed, increasing amounts of apyrase corresponded to increased $A_{360}$ readings, indicating that the enzyme hydrolyzed ATP in proportion to its concentration (Fig. 3B). Positive readings were absolutely dependent on the addition of ATP to the reaction and on the presence of apyrase (data not shown), indicating that the source of Pi was enzymatically hydrolyzed nucleotides.

Likewise, purified DotB liberated Pi from ATP in a concentration-dependent fashion, though to a lesser extent than the very active ATPase apyrase (Fig. 3C). DotB-specific activity was calculated to be 6.4 nmol of ATP/min/mg of protein, while that of apyrase was found to be 3.0 μmol/min/mg. Because the activity of DotB was quite low, we needed to demonstrate that it was due to the presence of DotB rather than a contaminating ATPase that might be present in the preparation in trace amounts. To eliminate this possibility, we subjected purified DotB to gel filtration analysis. The protein was found to have a native molecular mass of ~259 kDa, a value consistent with the predicted molecular mass of a hexamer (252 kDa) (Fig. 4). In addition, the gel filtration elution profile for DotB K162Q was identical to that of wild-type DotB, suggesting that it also can form a hexamer (data not shown).

Next, we employed quick-freeze, deep-etch electron microscopy (11, 12), one of the most sensitive and accurate techniques available for visual examination of proteins, to observe the conformation of DotB. Purified protein was diluted in KH2PO4 buffer and incubated with no nucleotides, with ADP, or with ATPγS and then prepared and visualized with platinum replicas as described in Materials and Methods. Wild-type DotB appeared to exist solely and uniformly as rings of ~10 nm in diameter, each with an electron-dense center that may represent a completely open hole—as in a doughnut shape—or perhaps the hollow chamber of a bowl-shaped molecule (Fig. 5A). Frequently, these rings were closely juxtaposed, even sometimes appearing to be linked. The protein was found in the same ring conformation regardless of the presence of nucleotides, confirming that nucleotide binding is not needed for hexamerization (Fig. 5B and C). Although changes in individual protein molecules were not discernible, the DotB sample containing ATPγS appeared to contain an increased number of linked rings (data not shown), reminiscent of tube-like structures observed for R388 TrwD (15). A preparation of purified DotB K162Q was also subjected to analysis, with the prediction that its loss of ability to hydrolyze nucleotides might be related to an altered conformation. However the mutant protein, like the wild type, appeared as ~10-nm rings and was not affected by the presence of nucleotides (Fig. 5D and data not shown).

**DotB is a hexameric ring.** The discovery that several type IVA ATPases exist as homohexameric rings has inspired a model of function wherein the central chamber is the site of potential chaperone activity that is required for translocation and assembly of secretion complex components (14–16, 40).
this possibility, the capacity of the DotB K162Q mutant protein to multimerize with wild-type DotB was assayed by using a strain containing two different versions of epitope-tagged DotB. Wild-type DotB with an N-terminal Flag tag was expressed from the L. pneumophila chromosome, while DotB K162Q with an N-terminal His tag was expressed from a plasmid. Both fusion proteins were confirmed to be functional by intracellular growth assays (data not shown). Cell lysates of strains containing Flag-DotB and empty vector, Flag-DotB and the His-DotB complementing clone, or Flag-DotB and the His-DotB K162Q clone were made and passed over Ni-NTA–agarose. As expected, Flag-DotB in the absence of His-DotB did not bind to the Ni²⁺ matrix and was present in the flowthrough fraction rather than the elution fraction (Fig. 6, compare lanes 2 and 3). However, when Flag-DotB was in the presence of His-DotB, it appeared in the Ni-NTA-agarose elution fraction (Fig. 6, compare lanes 5 and 6), indicating an interaction between Flag- and His-tagged wild-type DotB. Moreover, the same result was obtained when Flag-DotB was in the presence of His-DotB K162Q (Fig. 6, compare lanes 8 and 9). The elution fraction containing Flag-DotB and His-

FIG. 4. DotB is a hexamer. (A) Superose 12 elution profile for purified wild-type DotB. Milli-absorbance units (mAU) are shown as a function of elution volume. DotB eluted as a single peak corresponding to a molecular mass of 259 kDa. Arrows show elution peaks for standards of known molecular masses (Amersham Biosciences): 1, thyroglobulin (669 kDa); 2, ferritin (440 kDa); 3, catalase (232 kDa); 4, aldolase (158 kDa); 5, BSA (67 kDa). (B) Coomassie-stained SDS-PAGE gel demonstrating that the quantities of DotB in elution fractions (Fxn) 7 to 15 correlate with the single protein elution peak. The elution profile is representative of three experiments and is identical to that for DotB K162Q (data not shown).

FIG. 5. Purified DotB and DotB K162Q proteins form hexameric rings ~10 nm in diameter. (A to C) Wild-type DotB was visualized in the absence of added nucleotides (A), revealing the putative apo form, as well as in the presence of 1 mM ADP (B) or 1 mM ATP-S (C). (D) DotB K162Q was also visualized in the putative apoprotein (shown here) and nucleotide-bound (not shown) forms. Scale bar, 50 nm. Images are representative of several thousand molecules visualized for each condition.
DotB K162Q was further subjected to gel filtration and Western blot analysis to confirm the presence of both proteins in hexameric multimers (data not shown). Thus, the Walker box mutant protein DotB K162Q can interact with wild-type DotB to form mixed hexamers.

**DotB K162Q shows enhanced membrane localization specific to *L. pneumophila***. Though the DotB protein lacks any obvious hydrophobic regions and therefore does not appear to have membrane-spanning domains, there is a detectable amount of DotB in *L. pneumophila* membrane fractions (Fig. 7A, lane 5). This is consistent with observations of numerous secretion ATPases from type II and type IV systems, which partition to various degrees to the cytoplasmic and membrane fractions (10, 25, 27, 29, 30). Interestingly, a Walker A box mutant version of the *A. tumefaciens* VirB11 protein, VirB11 K175A, displays significantly enhanced membrane association relative to wild-type VirB11 (25). To examine the possibility that DotB K162Q might exhibit an altered localization profile, we prepared cell fractions from the *L. pneumophila* ΔdotB strain JV918 containing either empty vector, the wild-type DotB complementing clone, or the DotB K162Q clone and compared them by Western blotting to determine DotB and DotB K162Q localization.

It appeared that a significant portion of the Walker box mutant protein was associated with *L. pneumophila* membranes. While soluble protein fractions (whole-cell lysate) contained less total DotB K162Q than wild-type DotB (Fig. 7A, lane 3 versus 2), indicating a relative lack of DotB K162Q stability, fractions comprised of only membrane proteins contained more DotB K162Q than wild-type DotB (Fig. 7A, lane 6 versus 5). Analysis of serially diluted cell fractions allowed an estimation that, while approximately 5% of wild-type DotB was membrane associated, 40% of the Walker box mutant protein DotB K162Q was present in the membrane fraction (data not shown). Importantly, when this same experiment was repeated using *E. coli* as a host strain, equivalent amounts of DotB and DotB K162Q were localized to the membrane fractions (Fig. 7B, compare lanes 3 and 4). Thus, the enhanced membrane localization of the DotB K162Q protein is a *Legionella*-specific phenomenon and may indicate the presence of a specific receptor for DotB in the *L. pneumophila* inner membrane.

**DotB K162Q cannot bind nucleotides**. In search of an explanation for the enhanced membrane affinity of DotB K162Q, we wondered whether its association with the membrane might be affected by its capacity to bind nucleotides. To examine this ability, we took two approaches, exposing either purified protein or *L. pneumophila* whole-cell lysate to ATP- or AMP-agarose beads (Sigma). The beads were washed, and the eluate was analyzed via Coomassie-stained protein gels (Fig. 8A) or DotB Western blotting (Fig. 8B and C). Purified wild-type protein was present in the ATP-agarose eluate and was not
present in eluate from AMP-agarose, to which it should not bind, or in eluate from ATP-agarose with competing free ATP (Fig. 8A, compare lanes 1, 2, and 3). Likewise, DotB from L. pneumophila lysate displayed the same pattern in the analogous elution fractions (Fig. 8B, compare lanes 3, 5, and 7). In contrast, DotB K162Q was not present in either ATP-agarose elution fraction (Fig. 8A, lane 4, and C, lane 3), indicating that it could not bind ATP either as a purified protein or when present in L. pneumophila lysate. Thus, DotB K162Q cannot bind ATP, a property which may help to explain its enhanced membrane affinity.

DISCUSSION

We have purified the L. pneumophila DotB protein, shown that it forms homohexameric rings, and demonstrated for the first time that it exhibits ATPase activity. Moreover, ATPase activity is critical to DotB function, since a Walker A box mutant protein (DotB K162Q) that is deficient in ATP binding and hydrolysis cannot complement a ΔdotB strain for intracellular growth. We have also observed that the dotB K162Q mutation is dominant negative, likely due to the capacity of the mutant protein to form mixed multimers with wild-type DotB. Finally, we have demonstrated that the DotB K162Q protein has enhanced membrane localization in L. pneumophila but not in E. coli, suggesting the existence of a DotB-specific inner membrane receptor.

The ATPase activity measured for DotB is equivalent to that seen for several other secretion ATPases. R64 PilQ, Ag uzex aeolicus PilT, R388 TrwD, and Actinobacillus actinomycetemcomitans TadA have similarly modest activities of between 1 and 15 nmol/min/mg (3, 10, 27, 29). Because this level of activity appears to be inconsistent with the idea that type II and type IV secretion ATPases are molecular motors, it has been proposed that they may function as chaperones facilitating the assembly or disassembly of secretion complexes and pil (10). Alternatively, modest activity could be due to the absence of stimulatory cofactors in ATPase reactions. For example, the addition of phospholipids to purified H. pylori HP0525, RP4 TrbB, TrwD, and TadA increased their enzymatic activity 2- to 10-fold (3, 15, 27), suggesting that interactions with the cytoplasmic membrane may regulate their function.

To confirm the importance of DotB ATPase activity, we constructed a mutant version of the protein which was enzymatically null and tested it for functionality in the context of L. pneumophila intracellular growth. Similar to a strain lacking DotB, a strain containing the DotB K162Q Walker A box mutant protein in place of the wild-type protein was completely defective for growth inside macrophages. Thus, DotB ATPase activity appears to be absolutely essential to its function in the Dot/Icm complex. Additionally, we observed that the DotB K162Q protein inhibited the intracellular growth of a wild-type L. pneumophila strain; this is the first description of a dominant negative mutation in Legionella. The DotB K162Q protein should prove to be a useful tool; potential applications include selective inactivation of the Dot/Icm complex at various stages of infection and inactivation of the DotB homologue in C. burnetti. The latter would be especially useful because genetic disruptions are not yet feasible in this system (33, 41, 42).

Other examples of secretion ATPase Walker A box mutations that are dominant negative in character include pilQ K238Q and trwDK203Q (27, 29). In these cases, it was proposed that dominance resulted from the formation of wild-type and mutant mixed multimers; however, this remained untested. Here we have successfully demonstrated that DotB K162Q is capable of forming mixed multimers with wild-type DotB in vivo, and this likely explains the dominant negative phenotype of the dotB K162Q mutation. Consistent with this idea, a model derived from several crystal structures of the H. pylori type IVA secretion ATPase HP0525 proposes that the ATPase cycles between at least three conformations via concerted changes that are likely to depend on the functionality of all six subunits (31, 40). Thus, inactivation of even one subunit may be sufficient to render the entire complex nonfunctional, so that mixed multimers of functional and nonfunctional monomers would exhibit a null phenotype.

In addition to its nonfunctional and dominant negative properties, the DotB K162Q mutant protein exhibited enhanced membrane localization. Such augmented membrane localization was likewise observed for the A. tumefaciens Walker box VirB11 K175A mutant protein (25). Though the membrane association of VirB11 does not require other VirB proteins (25, 35), several type II secretion ATPases have been shown to localize to the bacterial membrane only in the presence of specific components of their respective secretion complexes (1, 24, 30). Because the DotB K162Q mutant protein displays enhanced membrane localization only in the context of L. pneumophila and not in E. coli, this suggests that there may be an inner membrane receptor for DotB, perhaps another Dot/Icm protein. Further characterization of DotB K162Q should help to confirm the existence of such a receptor.

It is not clear what dictates the increased membrane localization of the DotB and VirB11 Walker A box mutant proteins. One possibility is that these proteins are locked in an altered conformation that is more conducive to membrane association. Experiments with PilQ have shown that it, like HP0525, changes conformation upon ATP binding. Interestingly, when a Walker A box mutant version of PilQ was examined, it was found to exist only in what appeared to be the ATP-bound conformation (29). To check DotB K162Q for an altered conformation, high-resolution electron microscopy comparing purified wild-type and mutant proteins was performed. We could not detect gross conformational differences between them, either in the presence or absence of nucleotides. Furthermore, limited proteolysis failed to reveal any differences (data not shown). In both cases, such changes may be too subtle to detect. Regardless, it is clear that the mutant protein differs from wild-type DotB in that it is no longer able to bind and hydrolyze nucleotides.

Our work is in accordance with a model where secretion ATPases cycle between cytoplasmic and membrane-linked states by associating and disassociating with secretion complexes at the inner membrane. While at the membrane, secretion ATPases may function as gating molecules, cycling through closed and open forms regulated by ATP binding and hydrolysis. For DotB K162Q, its inability to bind and hydrolyze nucleotides is likely to abolish this mode of action, leaving it trapped in an intermediate step of normal DotB cycling at the L. pneumophila membrane.

In this study, we have demonstrated that the L. pneumophila
DotB protein has several characteristics in common with assembly ATPases of type II and type IVA secretion systems and with the retraction ATPase PilT: specifically, DotB is a hydrophilic, membrane-associated ATPase that exists as a hexameric ring, the enzymatic activity of which is critical to its function. The significance of the intriguing homology between DotB and the pilus retraction protein PilT remains to be determined, and a potential role for DotB in pilus retraction awaits identification of a putative Dot/Icm pilus. We have also demonstrated here, based on observations of the mutant protein DotB K162Q, that DotB hexamers likely need to hydrolyze ATP in a concerted or rapidly successive fashion in order to function effectively. These data will serve as the foundation for further analysis of the DotB protein and should lead to a better understanding of its function on molecular and macromolecular levels.

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