Chaperone-subunit-usher interactions required for donor strand exchange during bacterial pilus assembly

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Chaperone-Subunit-Usher Interactions Required for Donor Strand Exchange during Bacterial Pilus Assembly

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The assembly of type 1 pili on the surface of uropathogenic Escherichia coli proceeds via the chaperone-usher pathway. Chaperone-subunit complexes interact with one another via a process termed donor strand complementation whereby the G1β strand of the chaperone completes the immunoglobulin (Ig) fold of the pilus subunit. Chaperone-subunit complexes are targeted to the usher, which forms a channel across the outer membrane through which pilus subunits are translocated and assembled into pili via a mechanism known as donor strand exchange. This is a mechanism whereby chaperone uncapping from a subunit is coupled with the simultaneous assembly of the subunit into the pilus fiber. Thus, in the pilus fiber, the N-terminal extension of every subunit completes the Ig fold of its neighboring subunit by occupying the same site previously occupied by the chaperone. Here, we investigated details of the donor strand exchange assembly mechanism. We discovered that the information necessary for targeting the FimC-FimH complex to the usher resides mainly in the FimH protein. This interaction is an initiating event in pilus biogenesis. We discovered that the ability of an incoming subunit (in a chaperone-subunit complex) to participate in donor strand exchange with the growing pilus depended on a previously unrecognized function of the chaperone. Furthermore, the donor strand exchange assembly mechanism between subunits was found to be necessary for subunit translocation across the outer membrane usher.

Type 1 pili are assembled via the highly conserved chaperone-usher pathway, which directs the synthesis of over 30 different adhesive organelles expressed by a multitude of pathogenic bacteria (20, 45). Two prototypical members of the chaperone-usher pathway are type 1 and P pili, which are produced by uropathogenic Escherichia coli. Both of these adhesive organelles are important in mediating attachment to epithelial cells during urinary tract infections. Type 1 pili bind to mannosylated residues present on the bladder epithelium via the FimH adhesin (18) and are therefore critical for the establishment of cystitis (9, 25, 28, 33, 51). P pili mediate epithelial binding to Galα(1-4)Gal disaccharides present on the kidney epithelium via the PapG adhesin and are important for the development of pyelonephritis (5, 11, 26, 29, 36, 47, 52). Genes important for type 1 pilus production are encoded by the fim gene cluster (fimA to fimH) (35, 49), while genes important for P pili are encoded by the pap gene cluster (papA to papG) (15, 37). Both of these pili are heteropolymeric structures composed of rigid pilus rods joined to thinner and more flexible tip fibrillae with the tip fibrillum of type 1 pili being short and stubby in comparison to that of P pili (22, 26). The type 1 pilus rod is comprised of repeating monomers of FimA arranged in a right-handed helical cylinder, and the tip fibrillum is composed of FimF, FimG, and the adhesin FimH (6, 22).

Both the chaperone and the usher, FimC and FimD in the type 1 pilus system, are absolutely required for pilus biogenesis to occur, as mutations in both genes result in nonpiliated bacteria (24, 30). Mutations in fimC result in the degradation of pilus subunits in the periplasm (21, 30), and mutations in fimD result in the accumulation of chaperone-subunit complexes in the periplasm (24, 34). The chaperone interacts with pilus subunits in a mechanism called donor strand complementation, which facilitates subunit folding on the chaperone template (8, 38). Pilus subunits are incomplete immunoglobulin (Ig) folds, resulting in a groove or scar present in the subunit exposing its hydrophobic core. In complex with the chaperone, the Ig fold of the pilus subunit is completed by the G1β strand of the chaperone, which is inserted into the groove and protects the hydrophobic core of the subunit. The chaperone completes the Ig fold of the subunit in an atypical fashion by inserting its G1β strand parallel to the F strand of the subunit. The folded subunit remains bound to the chaperone so that the folding reaction is simultaneously coupled with the capping of the interactive groove of the subunit (7, 27, 44), stabilizing the subunit in an assembly-competent conformation.

During type 1 pilus assembly, chaperone-subunit complexes are targeted to the usher FimD, which forms a pore in the outer membrane allowing the translocation of pilus subunits to the cell surface (24, 42, 50). Pilus subunits are targeted to the usher in a specific order reflecting their final order in the pilus (10, 42). The chaperone-adhesin complex binds first, most tightly, and fastest to the usher, suggesting that adhesins initiate pilus assembly (10, 41, 42). In support of this hypothesis, clinical isolates lacking a functional fimH gene did not produce type 1 pili (9, 28). Furthermore, the binding of FimC-FimH to FimD induces a conformational change in FimD, presumably into an assembly-competent state (42). At the usher, pilus assembly is thought to occur by a reaction termed donor strand exchange (3, 8, 38). Donor strand exchange predicts that the N-terminal extension of one subunit will displace the G1β strand of the chaperone from its neighboring subunit and in-
sert itself antiparallel to the F strand of the subunit to complete a canonical Ig fold. Thus, the pilus would consist of perfectly canonical Ig domains, each of which contributes a strand to the fold of its neighboring subunit. In support of the donor strand exchange hypothesis, fusion of the N-terminal extension of FimG onto the C terminus of FimH created donor strand-complemented FimH (dscFimH), which was stable in the periplasm in the absence of FimC and folded on its own (3). In contrast, FimH required FimC for proper folding and stability in the periplasm (3). In addition, we have recently co-crystallized and solved the structure of the N-terminal extension of PapK bound to the PapE pilin (40). The structure revealed that the N-terminal extension completes the Ig fold of the pilin in a canonical fashion, thus proving the donor strand exchange hypothesis. Thus, pilus subunits do not contain all of the information necessary for folding, and this missing information is supplied by the chaperone during donor strand complementation and by the N-terminal extension of neighboring subunits in the pilus fiber. The chaperone primes the subunit for assembly by holding the groove in an open, activated conformation. During donor strand exchange, the subunit undergoes a topological transition that triggers the closure of the groove and seals the N-terminal extension in place. It is this topological transition, made possible only by the priming action of the chaperone, which drives subunit assembly into the fiber (40).

Here, we elucidated factors governing donor strand exchange, assembly, and translocation across the outer membrane usher. We also demonstrated that the information required for targeting the FimC-FimH complex to the usher was contained primarily within the FimH protein and did not require the FimC chaperone. FimH is the first protein to be incorporated into the pilus, and its interaction with the usher initiates pilus assembly (10, 41, 42). The incorporation of subsequent subunits into the pilus and their translocation across the usher depend on a previously unrecognized function of the chaperone necessary to facilitate the donor strand exchange process.

**MATERIALS AND METHODS**

**Genetic constructs.** To create pTc-FimGH, FimG was PCR amplified from pETSA2 (42) by using the two oligonucleotides FimGH top and bottom. PCR products were cloned into the ClaI and BamHI sites of pTc-dscFimH (3). pETSA2 was cleaved from pTc-FimGH. FimGH was subcloned from pTc-FimGH into pMMB91 by using the EcoRI and BamHI sites to create pMMB-FimG. pMMB-FimG was then subcloned from pTc-FimGH into pBad-FimGH with the SpI and NheI sites into the SpI and XbeI sites of pBad18-Kn (13). FimG was PCR amplified from pETSA2 by using the two oligonucleotides FimGH top and bottom. PCR products were cloned into the EcoRI site of pUC-dscFimH (D. L. Hung and S. J. Hultgren, unpublished data) with the KpnI, XhoI, and NotI sites into the KpnI, XhoI, and NotI sites of pBad-dscFimH (3). 

**In vitro subunit-subunit binding assays.** FimC-FimH complexes were purified from the strain C600/pETSA100/pETSA2 as described previously (42), and samples were analyzed by sodium dodecyl sulfate (SDS)-polyacrylamide gel electrophoresis followed by Western blotting with anti-FimC antiseraum (MedImmune, Inc.). FimC-FimH antibodies are polyclonal and were used at 1:2000 dilution. 

**TABLE 1. List of plasmids used in this work**

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**Periplasmic preparations.** Bacterial strains were grown to an optical density at 600 nm of 0.8 and induced with 0.1% arabinose and 0.05 mM IPTG (isopropyl-β-D-thiogalactopyranoside) for 1 h. Periplasms were prepared as described previously (43), and samples were analyzed by sodium dodecyl sulfate (SDS)-polyacrylamide gel electrophoresis followed by Western blotting with anti-FimC antiseraum (MedImmune, Inc.). FimC-FimH antibodies are polyclonal and were used at 1:2000 dilution. 

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independent experiments. Results are representative of three flooded with 0.1 mM IPTG for 48 h. The cells were harvested, and hemagglutination assays were generated against peptides.

clonal and were generated against native protein. FimF and FimG antibodies staining with Coomassie blue or Western blotting with anti-FimCH (MedIm-

Samples were analyzed by SDS-polyacrylamide gel electrophoresis followed by using the same buffer containing 30 to 100 mM EDTA instead of imidazole. Nickel-nitrilotriacetic acid beads (Qiagen) were added to the outer membranes and rocked overnight at 4°C (48, 50). FimC and the appropriate subunit(s) with FimDHis (41, 42). Bacterial strains were grown to an optical density at 600 nm of 0.8 and induced with 0.1 mM IPTG and 0.1% arabinose for 1 h. The cells were harvested, and outer membranes were prepared as described previously (48, 50). Nickel-nitritriacetic acid beads (Qiagen) were added to the outer membranes and rocked overnight at 4°C. The beads were washed several times in buffer containing 0.3 M NaCl, 20 mM HEPES (pH 7.4), and 0.1% dodecyl maltoside with 10 to 20 mM imidazole. Protein was eluted from the beads by in buffer containing 0.3 M NaCl, 20 mM HEPES (pH 7.4), and 0.1% dodecyl maltoside with 10 to 20 mM imidazole. Protein was eluted from the beads by

C. The beads were washed several times with FimDHis (Fig. 2B and D, lanes 5). These results demonstrated that both the FimHp and FimHr domains of FimH were individually cloned (Fig. 1), and the ability of these two proteins to bind to FimD was assessed. Both FimHr and FimHp were tagged with HA for detection by Western blotting. FimHr was stable in the periplasm, and FimHr required FimC for stability in the periplasm as expected (data not shown). Both FimHr and FimHp copurified with FimDHis (Fig. 2B and D, lanes 3 and 4) as did FimC-FimH complexes (Fig. 2B and C, lanes 2). Surprisingly, no detectable FimC copurified with FimHr-FimD complexes (Fig. 2C and D, lanes 4). FimC stabilizes subunits via donor strand complementation and accordingly is required for FimHr stability. It is unclear why or when FimC dissociates during the purification process. Nevertheless, FimHr clearly binds to FimD, indicating that FimHr has information necessary for FimD binding. As a control an unrelated HA-tagged periplasmic protein, CsgE, was coexpressed with FimDHis. Although CsgE is stably expressed in the periplasm, it did not copurify with FimDHis (Fig. 2B and D, lanes 5). These results demonstrate that both the FimHr and FimHp domains contain surfaces that bind to FimD. Since FimH is L shaped (8), we propose that FimHR is inserted into the usher pore while the FimHP domains would then straddle the periplasmic surface of FimD (Fig. 5). Presumably, the groove occupied by the chaperone is oriented toward the periplasm in order to facilitate a donor strand exchange reaction with an incoming FimC-FimG complex.

FIG. 1. Schematic diagram of some of the constructs used in this work. FimHR is the FimH receptor binding domain with an HA tag at its C terminus. FimHp is the FimH pilin domain with an HA tag at its N terminus. dscFimH has the first 13 amino acids of FimG fused onto its C terminus with a 4-amino-acid linker sequence, DNKQ, preceding the FimG sequence (FimG amino terminus, DVSTITINGYVRDN). Abbreviations: RBD, receptor binding domain; PD, pilin domain; GN, FimG N-terminal extension; FN, FimF N-terminal extension.

Outer membrane preparation and usher copurification. Usher copurification experiments were performed by expressing FimC and the appropriate subunit(s) with FimDHis (41, 42). Bacterial strains were grown to an optical density at 600 nm of 0.8 and induced with 0.1 mM IPTG and 0.1% arabinose for 1 h. The cells were harvested, and outer membranes were prepared as described previously (48, 50). Nickel-nitritriacetic acid beads (Qiagen) were added to the outer membranes and rocked overnight at 4°C. The beads were washed several times in buffer containing 0.3 M NaCl, 20 mM HEPES (pH 7.4), and 0.1% dodecyl maltoside with 10 to 20 mM imidazole. Protein was eluted from the beads by using the same buffer containing 30 to 100 mM EDTA instead of imidazole. Samples were analyzed by SDS-polyacrylamide gel electrophoresis followed by staining with Coomassie blue or Western blotting with anti-FimCH (MedImmune, Inc.), anti-FimD (MedImmune, Inc.), anti-FimF (Soman Abraham), anti-FimG (1), and/or anti-HA (Convance) antiserum. FimD antibodies are polyclonal and were generated against native protein. FimF and FimG antibodies were generated against peptides.

Hemagglutination assays. The strain Orn103pUT3002 (32) was transformed with pTrc99A, pTrc-FimH, or pTrc-FimGH and grown statically in the presence of 0.1 mM IPTG for 48 h. The cells were harvested, and hemagglutination assays were performed as described previously (16). Results are representative of three independent experiments.

RESULTS

FimH has sufficient information for FimD binding. The ability of dsc pilus subunits to bind to the usher was measured to test the requirement of the chaperone in usher binding. dsc subunits have the amino-terminal extension of their respective neighboring subunit fused to their C terminus (Fig. 1). The presence of this added β strand completes the Ig fold of the subunit and alleviates the requirement of the chaperone for folding and stability in the periplasm (3). The FimH adhesin is the first subunit incorporated into the pilus, and FimC-FimH complexes bind first, most tightly, and fastest to FimD (42). The PapG adhesin of the P pilus system also binds first to its cognate usher protein (10). Since pilus adhesins bind first to the usher, we hypothesized that the primary information necessary for usher binding resides in the adhesin protein itself. To test this hypothesis, the ability of dscFimH (Fig. 1) to bind to FimD was determined. dscFimH, FimH, or FimC-FimH was coexpressed with FimDHis and outer membrane extracts were subjected to nickel chromatography. FimDHis expressed by itself and purified by nickel chromatography is shown in Fig. 2A, lane 1. The lower-molecular-weight bands represent FimD degradation products. FimH expressed in the absence of FimC did not copurify with FimD (Fig. 2A, lane 2) because FimH is unstable in the absence of FimC. dscFimH copurified with FimD (Fig. 2A, lane 4), as did FimC-FimH complexes (42) (Fig. 2A, lane 3). These results suggest that FimC is not required for FimH binding to FimD and that folded FimH has sufficient information necessary for FimD binding.

Pilus adhesins are distinct from other pilus subunits because they contain an extra domain, an N-terminal receptor binding domain that is linked to the pilin domain. We hypothesized that the FimH receptor binding domain is the portion of FimH that allows it to bind to FimD first because the pilin domain must remain accessible, and exposed in the periplasm, in order to participate in donor strand exchange with the subsequent incoming subunit (FimG). The receptor binding (FimHR) and pilin (FimHP) domains of FimH were individually cloned (Fig. 1), and the ability of these two proteins to bind to FimD was assessed. Both FimHR and FimHp were tagged with HA for detection by Western blotting. FimHR was stable in the periplasm, and FimHR required FimC for stability in the periplasm as expected (data not shown). Both FimHR and FimHp copurified with FimDHis (Fig. 2B and D, lanes 3 and 4) as did FimC-FimH complexes (Fig. 2B and C, lanes 2). Surprisingly, no detectable FimC copurified with FimHR-FimD complexes (Fig. 2C and D, lanes 4). FimC stabilizes subunits via donor strand complementation and accordingly is required for FimHP stability. It is unclear why or when FimC dissociates during the purification process. Nevertheless, FimHp clearly binds to FimD, indicating that FimHp has information necessary for FimD binding. As a control an unrelated HA-tagged periplasmic protein, CsgE, was coexpressed with FimDHis. Although CsgE is stably expressed in the periplasm, it did not copurify with FimDHis (Fig. 2B and D, lanes 5). These results demonstrate that both the FimHR and FimHP domains contain surfaces that bind to FimD. Since FimH is L shaped (8), we propose that FimHR is inserted into the usher pore while the FimHP domain would then straddle the periplasmic surface of FimD (Fig. 5). Presumably, the groove occupied by the chaperone is oriented toward the periplasm in order to facilitate a donor strand exchange reaction with an incoming FimC-FimG complex.

The chaperone is required for donor strand exchange. Next, we wanted to analyze the ability of a dsc subunit to be incorporated into a growing pilus to determine if the chaperone is required during the donor strand exchange reaction. dscFimH was not used in these studies because after it binds to the usher pilus assembly is terminated, since its interactive groove is already filled with the added donor strand (3). Thus, dscFimG was constructed to test the role of the chaperone during donor
The in vitro reconstitution experiments described above prove that dscFimG interacts with FimH. Thus, we next investigated the ability of dscFimG to be incorporated into the growing pilus. Previously, it was shown that assembly intermediates can be purified in a complex with FimDHis, by nickel chromatography. Thus, coexpression of FimC, FimG, and FimH with FimDHis resulted in the formation of a FimC-FimG-FimH-FimDHis complex that can be purified by nickel chromatography (41) (Fig. 3B to D, lanes 2). The ability of dscFimG to dissociate FimC from the FimC-FimH-FimD complex and form a dscFimG-FimH-FimD complex was analyzed to determine if a subunit, in the absence of the chaperone, could allow donor strand exchange to occur. dscFimG did not carry out donor strand exchange with the FibFH-Fim-D ternary complex, and thus, a dscFimG-FimH-FimD complex was not formed (Fig. 3B to D, lanes 3). These results argue that the chaperone, in an incoming chaperone-subunit complex, plays a critical role in the donor strand exchange reaction.

Type 1 pilus assembly can be monitored by hemagglutination. FimG-FimH tip fibrillae assemble on the bacterial surface when coexpressed with FimD and FimC, resulting in HA-positive cells (Fig. 3D) (41). However, replacing FimG with dscFimG resulted in HA-negative bacteria (Fig. 3D), confirming the copurification experiments showing that dscFimG is not incorporated into the growing pili and supporting the conclusion that the chaperone is needed for donor strand exchange to occur.

**Genetically linked FimGH does not produce functional pili.**

Other bacterial adhesins, such as invasin of *Yersinia pseudotuberculosis* (14) and intimin of enteropathogenic *E. coli* (4, 23, 31), are single proteins composed of multiple Ig domains, with a specialized adhesive domain at their end. This is similar to the pilus, which is also comprised of multiple Ig domains, with an adhesin at its tip. However, in the pilus, each Ig domain is a separate protein with an incomplete Ig fold that is completed by its neighboring subunit (40). A FimG-FimH fusion protein (FimGH) (Fig. 1) was constructed to investigate the role of individual subunits in comprising a pilus. The *fimH* gene was fused onto the 3' end of *fimH*, so that the N-terminal extension of FimG should complete the Ig fold of the FimH pilin domain in the fusion protein. However, the FimG pilin would still require FimC for stability. The production of FimGH in the periplasm in the absence and presence of FimC was monitored. FimGH was stable in the periplasm only when FimC was
coexpressed (Fig. 4A, lanes 3 and 4). Additionally, FimGH bound to mannose and formed a complex with FimC, indicating that it was properly folded (data not shown).

Next, FimGH binding to FimD was assessed to determine if FimGH was targeted for pilus assembly. FimC-FimGH complexes copurified with FimDHis by nickel chromatography (Fig. 4B and C, lanes 1), indicating that FimGH was appropriately targeted to FimD for pilus assembly. Hemagglutination assays were performed to determine if FimGH is incorporated into the pilus. For strains Orn103/pUT2002/pTrc99A, Orn103/pUT2002/pTrc-FimH, and Orn103/pUT2002/pTrc-FimGH, the HA titers were 0, 32, and 0, respectively. Plasmid pUT2002 encodes a fimH mutant type 1 gene cluster, and strain Orn103 does not produce type 1 pili. Thus, the coexpression of FimGH with a fimH mutant type 1 gene cluster resulted in HA-negative bacteria, while coexpression of FimH restored the HA titer. We wanted to determine why FimGH did not produce functional pili. After FimC-FimGH binds to FimD, the next step in the biogenesis pathway is the binding of the next chaperone-subunit complex to the FimC-FimGH-FimD complex, which would be either FimC-FimF or FimC-FimG. Thus, the ability of either FimG or FimF to copurify with FimC-FimGH-FimD complexes was assayed. Both FimG and FimF copurified with FimC-FimGH-FimDHis complexes (Fig. 4B to E, lanes 2 and 3), indicating that FimGH formed appropriate interactions with other pilus subunits. Even though FimGH was properly targeted for pilus assembly and interacted with other pilus subunits (Fig. 4), functional type 1 pili were not produced when FimGH was coexpressed with a fimH mutant type 1 gene cluster (above). Thus, we conclude that the donor strand exchange reaction between individual subunits provides the fiber with the necessary steric properties to be translocated through the usher. The FimGH fusion, while properly folded and capable of targeting to the usher and participating in donor strand exchange with incoming FimC-FimG and/or FimC-FimF complexes, may be unable to be translocated across the usher. An alternative hypothesis is that FimGH is translocated across the usher but the FimGH fusion protein in the pilus is unable to bind mannose. We favor the first hypothesis because FimH in the FimGH fusion protein is capable of binding mannose. When coexpressed with FimC, the FimGH fusion protein can be purified from the periplasm by using mannose Sepharose beads (data not shown).

**DISCUSSION**

Pilus assembly is thought to occur via a donor strand exchange reaction at the usher, where the G1β strand of the chaperone, occupying the groove of a subunit, is exchanged for the N-terminal extension of an incoming and neighboring subunit (8, 38, 40). During type 1 pilus biogenesis, FimH is the first
protein to be incorporated into the growing pilus (10, 42). The absence of FimH results in a severe assembly defect, suggesting that the FimH-FimD interaction plays a critical role in initiating pilus assembly (9, 28). The next event in the biogenesis cascade is the targeting of the FimC-FimG complex to the FimC-FimH-FimD ternary complex where donor strand exchange occurs. This results in the dissociation of the G1β strand of FimC from FimH in the FimC-FimH-FimD complex and the replacement of this strand by the N-terminal extension of FimG (3, 8, 38, 41). We used the type 1 pilus assembly system as a model to investigate the mechanistic details and structural requirements of donor strand exchange.

The role of the adhesin in initiating pilus assembly suggests that it contains structural properties distinct from those of the other subunits. The FimC-FimH complex is in fact the only chaperone-subunit complex to bind strongly to the usher (42). We hypothesized that the unique information must therefore reside in the FimH protein itself. Thus, we used dscFimH to test this hypothesis. dscFimH does not require FimC for folding, since it contains its naturally missing β strand (as a C-terminal fusion) that is otherwise transiently provided by FimC during folding and the N-terminal extension of FimG during pilus assembly (3). We discovered that dscFimH was able to target to FimD and form a stable complex (Fig. 2A). We interpreted this result as indicating that FimH has sufficient information necessary for FimD binding. Structurally, the only difference between FimH and other pilus subunits is the presence of an additional domain, the N-terminal receptor binding domain, suggesting that this is the domain that interacts with FimD. However, we went on to show that both the receptor binding and pilin domains of FimH bound to FimD (Fig. 2B to D). Interestingly, other pilus subunits, like FimG or FimF, do not bind well to FimD (41, 42), suggesting that the pilin domain of FimH has unique properties enabling it to interact

![FIG. 4. FimGH is stable in the periplasm and is targeted for pilus assembly. (A) Western blot of periplasms prepared from strains C600/pMMB-FimH (FimH) (lane 1), C600/pHJ9205/pMMB-FimH (FimC + FimH) (lane 2), C600/pMMB-FimGH (FimGH) (lane 3), and C600/pHJ9205/pMMB-FimGH (FimC + FimGH) (lane 4). The Western blot was developed with anti-FimCH antiserum. (B to E) Coomassie blue-stained SDS-polyacrylamide gel (B), Western blot developed with anti-FimCH antiserum (C), Western blot developed with anti-FimG antiserum (D), or Western blot developed with anti-FimF antiserum (E) of outer membrane preparations after nickel chromatography from strains C600/pCD-Kn/pMB10/pTrc99A (FimC + FimDHis + FimGH) (lanes 1), C600/pCD-Kn/pMB10/pTrc-FimG (FimC + FimDHis + FimGH + FimG) (lanes 2), and C600/pCD-Kn/pMB10/pTrc-FimF (FimC + FimDHis + FimGH + FimF) (lanes 3).](http://jb.asm.org/)

![FIG. 5. Model of type 1 pilus assembly at the usher. The FimC-FimH complex binds to the FimD usher, inducing a conformation change in FimD (42), presumably into an assembly-competent state. We hypothesize that the FimH receptor binding domain (HR) is inserted into the FimD pore, allowing the FimH pilin domain (H9252) to be exposed on the periplasmic side of FimD to remain available for donor strand exchange with FimC-FimG complexes. dscFimG was not incorporated into the growing pilus, suggesting that the chaperone is required for appropriate targeting and assembly of subunits into the pilus. The black line on FimC represents the FimC G1β strand completing the Ig fold of either FimG or FimH. The yellow line of dscFimG represents the N-terminal extension of FimF completing the Ig fold of FimG.](http://jb.asm.org/)
with FimD. Since FimH is L shaped, we propose that the receptor binding domain is inserted into the channel of FimD, allowing the simultaneous docking of the pilin domain of FimH to the periplasmic surface of FimD (Fig. 5). The interactive groove of FimH occupied by the FimC chaperone is presumably exposed to the periplasm in order to properly orient it for participation in a donor strand exchange reaction with an incoming chaperone-subunit complex.

The efficient targeting of all subsequent chaperone-subunit complexes to the FimD usher (and their subsequent incorporation into the pilus) requires the presence of FimH to make the initiating interactions described above. Thus, FimC-FimH forms a ternary complex with FimD (41, 42), which is primed to participate in a donor strand exchange reaction with an incoming FimC-FimG complex. The N-terminal extension of FimG is exposed in the FimC-FimG complex. It is thus presumably free to exchange with the G1β strand of the chaperone to facilitate chaperone dissociation (38) and the assembly of FimG to the pilin domain of FimH. We investigated the requirement for the FimC chaperone in the FimC-FimG complex to carry out this reaction by examining the ability of dscFimG to be incorporated into the growing pilus. dscFimG was shown to have all of the information necessary to bind and assemble to FimH in an in vitro reconstitution assay (Fig. 3A). However, in vivo, dscFimG was not able to dissociate FimC from the FimC-FimH-FimD ternary complex and it was unable to form a dscFimG-FimH-FimD complex (Fig. 3B to D and Fig. 5). The best interpretation of this result is that the donor strand exchange reaction requires the presence of the chaperone bound to an incoming subunit. This is consistent with previous work demonstrating that the chaperone is required for pilus assembly at a step after chaperone-adhesin binding to the usher (19).

FimGH was created to investigate the requirement of individual subunits in comprising a growing pilus. FimGH was functional in every aspect of pilus assembly tested except for its ability to be translocated across the outer membrane usher. It bound to the FimD usher and participated in donor strand exchange assembly reactions with incoming FimC-FimG and FimC-FimF complexes (Fig. 4). Yet, it did not produce functional pilus when coexpressed with a fimH mutant type 1 gene cluster (see above). Instead, expression of FimGH blocked pilus assembly presumably by jamming the usher and preventing outward growth of the fiber. Thus, individual subunits assembled via donor strand exchange may provide the needed steric freedom to traverse the FimD pore.

The results presented here provide new insights into the assembly of pilus via the chaperone-usher pathway. We have demonstrated that the receptor binding domain of FimH probably makes the first interaction with FimD, presumably being inserted into the pore, allowing the FimH pilin domain (bound to the chaperone) to lock onto the periplasmic surface of FimD and become properly oriented for donor strand exchange with incoming FimC-FimG complexes (Fig. 5). With the exception of chaperone-adhesin complexes, all other chaperone-subunit complexes bind poorly or not at all to the usher (10, 42). However, when the usher has been primed by an interaction with FimH, proper targeting and assembly of all other chaperone-subunit complexes occurs. It is well established that the chaperone is critical for appropriate pilus assembly because it is required to facilitate subunit folding and to prevent nonproductive aggregation (3, 17, 21, 30, 39). However, here we have shown that the chaperone also plays a critical role at the usher during donor strand exchange. It is required to facilitate the necessary interactions at the usher site for pilus assembly to occur. The finding that the targeting and donor strand exchange reactions during pilus assembly depend on properties of the chaperone opens up new insights and paves the way for future studies investigating the mechanistic details of the donor strand exchange reaction at the outer membrane usher.

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References


