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Kurt H. Piepenbrink
University of Maryland at Baltimore

Erik Lillehoj
University of Maryland at Baltimore

Christian M. Harding
Washington University School of Medicine in St. Louis

Jason W. Labonte
The Johns Hopkins University

Xiaotong Zuo
The Johns Hopkins University

See next page for additional authors

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Recommended Citation
Piepenbrink, Kurt H.; Lillehoj, Erik; Harding, Christian M.; Labonte, Jason W.; Zuo, Xiaotong; Rapp, Chelsea A.; Munson, Robert S. Jr.; Goldblum, Simeon E.; Feldman, Mario F.; Gray, Jeffrey J.; and Sundberg, Eric J., "Structural diversity in the type IV pili of multidrug-resistant Acinetobacter." The Journal of Biological Chemistry. 291,44. 22924-22935. (2016).
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Authors
Kurt H. Piepenbrink, Erik Lillehoj, Christian M. Harding, Jason W. Labonte, Xiaotong Zuo, Chelsea A. Rapp, Robert S. Munson Jr., Simeon E. Goldblum, Mario F. Feldman, Jeffrey J. Gray, and Eric J. Sundberg
Structural Diversity in the Type IV Pili of Multidrug-resistant Acinetobacter*

Kurt H. Piepenbrink†, Erik Lilleshøj§, Christian M. Harding*, Jason W. Labonte‡, Xiaotong Zuo∥, Chelsea A. Rapp∥∥, Robert S. Munson, Jr.∗∗, Simeon E. Goldblum†††‡‡‡, Mario F. Feldman*, Jeffrey J. Gray∥∥∥, and Eric J. Sundberg††††

Received for publication, August 1, 2016, and in revised form, September 7, 2016. Published, JBC Papers in Press, September 15, 2016, DOI 10.1074/jbc.M116.751099

Acinetobacter baumannii is a Gram-negative coccobacillus found primarily in hospital settings that has recently emerged as a source of hospital-acquired infections. A. baumannii expresses a variety of virulence factors, including type IV pili, bacterial extracellular appendages often essential for attachment to host cells. Here, we report the high resolution structures of the major pilin subunit, PilA, from three Acinetobacter strains, demonstrating that A. baumannii subsets produce morphologically distinct type IV pilin glycoproteins. We examine the consequences of this heterogeneity for protein folding and assembly as well as host-cell adhesion by Acinetobacter. Comparisons of genomic and structural data with pilins proteins from other species of soil gammaproteobacteria suggest that these structural differences stem from evolutionary pressure that has resulted in three distinct classes of type IVa pilins, each found in multiple species.

Type IV pili are extracellular adhesive appendages primarily comprising a single protein subunit, called the major pilin, which is assembled into a narrow (~6–9-nm) helical fiber of variable length (up to 2.5 μm) (1). One or more other proteins, called minor pilins, are also incorporated into the fiber at low levels. All pilins contain an N-terminal signal sequence followed by a soluble 15-kDa globular domain referred to as the pilin headgroup; the hydrophobic helical regions are buried together in the center of the fiber, whereas portions of the C-terminal headgroup are exposed (2, 3).

Type IV pili are found in both Gram-negative (4, 5) and Gram-positive (6–8) bacteria as well as Archea (9). They are involved in a wide range of processes, including twitching motility (10), horizontal gene transfer (11), host-cell adhesion (12), and microcolony/biofilm formation (13). This functional diversity is reflected in the sequence of the pilin proteins that typically have little or no sequence identity beyond the hydrophobic portion of the N-terminal α-helix. This lack of sequence identity is apparent even in cases where there is high structural similarity.

In contrast, within a given species, the minor pilins are typically well conserved. Only the major pilin is highly variable (14–16) and then only in those regions left exposed in the assembled pilus (17). This sequence diversity may result from diversifying selection as a mechanism by which to avoid detection by the host immune system (18). However, such diversity can also be found in species whose life cycle is primarily environmental (19). Glycosylation is an additional source of variability in some type IV pilins; O-linked glycosylation has been observed in multiple strains of both Pseudomonas aeruginosa (20–22) and Neisseria (23, 24). Additional glycosylation sites have been found in class II strains of Neisseria meningitidis where they have been hypothesized to play a role in immune evasion (25).

Among the many genera of Gram-negative bacteria that express type IV pili is Acinetobacter, a coccobacillus that is widely distributed in nature and can be isolated from the environment in the soil and in water as well as from a variety of mammalian hosts (26, 27). Several species of Acinetobacter, chiefly Acinetobacter baumannii, Acinetobacter calcoaceticus, Acinetobacter nosocomialis, and Acinetobacter pittii, are collectively referred to as the A. calcoaceticus-baumannii (Acb) complex and constitute an increasingly common source of nosocomial infections (28–30). Although reports of infections by A. baumannii predominate in the literature, phenotypic similarity makes it difficult to differentiate between related Acinetobacter calcoaceticus-baumannii complex and Acinetobacter nosocomialis, both of which have been hypothesized to play a role in immune evasion (25).
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Like other Acinetobacter species, A. baumannii lacks flagella but exhibits twitching motility, which is dependent on type IV pili (33). Type IV pili are also required for its natural transformation (33, 34), but their role in other biological processes is unclear. Virstatin, a known inhibitor of type IV pilus formation in Vibrio cholerae, was shown to both reduce type IV pilus expression and inhibit biofilm formation in A. baumannii (35). In another study, no correlation could be demonstrated between antigenic variation in the A. baumannii major pilin, pilA, and biofilm formation in vitro (36). More recently, Oh and Choi (37) reported that deletion of a LuxR-type regulator, AnoR, reduces both biofilm formation and surface motility in A. nosocomialis ATCC 17903. In addition to variation in the sequence of pilA, some Acinetobacter strains utilize an O-oligosaccharidyltransferase to specifically glycosylate the major pilin at a C-terminal serine with the major capsule polysaccharide repeat unit (38, 39). These post-translational modifications are independent of the more general protein O-glycosylation system common to many gamma proteobacteria (including P. aeruginosa and Dichelobacter nodosus) (40–43). However, Harding et al. (38) reported that pilin C-terminal glycosylation is not required for either competence or twitching motility.

To understand the basis for the variability in sequence and glycosylation of Acinetobacter PilA, we have resolved the x-ray crystal structures of the major type IV pilin from three members of the Acb complex, strains ACICU and BIDMC 57 of A. baumannii and strain M2 of A. nosocomialis. In these three structures, we observe structural divergence independent of species within Acinetobacter. We demonstrate that Acinetobacter type IV pili promote host-cell adhesion in a manner independent of C-terminal glycosylation. We also provide evidence that the structural variation of Acinetobacter pilins is underpinned by functional differentiation.

Experimental Procedures

Protein Expression and Purification—Codon-optimized sequences of PilA from A. baumannii ACICU and A. nosocomialis M2, starting with alanine 23, were cloned into a pETM44 vector with an N-terminal His6 tag. These clones were transformed into BL21 (DE3) pLysS cells and grown to saturation overnight with shaking at 37 °C in LB medium with 50 μg/ml ampicillin. These saturation cultures were then diluted into LB-ampicillin and grown to an optical density (OD) of 0.4–0.6 at 37 °C. These flask cultures were transferred to a refrigerated orbital shaker and cooled to 18 °C before induction with 30 mM isopropyl β-D-1-thiogalactopyranoside. These flask cultures were allowed to grow overnight before being harvested by centrifugation at 7500 × g for 10 min. The cells were then lysed using lysozyme (0.25 mg/ml final concentration) for 10 min, and the resulting lysate was centrifuged again, this time at 20,000 × g for 30 min. The supernatant was purified using a nickel-nitritolactiacid column, and the elution was further purified by size exclusion chromatography over a GE Healthcare S200 Superdex column using an ÄKTA Purifier FPLC.

For crystallization, MBP-PilAACICU, MBP-PilABIDMC57, and MBP-PilAM2 were cloned and expressed as described previously (7). Briefly, the sequences of PilA from A. baumannii ACICU and A. nosocomialis M2, starting with alanine 23, were cloned into a maltose-binding protein fusion vector, making use of surface entropy reduction mutations (pMal E) described previously (44). A C-terminal His6 tag was included for ease of purification. These clones were transformed, expressed, and purified as described above.

Structure Determination and Refinement—All MBP fusion proteins were initially screened by sitting drop vapor diffusion at a concentration of 20 mg/ml in 20 mM Bis-Tris, pH 6.0, 50 mM maltose.

MBP-PilAACICU—MBP-PilACICU was initially crystallized in the Hampton Research Index screen, condition D6: 0.1 m Bis-Tris, pH 5.5, 25% (w/v) polyethylene glycol 3350. These conditions were optimized to 0.1 m Bis-Tris, pH 5.5, 22.5% (w/v) polyethylene glycol 3000, 0.3 m 1,6-hexanediol, 5 mM maltooltriose in place of maltose. Crystals were grown in sitting drops at room temperature and took ~48 h to grow at a protein concentration of 5 mg/ml. They were then harvested and flash cooled in the mother liquor supplemented with 20% glycerol. Data were collected at the Stanford Radiation Source, the National Light Source beam line X25 in Brookhaven, NY, and eventually the data set used to resolve the structure was collected at the Advanced Photon Source, General Medical Sciences and Cancer Institutes Structural Biology Facility, beam line 23-ID-D.

MBP-PilABIDMC57—MBP-PilABIDMC57 was initially crystallized in the Molecular Dimensions Morpheus screen, condition A12: 0.1 m Bicine/Trizma (Tris base), pH 8.5, 12.5% (w/v) PEG 1000, 12.5% (w/v) PEG 3350, 12.5% (v/v) MPD, 0.03 m CaCl2, 0.03 m MgCl2. The optimal conditions were 0.1 m Bicine/Trizma, pH 8.0, 12.5% (w/v) PEG 1000, 12.5% (w/v) PEG 3350, 12.5% (v/v) MPD, 0.06 m CaCl2, 0.06 m MgCl2, 50 mM NaCl, 3% EtOH. Crystals were grown in hanging drops at room temperature and took ~72 h to grow at a protein concentration of 10 mg/ml. They were then harvested and flash cooled in the mother liquor supplemented with 20% glycerol. Data were collected at the Stanford Synchrotron Radiation Lightsource, beam line 12-2.

MBP-PilAM2—MBP-PilAM2 was initially crystallized in the Molecular Dimensions Morpheus screen, condition A12: 0.1 m Bicine/Trizma base, pH 8.5, 12.5% (w/v) PEG 1000, 12.5% (w/v) PEG 3350, 12.5% (v/v) MPD, 0.03 m CaCl2, 0.03 m MgCl2. The optimal conditions were 0.1 m Bicine/Trizma, pH 8.0, 12.5% (w/v) PEG 1000, 12.5% (w/v) PEG 3350, 12.5% (v/v) MPD, 0.06 m CaCl2, 0.06 m MgCl2. Crystals were grown in sitting drops at room temperature and took ~72 h to grow at a protein concentration of 10 mg/ml. They were then harvested and flash cooled in the mother liquor supplemented with 20% glycerol. Data were collected at the Advanced Photon Source, GM/CA, beam line 23-ID-B.

The ACICU and M2 data sets were processed with XDS (45); the BIDMC 57 data set was processed with HKL2000 (46). Molecular replacement was carried out by Phaser (47) using a sequential search of 1) maltose-binding protein and 2) PilA from P. aeruginosa strain K (PAK). Phenix and Coot were used for phasing, building, and refinement (48–51). The
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crystallographic parameters of the refined data are summarized in Table 1.

Differential Scanning Fluorometry—Melting curves for pilin headgroups were obtained by the addition of SYPRO Orange protein stain (Sigma-Aldrich) and thermal denaturation in an iQ5 RT-PCR cycler. The buffer conditions were 10 mM NaPO4, 150 mM NaCl, 25 mM DTT. All measurements were made in triplicate. The resulting curves were normalized and fit using the Boltzmann equation to determine the melting temperature for each protein. Similar Tm values were obtained by circular dichroism (supplemental Fig. 6) (6, 52).

Pilus Modeling—Full-length PilAACICU and PilAM2 were modeled based on the structure of the full-length PAK pilin (53). The initial models of the pili were created by superimposition onto a model of the Neisseria gonorrhoeae type IV pilus filament (Protein Data Bank code 2HIL) (54), and the N-terminal helix position was adjusted to eliminate clashes between subunits. The resulting models were then minimized as rigid bodies using UCSF Chimera (55).

Glycan Modeling—The glycans attached to PilAACICU and PilAM2 (supplemental Fig. 2) were modeled using the PyRosetta protein structural modeling suite (56) with extensions for non-protein polymer units for the glycans (57). The initial models were generated in the Discovery Studio Visualizer (BIOVIA, Discovery Studio Modeling Environment, Release 4.5, 2015, Dassault Systèmes, San Diego, CA). Then the glycans were modeled using the FloppyTail algorithm (58) altered for use in glycans. The protocol consists of two parts. In the low resolution part, a random perturbation of the torsion angles was applied. The high resolution parts of the structures were refined by applying a smaller perturbation of the torsion angles, sidechain packing, and minimization. With this protocol, 6000 structures of PilAACICU and 6000 structures of PilAM2 were generated.

Surface Area Calculations—The 10 best scoring models were used for surface area calculations for each pilus. Exposed surface areas for pilins with and without glycans were calculated using the pilus and glycan models described above and the ArealMol module of CCP4 (59) using a 1-nm spherical probe. C-terminal glycosylation reduces the exposed surface area from 22926 Å2 to 1801 Å2 (PilAACICU) and from 2938 Å2 to 2218 Å2 (PilAM2). The high resolution parts of the structures were refined by the ArealMol module of CCP4 (59) using a 1-nm spherical probe. C-terminal glycosylation reduces the exposed surface area from 22926 Å2 to 1801 Å2 (PilAACICU) and from 2938 Å2 to 2218 Å2 (PilAM2).

Cell Adhesion—A549 human airway adenocarcinoma cells (52) (CCL 185, American Type Culture Collection (ATCC), Manassas, VA) or Detroit 562 pharyngeal carcinoma cells (53) (ATCC CCL 138) were seeded in 24-well culture plates and cultured at 37 °C in 5% CO2 to 2.0 × 105 cells/well in Dulbecco’s modified Eagle’s medium containing 10% fetal bovine serum, 2.0 mm glutamine, 100 units/ml penicillin, and 100 μg/ml streptomycin. The cells were washed twice with PBS, pH 7.2; fixed for 10 min at room temperature with 2.5% (v/v) glutaraldehyde in PBS, pH 7.2; and washed three times with PBS, pH 7.2 as described (60, 61). A. nosocomialis M2 was cultured over-night in Luria-Bertani broth; washed twice with PBS, pH 7.2; resuspended in PBS, pH 7.2 containing 2.0 mg/ml glucose; and quantified spectrophotometrically at A600. Fixed A549 or Detroit 562 cells (2.0 × 105/well) were incubated with 2.0 × 107 colony-forming units (cfu)/well A. nosocomialis M2 in 0.5 ml for 40 min at 37 °C and washed three times with PBS, pH 7.2.

Bound bacteria were released with 0.05% trypsin, EDTA, and bound cfu were quantified on Luria-Bertani agar plates as described (60, 61). Significance was determined by Student’s t test.

Results

Acinetobacter Species Produce Type IV Pilins with Diverse C Termini—Although all strains of Acinetobacter carry the genes necessary to produce type IV pili, and the majority of those genes are highly conserved, the protein sequence of the major pilin, PilA, exhibits considerable variation in the soluble domain. In addition to this variation in amino acid sequence, Harding et al. (38) noted that strains from multiple Acinetobacter species with a serine residue at the C terminus of the major pilin also expressed an O-OTase similar to TfpO/PilO O-OTase from P. aeruginosa in addition to the PgL-like O-OTase found in all Acinetobacter strains. Analysis of pilA in 49 publically available A. baumannii genomes, 25 with a tfpO-like O-oligosaccharide transferase gene immediately after pilA and 24 without, shows considerable variation in both groups. All 25 tfpO+ strains also have pilA genes with C-terminal serine residues.

Fig. 1 shows dendograms of PilA sequences for each of the four Acinetobacter species in the Acb complex. Those strains that contain a tfpO gene and end their PilA sequence with a serine residue are marked with an asterisk to indicate putative glycosylation at the C terminus. In A. baumannii, the majority of these strains can be divided into two large clusters. The first (highlighted in orange) corresponds to the international clone II group, which is responsible for 50% of hospital infections worldwide (62). The second cluster (highlighted in blue) contains the type strain ATCC 19606. The largest cluster of tfpO—strains includes the international clone I group. Importantly, representatives of these two clusters can be found in each of the other members of the Acb complex. In particular, PilA proteins from A. baumannii PilA BIDMC 57 and A. nosocomialis PilA M2 are highlighted because their nucleotide sequences are over 99% identical.

To better understand why such diversity exists in the type IV pili of A. baumannii, we resolved high resolution structures of PilA proteins representative of these two major clusters. From the largest cluster, A. baumannii ACICU (also known as H34) is an epidemic, multidrug-resistant strain belonging to the European clone II group that was isolated in an outbreak in Rome in 2005 (63). From the other large cluster, A. baumannii BIDMC 57 was isolated in 2013 at Beth Israel Deaconess Medical Center (Boston, MA) and sequenced at the Broad Institute (Cambridge, MA), and A. nosocomialis M2 (referred to as A. baumannii M2 in some earlier publications) (33, 64, 65) was isolated in 1996 from a hip infection of a patient at Cleveland MetroHealth Systems (Cleveland, OH).

High Resolution Structure of PilAACICU—We determined the x-ray crystal structure of PilA from A. baumannii ACICU as a C-terminal fusion to maltose-binding protein to a resolution of 2.0 Å (Table 1). As depicted in Fig. 2, the overall fold of PilAACICU is very similar (r.m.s.d. = 2.19 Å) to PilA from PAK, differ-
ing primarily in the $\alpha\beta$-loop (the loop beginning with the end of the initial $\alpha$-helix and ending with the beginning of the first $\beta$-strand) (53). Among the differences between PilA from PAK and from ACICU are the $\alpha$-helical character of the ACICU $\alpha\beta$-loop and the longer length of the loop between the third and fourth strands of the central $\beta$-sheet. Combined, these features give PilA ACICU an axis of pseudosymmetry running diagonally across the molecule from the helix in the $\alpha\beta$-loop to the small

![Diagram](Image)

FIGURE 1. Dendrogram of Acinetobacter PilA. Dendrograms of PilA from A. baumannii, A. nosocomialis, A. calcoaceticus, and A. pittii are shown. Highlighted in orange are strains similar to PilAACICU and highlighted in blue are those similar to PilABIDMC57. Strains with a gene homologous to tfpO following their pilA gene and a C-terminal serine in PilA are marked with an asterisk.

### TABLE 1

| Crystallographic parameters | MBP- PilAACICU | MBP-PilABIDMC57 | MBP-PilAM2 |
|-----------------------------|----------------|-----------------|------------|
| Resolution (Å)              | 41.02–1.975    | 43.93–2.2       | 29.44–1.801|
| Space group                 | P 1 2 1        | C 1 2 1         | C 1 2 1    |
| Unit cell (Å)               | 41.018, 128.3, 92.505, 90, 90, 90 | 175.07, 56.636, 49.997, 90, 91.6, 90 | 173.883, 55.334, 49.67, 90, 91.52, 90 |
| Total reflections           | 105,740 (2.931) | 125,933 (2.2)  | 150,644 (8.909) |
| Unique reflections          | 53,305 (1.577) | 23,793 (2.036) | 42,472 (3.492) |
| Multiplicity                | 2.0 (1.9)      | 5.3 (2.7)       | 3.5 (2.6)  |
| Completeness (%)            | 79.68 (23.63)  | 94.85 (82.26)   | 96.82 (79.43) |
| Mean I/σ(I)                 | 12.43 (2.50)   | 11.1 (1.70)     | 14.90 (1.77) |
| Wilson B-factor             | 19.31          | 35.78           | 27.29       |
| $R_{merge}$                 | 0.04968 (0.6135) | 0.341 (1.10) | 0.05086 (0.5152) |
| $R_{int}$                   | 0.07026        | 0.375           | 0.06005    |
| CC1/2                       | 0.992 (0.184)  | 0.966 (0.314)   | 0.998 (0.791) |
| CC*                         | 0.998 (0.558)  | 0.991 (0.691)   | 1 (0.94)   |
| $R_{work}$                  | 0.1807 (0.2635) | 0.2109 (0.2950) | 0.1889 (0.3638) |
| $R_{free}$                  | 0.2408 (0.3457) | 0.2440 (0.3336) | 0.2280 (0.3943) |
| r.m.s. (bonds)              | 0.008          | 0.013           | 0.008      |
| r.m.s. (angles)             | 1.09           | 1.33            | 1.18       |
| Ramachandran favored (%)    | 98             | 97              | 96         |
| Ramachandran allowed (%)    | 2              | 2               | 1          |
| Ramachandran outliers (%)   | 0              | 0.62            | 0.83       |
| Clashscore                  | 5.03           | 2.43            | 9.08       |
| Average B-factor            | 26.3           | 28.10           | 37.1       |
| Macromolecules              | 25.9           | 27.30           | 37         |
| Ligands                     | 19.7           | 53.10           | 34.1       |
| Solvent                     | 30.6           | 41.90           | 40.20      |
helical region in the C terminus, a feature also found in the structure of PilA from *P. aeruginosa* K122-4 (66). Notably, contacts between pilin headgroups in a pilus typically occur primarily between these same regions of the protein (2).

Pil*A*CICU contains two disulfide bonds. One, between residues 123 and 136, is analogous to the C-terminal disulfide bond also found in Pil*A*PAK, which is nearly universal in type IV pili from Gram-negative bacteria. The other, between residues 74 and 91, spans the first two strands of the central β-sheet (Fig. 2B). However, we note that this additional disulfide bond in Pil*A*CICU (relative to Pil*A*PAK) does not result in any substantial rearrangement of the protein backbone.

### High Resolution Structures of Pil*A*BIDMC57 and Pil*A*M2

Although all *Acinetobacter* PilA sequences are nearly identical in the N-terminal hydrophobic α-helix, they diverge substantially beyond that point (e.g. Pil*A*CICU and Pil*A*BIDMC57 are 35% identical from alanine 23 onward). However, the sequence variability of type IV pili is such that homologs sharing only 30–40% sequence identity commonly have strikingly similar folds (the headgroups of Pil*A*PAK and Pil*A*CICU are 30% identical in sequence). To determine whether those pilins from the type strain cluster represented a distinct fold from those from the predominant international clone II cluster, we determined the x-ray crystal structures of PilA from *A. baumannii* BIDMC 57 and *A. nosocomialis* M2 as C-terminal fusions to MBP to resolutions of 2.2 and 1.8 Å, respectively (Table 1).

Although retaining the typical type IV pilin fold, the structure of Pil*A*BIDMC57 differs notably from that of Pil*A*CICU and Pil*A*PAK with its fold showing somewhat of an inversion along the previously described axis of pseudosymmetry (Fig. 3A), possessing an α-helix at the C terminus rather than the N terminus. The Pil*A*BIDMC57 αβ-loop contains 1) a short β-strand rather than an α-helix at its C terminus and 2) a seven-residue α-helix not found in Pil*A*CICU. This rearrangement results in the C terminus of Pil*A*BIDMC57 being shifted 13 Å relative to Pil*A*CICU when the two pilin headgroups are superimposed (Fig. 3D). Although there are few prior examples of multiple high resolution structures being solved from a single species, this degree of structural variation (r.m.s.d. = 4.17 Å) is greater than is expected within a given species. All three known structures of *Clostridium difficile* PilA1 are within 1 Å r.m.s.d. of each other (7), and Pil*A*PAK and Pil*A*K122-4 from *P. aeruginosa* are within 2 Å r.m.s.d. of each other and have superimposable C termini (53, 66). As expected from their sequence identity of over 99%, *A. baumannii* Pil*A*BIDMC57 and *A. nosocomialis* Pil*A*M2 have nearly identical structures as well, differing only in conformations of the αβ-loop and the loop between the fourth and fifth β-strands (Fig. 3B).

### Structural Implications for Pil*A*BIDMC57 and Pil*A*CICU Assembly

Of all the component proteins of a type IV pilus system, including major and minor pilins, extension and retraction ATPases, and other pilus biogenesis machinery, the major pilin protein is always the least conserved within a given species. However, the major pilin must retain the ability to assemble into a pilus, slowing the rate of variation in regions involved in intersubunit interactions. Although in some species the sequence variability of the major pilin is confined to hypervariable regions that are solvent-exposed in the assembled pilus (14), only the hydrophobic α1-N helix is well conserved in *A. baumannii* PilA (Fig. 3C). To understand how surface polymorphisms in PilA might impact pilin polymerization, we created models of *A. baumannii* pilus fibers from Pil*A*CICU and Pil*A*BIDMC57 based on the *N. gonorrhoeae* pilus (54) and compared the interactions between the pilin headgroups. Despite a sequence identify of only 35% between the Pil*A*CICU and Pil*A*BIDMC57 proteins (residues 23–136), many chemical moieties can be found in similar positions (Fig. 3D). These relationships are not obvious from a sequence alignment of the two
protein sequences (Fig. 3C) but become clear upon superimposition of the two structures. One implication of these data is that despite their divergence in sequence the major pilins of the various *Acinetobacter* strains may be assembled through similar networks of non-covalent interactions.

**Type IV Pili Promote Adhesion to A549 Cells**—The resemblance of *A. baumannii* type IV pili to other type IVa pilus systems (particularly *P. aeruginosa* and *D. nodosus*) led us to hypothesize that they may have overlapping functions. Previously, *Acinetobacter* type IV pili have been shown to be essential for natural transformation and twitching motility, but few data are available about their roles in infection-associated processes such as adherence to host cells or biofilm formation. To determine whether type IV pili play a role in bacterial host-cell adhesion, we measured the ability of wild type *A. nosocomialis* M2 and mutants with altered type IV pili biogenesis phenotypes to bind to immortalized lung (A549) and nasopharyngeal (Detroit 562) epithelial cells in vitro. We found that the pilA Δ strain, which produces no type IV pili, exhibited reduced adhesion to A549 cells in vitro and that wild type adhesion was restored after complementation with the wild type pilA gene (Fig. 4). To probe the importance of C-terminal glycosylation in this process, we also tested a pilA Δ strain complemented with pilA point mutant S136A, which cannot be glycosylated. Wild type PilA and PilA(S136A) are equally capable of complementing the adhesion defect of the ΔpilA mutant strain, indicating that pilin glycosylation plays no significant role in host cell adhesion. Increased binding by the ΔpilT mutant of M2, which is known to be hyperpiliated (33, 65), shows both that increased piliation increases adhesion and that the ability to retract type IV pili is not a component of type IV pilus-mediated bacterial host-cell adhesion. We found that universally M2 binds Detroit 562 cells much more weakly than A549 cells with only the ΔpilT strain showing any adhesion above background; this finding is similar to several strains tested by Eijkelkamp et al. (36). We also tested the ability of *A. nosocomialis* M2 to form a biofilm in vitro and found no significant difference among the wild type strain, the ΔpilA mutant, and the complemented mutant (supplemental Fig. 1).

**C-terminal Glycans Mask the PilA Protein in Models of Pilus Assembly**—There are four canonical functions for type IV pili: (i) twitching motility, (ii) horizontal gene transfer, (iii) host cell...
adhesion, and (iv) bacterial self-association (biofilm formation). As described above, none of these functions are dependent on C-terminal glycosylation of the major pilin in *Acinetobacter* in *vivo*. However, previous studies of C-terminal glycosylation in the major pilin of *P. aeruginosa* 1244 demonstrated a significant phenotype in *vivo*. Smedley et al. (21) demonstrated that deletion of the O-oligosaccharyltransferase tfpO (referred to by the authors as *pilO*) reduced survival of *P. aeruginosa* 1244 in a mouse model of lung infection. More recently, the *P. aeruginosa* 1244 ΔtfpO mutant was found to be more vulnerable to phagocytosis mediated by opsonization (67, 68).

Because opsonization is mediated by the binding of host immune proteins (commonly antibodies), the latter studies support the notion that the purpose of C-terminal glycosylation in the major pilin of *P. aeruginosa* 1244 was to interfere with immune recognition in *vivo*. Similarly, Gault et al. (25) recently showed that hypervirulent *N. meningitidis* strains with class II pilins are more heavily glycosylated than their class I counterparts.

To measure the extent to which C-terminal glycosylation of PilAACICU and PilAM2 would mask the pilin protein from binding, we modeled the full-length pilins and pilus fibers and measured the effect of glycosylation on the accessible surface area of each protein in its native context. We modeled an ensemble of each glycan based on the repeating unit of the major polysaccharide glycan and minimized each structure using Rosetta (69). The 10 best scoring glycan conformations were then combined to approximate the native conformational ensemble.

We then measured the differences in accessible surface area using a 10-Å particle probe to approximate the surface area needed for protein binding. The resulting models are shown in Fig. 5, and the change in accessible surface area for each protein is displayed in the *inset panel*. In both cases, C-terminal glycosylation reduces the exposed surface area (by 42% for PilAACICU and by 25% for PilAM2). The greater coverage of the PilAACICU protein stems from the greater flexibility of the linear PilAACICU glycan (in contrast to the branched PilAM2 glycan) (supplemental Fig. 2), which results in a more diverse conformational ensemble.

If C-terminal glycosylation in *Acinetobacter* type IV pili reduces recognition by host immune proteins, one might expect that the pilins from strains lacking a C-terminal glycan would face greater pressure to diversify as has been shown in *N. meningitidis* (25). Using our alignment of 49 PilA sequences, we separated protein sequences into *tfpO−* and *tfpO+* groups and compared the variability of their surface-exposed residues. For the *tfpO−* group, we modeled the structure of PilAAYE (an international clone I strain) based on the structure of PilAACICU. *Supplemental Fig. 3A* shows that, although overall the surface residue variability follows a similar pattern in the two groups, there is a region near the C terminus that is more conserved in the *tfpO+* strains. *Supplemental Fig. 3B* shows sequence logos of this region for both groups. These data support a model in which C-terminal glycosylation in type IV pili exists, at least in part, as a countermeasure to the host humoral immune response.

Variation in *Acinetobacter* pilA Is Driven by Evolutionary Pressure—To understand the basis for the structural resemblance of PilAACICU and PilABIDMC57 of *A. baumannii* to *P. aeruginosa* PilAPAK and *D. nodosus* FimA, respectively, we compared nucleotide and amino acid sequences for the major pilin from 11 representative genomes from each of the three species (Fig. 6). To evaluate the possibility that the cross-species similarities in pilA arose from horizontal gene transfer, we aligned the sequences of 54 nucleotides encoding the first 18 residues of the mature protein product, which is identical (FTLIELMIVVAIIGILAA) in all 33 amino acid sequences. Fig. 6A shows that, based on silent variations in these nucleotide sequences, the pilin genes can be separated neatly into three clusters based on species. That is, despite their dissimilarity in amino acid sequence, the nucleotide sequences for the α1-N domain of pilAACICU and pilABIDMC57 more closely resemble each other than their equivalents from *P. aeruginosa* and *D. nodosus*. However, when mature PilA amino acid sequences are aligned, all three of the resulting clusters contain representatives from multiple species. As they are labeled in Fig. 6B, cluster I contains the majority of the *D. nodosus* FimA serotypes (including serotype A, the sequence of Protein Data Bank code 3SOK) as well as *A. baumannii* PilAAICICU and PilABIDMC57. Cluster II contains PilAACICU as well as *P. aeruginosa* PilAPAK and PilAPAO1. Cluster III consists of two FimA sequences that contain C-terminal disulfide bonds, *A. baumannii* PilA135867 and PilA121738, and the *P. aeruginosa* PilA sequences with C-terminal serine residues.

The *A. baumannii* sequences from each of the three clusters are shown in Fig. 6C. Cluster II contains species from the international clone I group, whereas cluster III contains species from the international clone II group. Cysteine residues are highlighted in yellow and indicate differential disulfide bonding patterns between the three clusters; cluster III PilA sequences contain two disulfide bonds, and the majority of cluster I sequences do not contain a disulfide bond at the C terminus. However, all sequences in cluster I, from both *Acinetobacter* and *Dichelobacter*, contain hydrophobic residues aligned to isoleucine 106 and leucine 129 (highlighted in *violet*). These data support the hypothesis that variation in *Acinetobacter* pilA is the result of common evolutionary pressures that are common to *A. baun-
mannii BIDMC 57 and D. nodosus (serotype A) and conversely A. baumannii ACICU and P. aeruginosa PAK but not to A. baumannii as a whole, resulting in a structural divergence of A. baumannii PilA.

**Hydrophobic Interactions Stabilize the PilAM2 C Terminus**—One notable aspect of the PilABIDMC57 and PilAM2 structures is that, unlike PilAACICU, they contain only a single disulfide bond between residues 56 and 86 in the H9251/H9252-loop and the first strand of the H9252-sheet, respectively, rather than a disulfide bond at the C terminus of the pilin headgroup (Fig. 7 A). The addition of covalent disulfide bonds is typically understood to be a mechanism of stabilization in polypeptides, and hence the C-terminal disulfide bond, which is nearly ubiquitous in type IV pilins, is thought to be conserved to stabilize the pilin fold (3).

However, the lack of a C-terminal disulfide bond is not unique to Acinetobacter and, in fact, was observed previously in the structure of FimA from D. nodosus (serotype A) that PilABIDMC57 and PilAM2 closely resemble (Fig. 7 B). The principal difference between the two folds is that the shorter loops of Acinetobacter PilA BIDMC57 and PilAM2 result in a more compact structure. The lone disulfide bond in PilA BIDMC57 and PilAM2 is found in a position identical to the disulfide bond in FimA and the N-terminal disulfide bond in PilAM2 (Fig. 7 A). As PilA BIDMC57, PilAM2, and FimA have such similar folds and both lack a disulfide bond at the C terminus, we compared the structures of their C termini for common structural features that might explain the absence of a C-terminal disulfide bond. Because D. nodosus is an obligate anaerobe and cysteine residues are more likely to be reduced in anaerobic environments, one explanation for the structural convergence of PilAM2 and FimA that are in a similar position to the disulfide bond found in other pilins from Gram-negative bacteria: a backbone hydrogen bond between tyrosine 133 and valine 149, a hydrogen bond between the lysine 132 side chain and the backbone oxygen of lysine 150, and a van der Waals interaction between the tyrosine 133 phenyl ring and the aliphatic portion of the lysine 150 side chain. As no equivalents to these interactions can be found in the PilABIDMC57 and PilAM2 structures, we turned our attention to potentially stabilizing interactions between pairs of aliphatic side chains. In FimA, leucine 124, leucine 140, leucine 142, and isoleucine 145 can potentially form such pairs, and several would be superimposable with those formed by isoleucine 106, valine 126, leucine 129, and valine 134 in PilAM2 and PilAM2 (Fig. 7 B).

As noted above, this pattern is conserved in all 14 sequences in cluster I with two of these positions, Ile-106 and Leu-129, being universally isoleucine, leucine, or valine. Conversely, although Ile-106 is conserved in PilAACICU, the other three positions are occupied by glutamate, arginine, and glycine. To test our hypothesis that solvent exclusion from these aliphatic contacts stabilized PilAM2 in place of the canonical C-terminal disulfide bond, we measured the thermal stability of the PilAACICU and PilAM2 headgroups as well as a PilAM2 mutant with these four hydrophobic side chains truncated (I106A, V126A, L129A, V134A) using differential scanning fluorometry (Fig. 7 C) (71). We found that although the wild type PilAM2 ($T_m = 51.7 \pm 0.2 \degree C$) was less thermostable than PilAACICU ($T_m = 55.7 \pm 0.1 \degree C$), the hydrophobic C terminus of PilAM2 did contribute to the stability of the fold as evidenced by the lower melting temperature of the alanine mutant ($T_m = 45.0 \pm 0.5 \degree C$).
Discussion

From an evolutionary standpoint, the x-ray crystal structures reported here pose three questions for us. Why have the major pilins of *A. baumannii* diverged? Why are some, but not all, PilA proteins C-terminally glycosylated? And why do the major pilins from *A. baumannii* ACICU and BIDMC 57 resemble their counterparts from other bacterial species (*P. aeruginosa* and *D. nodosus*, respectively) more closely than they do each other?

The presence of close homologs to both PilAACICU and PilABIDMC57 in all four species that make up the Acb complex strongly implies that the divergence in *pilA* predates the divergence of *A. baumannii* and *A. nosocomialis*. This, combined with the similarities between PilA ACICU and PilAPAK and between PilABIDMC57 and FimA (serotype A), suggest that the divergence in *Acinetobacter pilA* is not due to functionally neutral diversifying selection, as is thought to be the case in *Neisseria pilE*, but instead due to functionally divergent evolution.

Determining which selective pressures favor a PilAACICU/PilABIDMC57-like structure over that of PilAPAK and FimA (serotype A), suggest that the divergence in *Acinetobacter pilA* is not due to functionally neutral diversifying selection, as is thought to be the case in *Neisseria pilE*, but instead due to functionally divergent evolution.

**FIGURE 7. Hydrophobic interactions in the PilAM2 C terminus.** *A*, schematic representations of various major pilins; disulfide bonds are marked with yellow spheres. *B*, superimposition of PilAM2 (blue) and FimA (gray); an inset panel shows the C-terminal region where a disulfide bond is typically found in type IV pilins. *C*, differential scanning fluorometry curves showing stability measurements for PilAACICU, PilAM2, and PilAM2(I106A,V126A,L129A,V134A).

It was this lack of observable phenotype that led us to search for alternative explanations for the prevalence of tfpO-mediated glycosylation in *Acinetobacter*. Previous work in *P. aeruginosa* 1244, demonstrating that a ΔtfpO mutant was more vulnerable to phagocytosis mediated by opsonization (67, 68), implied that C-terminal glycosylation formed an obstacle to binding by host immune proteins. Our quantification of the ability of *Acinetobacter* C-terminal glycans to mask their conjugate polypeptides shows that over 25% of the PilA surface area available for binding is occluded. C-terminal glycosylation...
should, therefore, offer an advantage provided that the glycan surface is less vulnerable to binding by antibodies or other opsonins.

The evolutionary distance between A. baumannii BIDMC 57 (and A. nosocomialis M2) and D. nodosus suggests that the close resemblance between their respective pilin proteins is the result of convergent evolution. Although the functional benefit of this fold to the soil gammaproteobacteria found in class I of the alignment in Fig. 6 remains to be determined, it seems unlikely that the absence of a C-terminal disulfide bond in 12 of the 14 cluster I sequences is due to chance. We speculate that the cluster I fold may be advantageous in an anaerobic environment.

A further implication of the diversity in Acinetobacter type IV pilins is the challenge it poses for vaccine development. Because of their abundance in the extracellular space, type IV pilis are obvious candidates for subunit vaccines and have been successfully used as such for other bacteria, including D. nodosus (75, 76). However, in Acinetobacter, the combination of variability in the PilA polypeptide with variation in polysaccharide structure in many strains may present a significant barrier to inducing a robust and durable immune response.

In conclusion, the results presented here reveal that type IV pilin in Acinetobacter have diverged in a manner unrelated to the genetic divergence of species within the Acb complex and that similarities in type IV pilin cross species, genus, and family lines. These data reinforce the principle that functional requirements determine protein structure while allowing considerable variation in sequence. These data also imply that three distinct functional classes of type IV pilin exist in Acinetobacter and other soil gammaproteobacteria.

Author Contributions—K. H. P. conducted most of the experiments, analyzed the results, and wrote the paper. E. L. conducted the cell binding measurements. C. M. H. created the mutant Acinetobacter strains used in this study (with the aid of R. S. M.) and provided valuable experimental input and commentary during writing. J. W. L. and X. Z. performed the glycan conformational simulations. C. A. R. conducted the in vitro biofilm formation experiments. S. E. G., M. F. E., J. J. G., and E. J. S. helped to coordinate the study and write the paper.

Acknowledgments—We thank the staff at Argonne National Laboratory Advanced Photon Source, General Medical Sciences and Cancer Institutes Structural Biology Facility, beam lines 23ID-D and 23ID-B, and the staff at Stanford Synchrotron Radiation Lightsource, beam line 12-2, for technical assistance with x-ray data collection. We also thank Dr. Angela Wilks for the use of the circular dichroism spectrophotometer.

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J. Biol. Chem. 2016, 291:22924-22935.
doi: 10.1074/jbc.M116.751099 originally published online September 15, 2016

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