

Unwrapping the Ciliary Coat: High-Resolution Structure and Function of the Ciliary Glycocalyx

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The glycocalyx, a highly heterogeneous glycoprotein layer of cilia regulates adhesion and force transduction and is involved in signaling. The high-resolution molecular architecture of this layer is currently not understood. The structure of the ciliary coat is described in the green alga *Chlamydomonas reinhardtii* by cryo-electron tomography and proteomic approaches and the high-resolution cryoEM structure of the main component, FMG1B is solved. FMG1B is described as a mucin orthologue which lacks the major O-glycosylation of mammalian mucins but is N-glycosylated. FMG1A, a previously undescribed isoform of FMG1B is expressed in *C. reinhardtii*. By microflow-based adhesion assays, increased surface adhesion in the glycocalyx deficient double-mutant *fmg1b-fmg1a* is observed. It is found this mutant is capable of surface-gliding, with neither isoform required for extracellular force transduction by intraflagellar transport. The results find FMG1 to form a protective layer with adhesion-regulative instead of adhesion-conferring properties and an example of an undescribed class of mucins.

also readily adhere to surfaces by their cilia, in which case the cilia are no longer beating. These cells are still able to move in a gliding fashion that is driven by intraflagellar transport (IFT). IFT is a system of polymeric trains moving along the microtubule-based axoneme that constitutes the core of all cilia. The rapid motion of IFT trains in *Chlamydomonas reinhardtii* is sufficient to pull the surface-adhered cell along the cilia. While the exact binding of IFT trains to components of the ciliary membrane remains unclear, it has been shown that moving trains can move beads attached to the outside of cilia.^[1] As such, the outer coat of the cilia, generally referred to as the glycocalyx, must act as the main force transducing element between IFT and the surroundings. Consequently, the adhesion of the glycocalyx is of significant importance to gliding in *C. reinhardtii* and we have recently demonstrated that changes

1. Introduction

The green alga *Chlamydomonas* uses its cilia, also referred to as eukaryotic flagella, as the primary means of motility and sensing of the external environment. In a liquid environment, *Chlamydomonas* cells swim by a breast-stroke motion. However, cells can

in N-glycosylation lead to reduced ciliary adhesion.^[2] In mammalian cilia, the glycocalyx of motile cilia is the main interactor with the mucosal layer covering the epithelial layer, but the precise nature of this interaction is currently unknown.^[3]

Bloodgood and Sloboda have shown that the flagellar membrane glycoprotein 1B (FMG1B), an unusually large ≈4546

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amino-acid long molecule, constitutes a major part of the glycocalyx of *C. reinhardtii*,^[4] which localizes to the ciliary coat and is visible as a densely stained layer in electron microscopy sections. However, the mutants used by Bloodgood have exhibited occasional instability of the phenotype with detectable levels of FMG1 atypical for *C. reinhardtii* insertional mutants. This reversal has primarily been attributed to the fact that the insertion in those specific mutants is in the 5'UTR of FMG1B which does not necessarily guarantee a complete null of the protein. In addition to FMG1B, *C. reinhardtii* has a homologous gene FMG1A with high primary sequence similarity to FMG1B that has been assumed to be not expressed. Recent proteomic studies have found evidence for the expression of FMG1A,^[2,5] but have not further studied the second isoform. Here, we use a combination of cryo-electron microscopy (cryoEM), cryo-electron tomography (cryoET), proteomic analysis as well as fluorescence microscopy and microfluidics on CRISPR/Cas mutants to demonstrate that: 1) Both FMG1 isoforms are expressed in *C. reinhardtii*, 2) are structurally highly similar and localize to the ciliary coat in the same manner; 3) the lack of both isoforms significantly increases ciliary adhesion and induces excessive microsphere binding; 4) that gliding motility is not impaired by lack of both isoforms. From our results, we conclude that the gliding mechanism in *C. reinhardtii* is likely not mediated by a single species but can be understood as a holistic effect of the entire membrane surrounding IFT trains. We suggest further that FMG1 exemplifies a new class of mucins and acts primarily as a protective layer with adhesion-regulating rather than adhesion-conferring properties.

2. Results

2.1. The Isoforms FMG1A and FMG1B are Expressed on the Surface of *C. reinhardtii* Cilia

With the recent extension of the CliP library^[6,7] we were able to obtain a mutant line with an insertion in the coding sequence of FMG1B (LMJ.RY0402.183636), specifically in the 5th exon (see Figure S1A, Supporting Information) and we have verified the presence of the CIB1 insert by PCR (see Figure S1B, Supporting Information). Analysis of whole CC-4533 *fmg1b* cells by liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS) confirms the complete absence of FMG1B (see Figure S1C, Supporting Information). Importantly, unique peptides are detected for FMG1A in both *fmg1b* cells as well as the background CC-4533 strain, confirming that the second isoform is expressed on a population level. The CC-4533 *fmg1b* strain readily adheres to glass surfaces in a gliding configuration and is indistinguishable from the background by phase-contrast microscopy (see Figure S1D, Supporting Information).

In order to facilitate the observation of gliding in CC-4533 *fmg1b*, we crossed the cells to *ift46::NIT IFT46-YFP* cells (a nitrate reductase insertional *ift46* mutant rescued with a full-length YFP tagged *IFT46* gene) and recorded the resulting cells in total internal reflection fluorescence (TIRF) microscopy. As shown in Figure 1A, these cells readily glide in the absence of FMG1B. We then proceeded to investigate whether the lack of FMG1B causes a difference in ciliary adhesion strength. We assayed this property by subjecting adhered cells in a microchannel to a fluid flow while observing the surface of the microchannel by bright-

field microscopy (see Figure S2A, Supporting Information). The drag force from the flow results in cells being detached over time (see Figure S2B, Supporting Information) and we measure the number of detached cells as a proxy for the adhesion strength. As such, we do not observe a significant difference in adhesion between CC-4533 and the *fmg1b* mutant cells, indicating that the adhesion is not solely mediated by FMG1B. This led us to ask whether FMG1A could assume the same function as FMG1B since both isoforms share an identical c-terminal tail region and have significant homology in the rest of the sequence (see Figure S1F, Supporting Information). To elucidate the 3D organization and distribution of FMG1s in the glycocalyx, we performed cryoET on the intact cilia extending from frozen life *C. reinhardtii* cells. In wild-type cells, the ciliary membrane that surrounds the central axonemal structure is coated with a diffuse inner layer of low electron density and an outer, electron-dense layer consisting entirely of FMG1 (see Figure 1C–E). Importantly, in tomographic slices of CC-124 as well as CC-4533 *fmg1b* cells, the same scale-like structure of the outer ciliary FMG1 coat can be observed (see Figure 1D,E), confirming that both FMG1 isoforms assume the same ultrastructural arrangement in the glycocalyx. We then wondered to what extent either isoform is present in the cilia of wild-type cells. Since proteomic analysis can only measure populations and we were unable to distinguish the isoforms in cryoET, we generated the fluorescent dual knock-in line *FMG1A-mScarlet1 FMG1B-mNeonGreen* using CRISPR/Cas-based precision genome editing (see Figure S1G, Supporting Information). Observation of this line by spinning-disk confocal microscopy showed that either one of the two isoforms usually dominates, but the presence of both isoforms in the cilia can be occasionally observed in the ciliary membrane (see Figure 1F). Further consolidating the similarity of the two FMG1 isoforms is a near-identical localization of the newly produced protein inside the cell body (see Figure S1H, Supporting Information).

2.2. Depletion of Both Isoforms of FMG1 Has no Impact on Gliding Ability but Increases Cilia-Substrate Adhesion

Having established the presence of a second isoform, we generated a CRISPR/Cas mediated dual null mutant line CC-124 *fmg1b-fmg1a* via an intermediate CC-124 *fmg1b* line and set out to characterize this new line with regard to gliding motility and adhesion (Figure S3A–C, Supporting Information). Despite a total lack of FMG1, these cells adhered to a microscope slide with their cilia in a gliding configuration (see Figure 2A).

To measure gliding activity, we crossed CC-124 *fmg1b-fmg1a* to *ift46::NIT IFT46-mNeonGreen (IFT46-mNG)* to produce an IFT labeled but glycocalyx deficient line and subjected cells to gliding analysis using TIRF microscopy (Figure S3B, Supporting Information). Unexpectedly, these cells were still able to glide (Figure 3B) with similar gliding velocities of $0.68 \mu\text{m s}^{-1} \pm 0.78$ in FMG1⁺ cells and $0.97 \mu\text{m s}^{-1} \pm 1.00$ in FMG1[−] cells (Figure 2C). Likewise, gliding distances were similar with a mean gliding distance of $5.2 \mu\text{m} \pm 2.4 \mu\text{m}$ in FMG1⁺ cells versus $6.9 \mu\text{m} \pm 2.8 \mu\text{m}$ in the FMG1[−] line (Figure 2D). To compare the relative adhesion strength of CC-124 and CC-124 *fmg1b-fmg1a*, cells were reconstituted in calcium-free HEPES/NMG buffer before transfer to

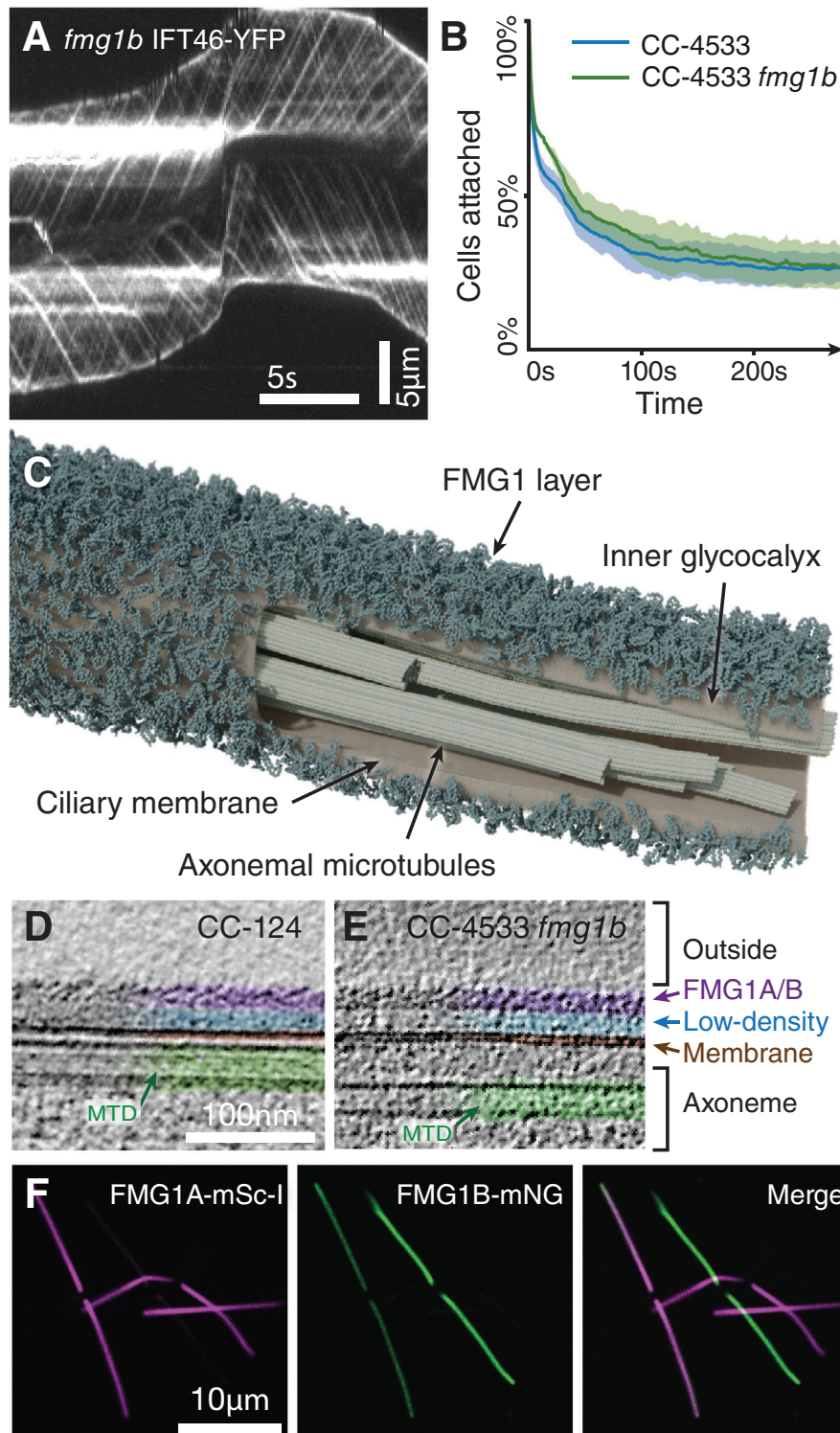


Figure 1. *C. reinhardtii* expresses both isoforms of the flagella membrane glycoprotein, FMG1-A and FMG1-B. A) Kymogram of the cilia of *fmg1b ift46::NIT* IFT46-YFP showing IFT-mediated gliding in the absence of FMG1B. Scale bars are 5 s and 5 μm. B) The absence of FMG1B does not cause loss of cellular adhesion to a polymer surface under 3.77 mL min⁻¹ flow. Average of three biological replicates. Shown error bars present the standard deviation. C) Tomographic segmentation of a wild-type cilium with membrane partially hidden to show the ultrastructural organization of the FMG1 layer coating the membrane that surrounds the central axonemal microtubules. D) Cryo-electron tomography (cryoET) slice of wild-type cilia showing the scale-like arrangement of FMG1 on the outer coat. The scale bar is 100 nm. E) CryoET slice of CC-4533 *fmg1b* cilia with intact scale-like layer. F) Spinning disk confocal slices of adherent FMG1A-mScarlet-I FMG1B-mNeonGreen cells showing facultative co-expression of both FMG1 isoforms. The scale bar is 10 μm. See also Figure S1 (Supporting Information).

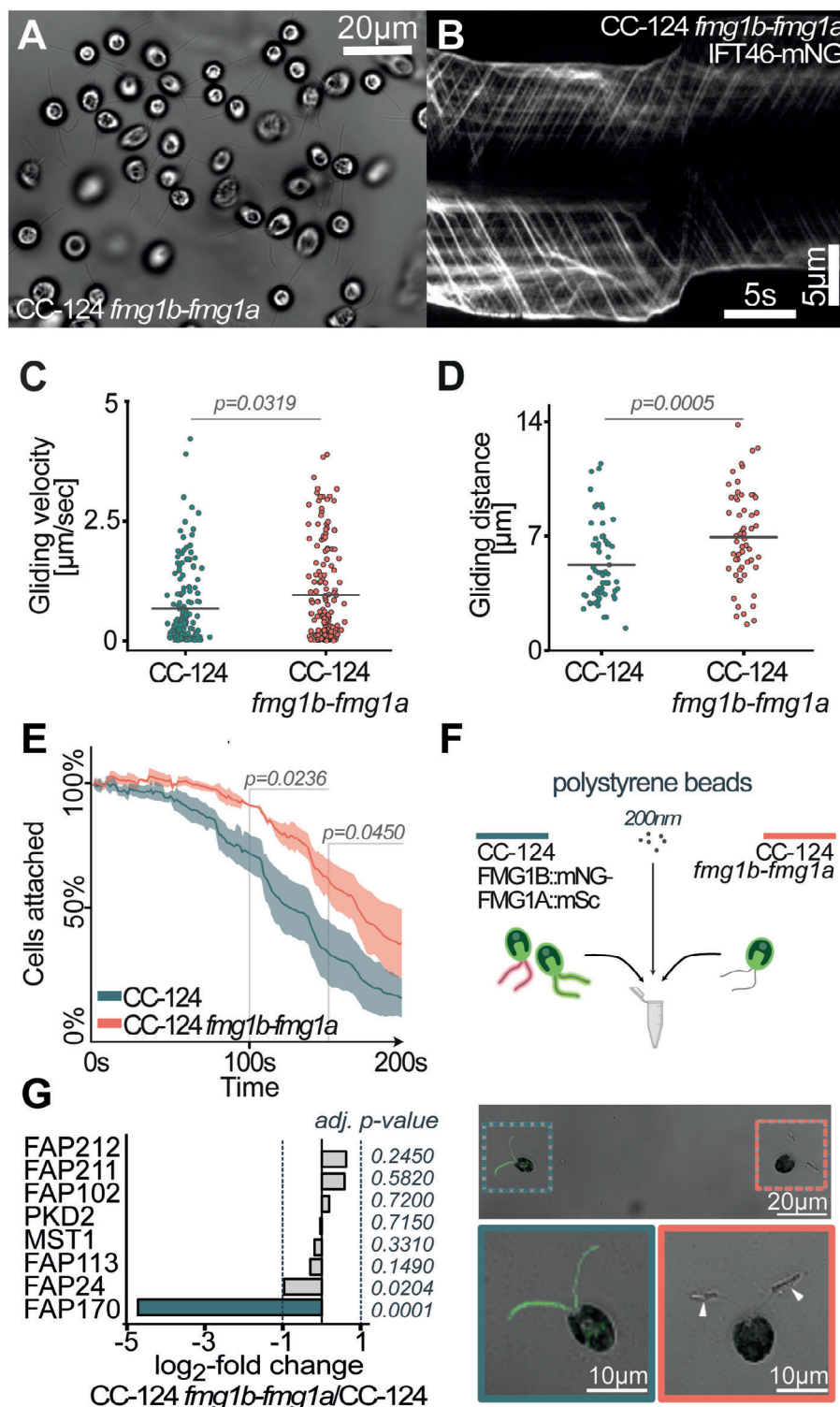


Figure 2. Depletion of FMG1 has no effect on gliding ability and renders cilia more adhesive. A) FMG1 deficient cells readily adhere in gliding configuration to glass coverslips. B) Kymogram of *fmg1b-fmg1a ift46::NIT IFT46-mNG* cilia showing IFT-mediated gliding in the absence of both FMG1 isoforms. Scale bars are 5 s and 5 μm. C) Detailed analysis of gliding velocities of surface-adhered cells. (WT cells: 40; events:161, MT. cells: 42; events: 218) D) Gliding distance of 60 gliding events per strain analyzed. E) Averaged detachment curves of CC-124 and CC-124 *fmg1b-fmg1a* under stepwise increasing flow rate every 30 s (3.77–51.94 mL min⁻¹). Three biological replicates were performed. Shown error bars present the standard deviation. Two sample t-test was performed for statistical validation. F) Analysis of polystyrene microsphere binding capacity of CC-124 *fmg1b-fmg1a* and CC-124 FMG1A-*mScarlet-I* FMG1B-*mNeonGreen*, shows excessive bead binding to cilia of CC-124 *fmg1b-fmg1a* (white arrow). G) Log₂fold change (CC-124 *fmg1b-fmg1a* / CC-124) of known N-glycosylated ciliary proteins quantified by LC-MS/MS. See also Figure S3D (Supporting Information).

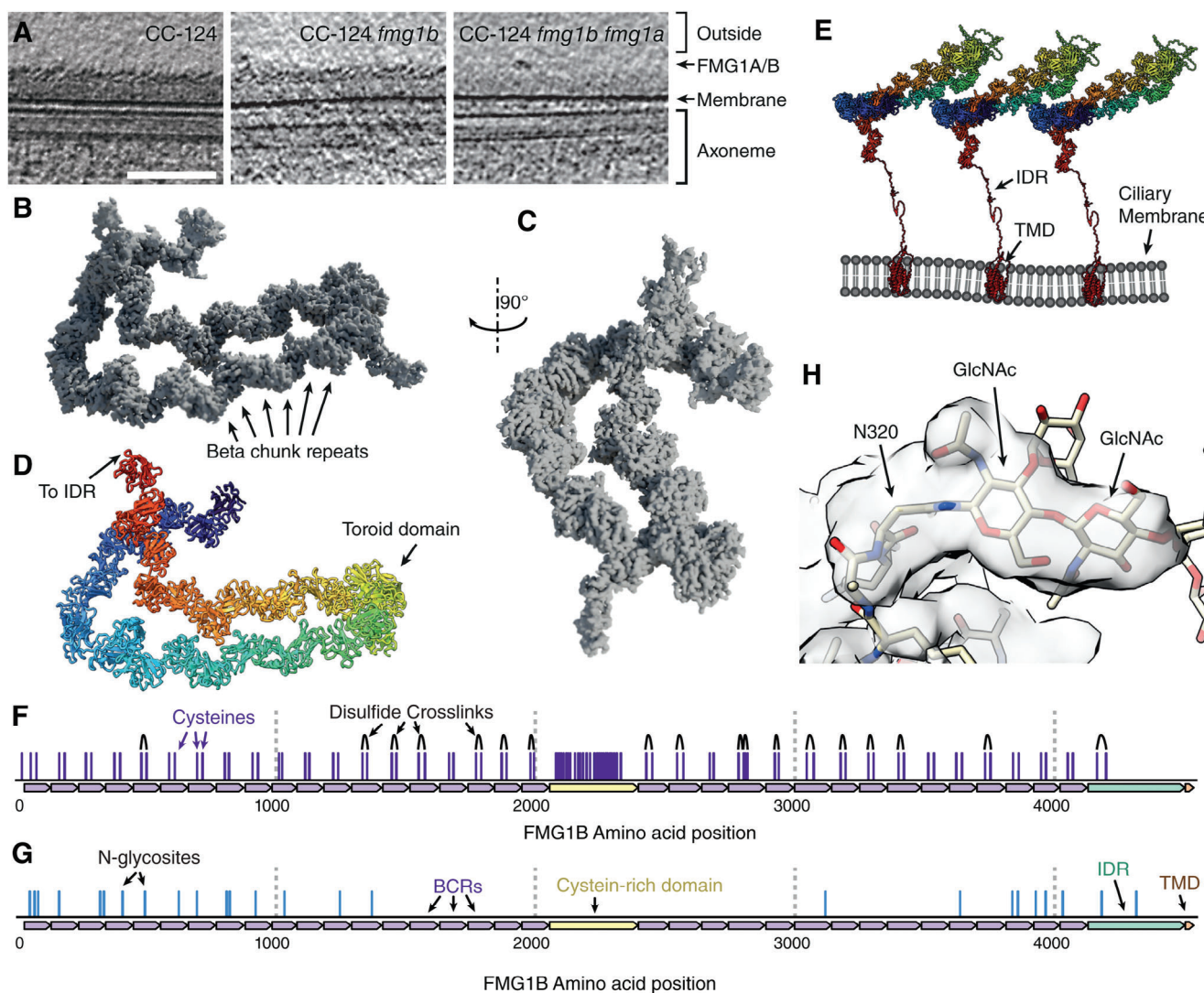


Figure 3. Cryo-electron microscopy and structure of FMG1. A) CryoET slices showing the presence of the scale-like outer coat in cilia of WT CC-124 cells as well as CC-124 *fmg1b* cells. Cilia of double-ko CC-124 *fmg1b-fmg1a* cells lack the scale-like outer coat with only a diffuse inner coat layer present. B) Side view of cryoEM reconstruction of isolated FMG1B. Boxed area detailed in (F). C) Front view of cryoEM reconstruction of isolated FMG1B. D) Integrative modeling-based structure of FMG1B. E) Schematic representation of the organization of FMG1 in the ciliary membrane (IDR, TMD and cysteine-rich regions predicted by AF2). F) Map of FMG1B cysteine residues with disulfide bridges identified by structural proteomics. G) Map of N-glycosites identified by combined proteomics and cryo-EM analysis (see also Table S1, Supporting Information). H) Representative detail view of Asn residue with bound N-glycan resulting in extra density.

the microchannel to encourage cells to settle on the surface. Under these conditions, CC-124 and CC-124 *fmg1b-fmg1a* showed strong adhesion when exposed to stepwise increasing shear stress from 3.77 to 51.94 mL min⁻¹ (Figure 2E). Surprisingly CC-124 *fmg1b-fmg1a* cells showed a significantly slower detachment of cells, suggesting a significantly increased ciliary adhesion strength of glycolyx-deficient cells. To confirm this observation in an independent approach, we compared the capacity of the cilia of CC-124 and CC-124 *fmg1b-fmg1a* to bind microbeads: We mixed equal cell numbers of CC-124 *fmg1b-fmg1a* and CC-124 FMG1A-*mScarlet-I* FMG1B-*mNeonGreen* with polystyrene beads in one sample, thus ensuring the same conditions for both cell lines. While CC-124 FMG1A-*mScarlet-I* FMG1B-*mNeonGreen*

cilia were largely devoid of microspheres, excessive binding of beads could be observed along cilia of CC-124 *fmg1b-fmg1a* accumulating primarily along the distal half of the cilium (Figure 2F). Considering these results, the absence of the major cilia glycolyx seems to render the cilium more adhesive. As ciliary adhesion is sensitive to tunicamycin and altered N-glycosylation impacts adhesion force,^[2,8] suggesting the requirement of N-glycosylated proteins, we analyzed protein abundance of confirmed ciliary N-glycoproteins^[9] that could compensate for the loss of FMG1 in gliding and adhesion (Figure 2G; Figure S3D, Supporting Information). Besides the uncharacterized membrane protein FAP170, no other known cilia N-glycoprotein showed significantly altered abundance.

2.3. FMG1 is Built From Structural Repeats with Low Sequence Self-Similarity

After establishing the phenotype of CC-124 *fmg1b-fmg1ab* we then investigated the resulting ultrastructural changes to the glycocalyx. CryoET on the intact cilia of these lines revealed the absence of the scale-like layer that constitutes the outermost layer of the ciliary coat for the dual-knockout, but not for the intermediate CC-124 *fmg1b* line (see Figure 3A). These data confirmed that the outer scale-like layer indeed consists of either an isoform of FMG1 or a mix of both.

Having thus confirmed the identity of the scale-like outer coat, we set out to solve the high-resolution structure of these unusual proteins. Due to the resolution limit of in-vivo cryoET we were not able to resolve a high-resolution structure of FMG1 directly from tomograms. Instead, we purified FMG1B from *C. reinhardtii* cilia by concanavalin A affinity chromatography and performed single particle cryoEM analysis.

The resulting ≈ 3 Å structure of FMG1B revealed the molecule as a long, twisted chain of 34 individual globular subdomains of 109.6 ± 10.9 amino acids and one cysteine-rich coiled domain (Figure 3B,C; Video S1, Supporting Information). We generated a corresponding peptide model of FMG1B by an initial prediction with AlphaFold3,^[10] followed by fitting with coarse-grained molecular dynamics^[11] and fine-tuning with ISOLDE.^[12] The individual subdomains fold into an Ig-like fold with each two orthogonal beta-sheets and one short alpha helix, which we call beta chunk repeats (BCR).

We modeled the semi-rigid structures composed of the chained BCRs to high confidence (see Figure 3D), while the flexible nature of the cysteine-rich domain resulted in a lower local resolution density which, together with the absence of bulky, recognizable amino acids, could not be assigned confidently. The C-terminus of FMG1B consists of an ≈ 100 amino-acid long intrinsically disordered region (IDR) linker followed by a multi-helix transmembrane domain (TMD). Due to the inherent flexibility of the linker region, no densities could be resolved for either the linker region or the TMD. Using our integrative model of FMG1 we could explain the densities measured in cryoET by the rigid BCR structure making up the scales of the ciliary membrane which are anchored in the ciliary lipid bilayer by the TMD (see Figure 3E). Despite the high sequence variability between individual BCRs, every BCR contained a single highly conserved disulfide bridge as confirmed by MS-assisted disulfide detection (Figure 3F), while no disulfide bridges were detectable in the cysteine-rich domain under our conditions. Interestingly, we observe protruding densities by cryoEM that cannot be explained by the primary peptide sequence. Since FMG1 is known to be heavily glycosylated from biochemical analysis, we performed In-Source collision-induced dissociation (IS-CID) MS/MS in combination with in-silico prediction^[13] to identify potential N-glycosites of FMG1B via mass spectrometry. Strikingly, we find a near-perfect correlation between the identified candidate sites and the unexplained electron densities (see Figure 3H; Table S1, Supporting Information). As such, we were able to directly confirm 25 glycosylation sites of FMG1B, which were mostly located to the 16 n-terminal and the 9 c-terminal BCRs, all of which were in proximity to each other on one side of the FMG1B molecule (see Figure 3G).

We then used AlphaFold predictions as a tool to assess the structural similarity of the two FMG1 isoforms. Despite the fact that FMG1A and FMG1B only share $\approx 61\%$ pairwise identity, the protein fold of the isoforms was predicted to be almost identical, with typical root mean square deviation (RMSD) values of less than one angstrom between corresponding subdomains of either isoform (see Figure 4A). These data suggested that FMG1A and FMG1B not only occupy the same space in the cilium but also have almost the same protein structure. Likewise, the individual BCRs composing either isoform share little sequence homology ($\approx 22\%$ pairwise identity, Figure 4B), but show a high degree of structural homology (Figure 4C,D).

Finally, suspecting that FMG1 might be just one example of a wider family of currently uncharacterized, related, proteins, we searched for homologs by linear alignment of individual domains and used AlphaFold predictions to verify potential hits. Unsurprisingly, the closely related *Chlamydomonas incerta* and *Chlamydomonas schlosseri*^[14] possess proteins that share a high similarity, particularly in the fold of their repeat units (Figure 4E,F). The number of repeats and the length—or presence—of a cysteine-rich domain varied among these examples. Strikingly, despite a large sequence variance in the structural repeats, these proteins shared a much more conserved IDR domain. Based on this conservation, we repeated our search by focusing on the IDR domain and were able to find an example of a different repeat-fold in the more distant green alga *Edaphochlamys debaryana*.^[14] These data suggest that FMG1 is indeed just one example of a highly variable family of mucin-like long and flexible proteins that are predicted to be targeted to the ciliary membrane of unicellular green algae.

3. Discussion

Using cryoET, MS-assisted protein quantification, and a fluorescent dual knock-in approach we provide strong evidence that *C. reinhardtii* expresses FMG1B and importantly FMG1A. The glycoproteins localize to the cilium and to an unknown compartment within the cell body. Both isoforms, despite the significant difference in amino acid sequence, seem to obtain the same ultrastructure in vivo as revealed by the unchanged appearance of the ciliary coat in two independent FMG1B knock-out mutants (Figures 1D,E and 3A), while knock-out of both isoforms confirms that the outer ciliary glycocalyx is indeed solely composed of one or both of these two isoforms (Figure 3A). While it is possible that other, unidentified components are localized to this layer and are lost in concert with the loss of FMG1, we do not detect additional unexplained densities in the outer coat at tomographic resolution. Loss of FMG1 is consistently correlated with a downregulation of FAP170 whose function is currently not known. Purifications of FMG1 from endogenous ciliary membranes do not contain detectable levels of FAP170 (in LC-MS/MS), indicating that there is no strong interaction between FAP170 and FMG1 and the partial loss of FAP170 in these mutants could be explained by translational regulation rather than a mechanically induced loss.

We suggest that FMG1 in *C. reinhardtii* is acting as a mucin orthologue. Mucins are ubiquitous in higher life forms and have evolved independently multiple times.^[15] The protein family serves primarily in a protective and adhesion-regulatory

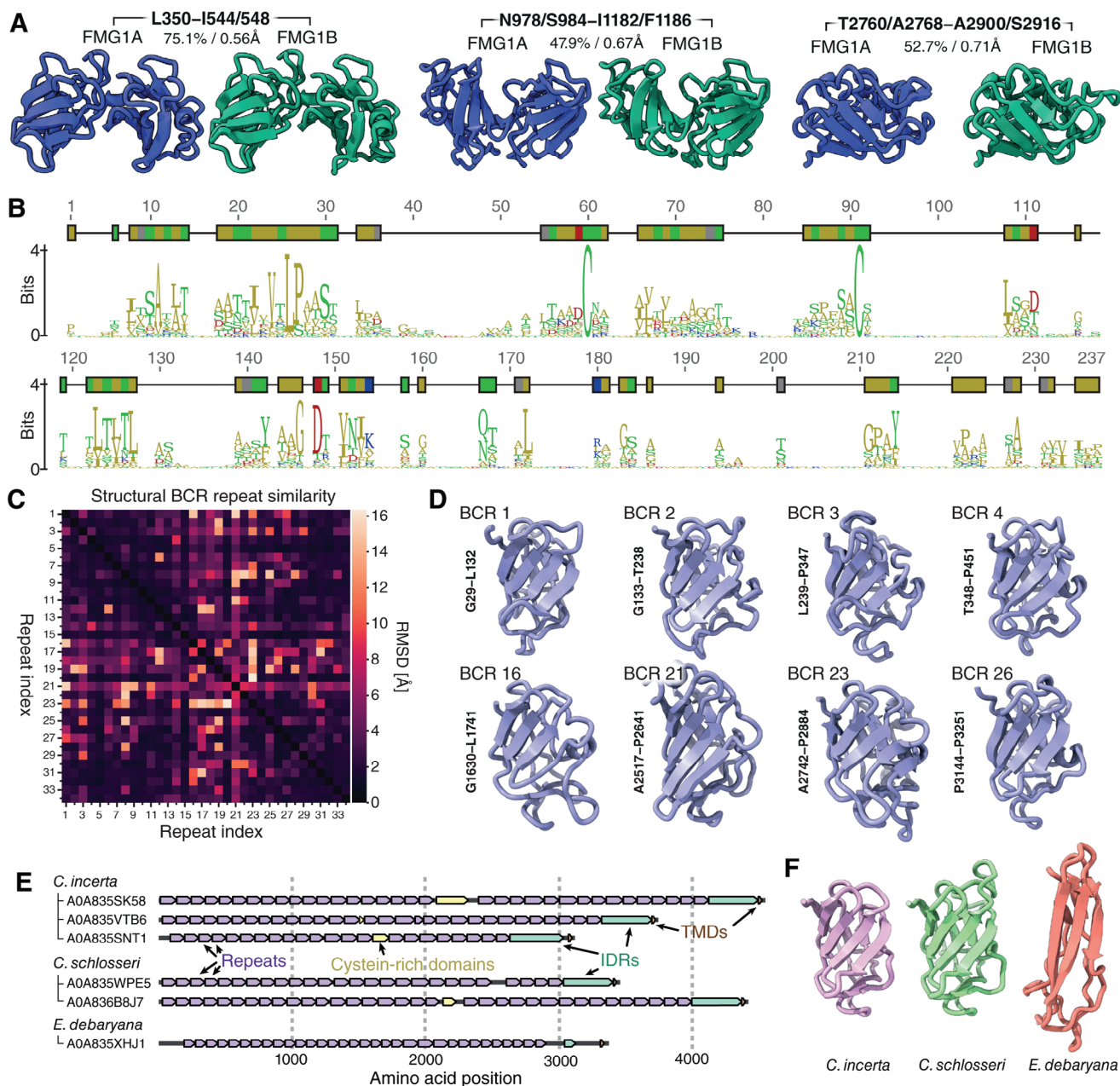


Figure 4. Structural characterization and conservation of FMG1 BCRs. A) Comparison of AlphaFold structures for FMG1A and FMG1B predict very high local structural homology despite significant sequence variability. Pairwise identity / RMSD values indicated for sequence and structural homology respectively. B) Sequence motif from all 34 aligned BCR repeats of FMG1B showing low overall sequence homology between BCRs except for a perfectly conserved pair of cysteines at positions 60 and 91. C) Pairwise root-mean-square atomic displacement (RMSD) map for all 34 BCRs showing a high degree of structural homology between all BCRs in FMG1B. D) Aligned example BCRs illustrating the conserved core beta-sheet fold and variable peripheral loops of different repeats. E) Structural annotation of transmembrane anchored homologues to FMG1 in three green algae *Chlamydomonas Incerta*, *Chlamydomonas Schlosseri* and *Edaphochlamys debaryana* showing examples of the wider family of the membrane-anchored folded-repeat based structure. F) Representative examples of the structural repeats annotated in E).

function as a major component of the epithelial glycocalyx. Linear alignment of FMG1 to the human proteome matches the serine, proline, and threonine-rich regions to human Mucin 4. The diverse known mucins are classically characterized by a repetitive primary amino acid sequence and abundant carbohydrate modification. The repetitive primary sequence results naturally in a

repetitive structural arrangement in known mucins. Conversely, both FMG1 isoforms consist of structural repeats of high similarity, but which share almost no primary sequence homology and as such raises the possibility of an entire class of currently not characterized mucin-like proteins that have been overlooked due to their lack of primary sequence repeats.

Interestingly, Mucin 4 specifically has been shown to localize to motile cilia of the airways, and anti-adhesive properties have been attributed to the protein due to an unspecific steric effect.^[16] Both FMG1 and Mucin 4 contain a cysteine-rich domain that is common to many mucins. The mechanochemical properties of known mucins arise due to the molecular interactions of long branched glycans.^[17] While mammalian mucins are primarily decorated by O-glycosylation, the detectable glycans of FMG1 in *C. reinhardtii* are all N-linked. This isomorphism could be another indication that this new class of mucins in *C. reinhardtii* has evolved independently to other major lineages. Finally, while O-glycosylation is poorly characterized in *C. reinhardtii*, recent structural work on mastigonemes^[18,19] implies that only monosaccharide adducts are fused during O-glycosylation of serine and threonine which likely do not confer the same rheological properties as the long glycan chains typical of mucins.

Contrary to expectations, depletion of FMG1 increases the ability of cells to adhere to surfaces in our flow-based and microsphere assays. This suggests that in contrast to the current understanding of FMG1 as an adhesion promoter, the molecule likely acts as an adhesion regulator to avoid unintentional adhesion. Mutation of a gliding associated kinase GDAK has been implied to be sufficient to inhibit adhesion and microsphere binding in the presence of FMG1^[20,21] and ciliary-mediated adhesion is modulated by light, with blue-light inducing cells to adhere while red light induces detachment. Importantly, the pronase treatment of cells under either light condition has further proposed protection of the peptidergic component required for adhesion under red light.^[22]

The ability to adhere to a surface is inherently required for gliding motility driven by IFT. Fundamentally, a single IFT train which is propelled along the axoneme has to transduce a force through the ciliary membrane and from there onto an extracellular surface to produce a relative motion. As the most abundant and the outermost positioned component of the ciliary coat, FMG1 has previously been thought to be a candidate to transduce this force.^[4] We show here that the complete absence of the outer ciliary coat does not cause any significant change to the ability of a cell to move by gliding motility. This indicates that FMG1 is not required for force transduction through the membrane. We cannot exclude that FMG1 together with other transmembrane components modulate IFT binding properties and act as force transducing elements.

The N-glycosylation inhibitor tunicamycin has been shown to impede cilia-microsphere interaction and adhesion forces are significantly reduced in mutants with altered N-glycan composition, suggesting that potential further adhesive candidates are likely to be N-glycosylated proteins.^[2,8] Besides FMG1, eight ciliary membrane proteins have been shown to be N-glycosylated of which FAP113 and PKD2, likely in a complex with mastigonemes, have already been implicated in ciliary surface interaction.^[23,24] Neither single knockouts of FAP113^[23] and PKD2/mastigoneme^[24] nor any combination of knockouts of FMG1A/FMG1B induced a detectable change in the ability of cells to glide it is therefore unlikely that either of these proteins is a key component of the gliding machinery. The remaining N-glycosylated ciliary proteins are namely: FAP170, FAP211, FAP212, FAP102, FAP24, and PKHD1.^[9] Additionally, there likely exist further ciliary membrane proteins that we have not yet been able to

identify with our current methods. Of particular interest among the identified candidates are FAP102, which contains two predicted fasciclin (FAS1) domains, and PKHD1. FAS1 domains are ancient cell adhesion molecules found in bacteria, yeast, plants, and mammals^[25] and have been identified as putative cell-surface adhesion-promoting proteins in the diatom *Phaeodactylum tricornutum*.^[26] Finally, the transmembrane protein PKHD1 has potentially sufficient size to induce significant motions in the ciliary membrane/coat to induce gliding and additionally has a sizable predicted intraciliary domain of 541 amino acids which could potentially bind IFT and could therefore be an interesting candidate for future experiments.

In nature, *C. reinhardtii* cells likely navigate through water rich in particles such as sand, wood, and fibers.^[27] Uncontrolled adhesion of such particles to cilia, as observed with polystyrene beads in this case, could significantly impair the motility of the cells. However, in environments like soil or silt, where water is confined to capillary microbridges between grains, the cells are likely capable of traversing dry patches by gliding when swimming is not an option. We conclude that FMG1 provides the essential adhesion-regulating properties needed to efficiently navigate through such diverse environments.

4. Experimental Section

Materials Availability: Strains and plasmids generated in this study have been deposited to the Chlamydomonas Resource Center. The collection numbers for the strains deposited are CC-6221 fmg1b, CC-6222 fmg1a-fmg1b, CC-6223 fmg1b fmg1a ift46::NIT IFT46-mNG, CC-6224 FMG1A-mScarlet-I FMG1B-mNeonGreen. These are also available upon reasonable request.

Experimental Model Details—Chlamydomonas Strains and Cell Culture Conditions: Chlamydomonas strains CC-4533 and CC-4533 fmg1b derive from the Chlamydomonas Library project. CC-124 (32M) was kindly provided by Susan Dutcher and used as background for newly generated CRISPR/Cas mutants in this work. ift46::NIT IFT46-YFP (HS211^[28]) was kindly provided by Kaiyao Huang. Cells were grown photoheterotrophically in tris-phosphate-acetate (TAP) medium in dark:light cycle 8 h:16 h at 50 $\mu\text{mol photons}\times\text{s}^{-1}\times\text{cm}^{-2}$. Strains were maintained on 1.5% TAP agar plates and kept either in incubators under light or in aluminum-coated trays under LED light bars.

Method Details—CRISPR/Cas Mutation: Mutants generated in this work were created by CRISPR/Cas-assisted precision genome editing, following the methods described in our previous work.^[29,30] Briefly, cells were grown on TAP 1.5% agar plates in 10 h:14 h dark:light under overhead LED illumination and harvested in the active growth phase by scraping into liquid TAP medium. Cell walls were removed by three rounds of autolysin treatment, followed by three rounds of washing with TAP + 40mM sucrose. All centrifugation steps were performed at 700 RCF for 3 min. About $5\cdot 10^6$ cells were mixed with 5 μL of 5 μM RNPs and 1.5 μg of donor DNA, electroporated in an Invitrogen Neon Electroporator with three pulses of 2300 V for 12 ms, then dispensed into 1 mL of TAPS in a 24 well plate for overnight recovery. Recovered reactions were plated on selective antibiotics (7.5 $\mu\text{g mL}^{-1}$ Nourseothricin, 100 $\mu\text{g mL}^{-1}$ Spectinomycin or 10 $\mu\text{g mL}^{-1}$ Paromomycin). Resulting colonies were picked into 96 well plates, grown up, and prescreened with primers flanking the insertions by qPCR on a QuantStudio 7 Pro. Identified candidate insertions were then amplified by PCR and sequenced by Sanger or nanopore sequencing (Eurofins or Plasmidsaurus respectively). CC-124 fmg1b-fmg1a was produced by an intermediate CC-124 fmg1b step, while CC-124 FMG1A-mScarlet-I FMG1B-mNeonGreen was produced in the background of CC-124 FMG1B-mNeonGreen (CC-6012).

Method Details—Cilia Isolation: Cilia isolation from cultures in the mid-log growth phase was performed as described elsewhere by the pH shock method.^[31] Pellets containing clean cilia samples were stored at -80°C until further use for sample preparation for mass spectrometric analysis.

Method Details—Sample Preparation for Mass Spectrometric Analysis: Cilia and whole cell samples were reconstituted in lysis buffer (Tris/HCl (100 mM, pH 8), SDS (2% v/v), PMSF (1 mM), Benzamidine (1 mM)) and subjected to sonication for 10 min. After pelleting cell debris, the protein concentration was determined using the bicinchoninic acid assay (BCA Protein Assay Kit by Thermo Scientific Pierce). Volumes corresponding to 60 μg of protein were tryptically digested and desalted as described elsewhere.^[32] For disulfide analysis cilia were reconstituted in lysis buffer + 1% Igpal, reduction of proteins was omitted before digestion with trypsin or chymotrypsin.

Method Details—Mass Spectrometry: Tryptic peptides were reconstituted in acetonitrile (2% v/v) / formic acid (0.1% v/v) in ultrapure water and separated with an Ultimate 3000 RSLCnano System (Thermo Scientific). Subsequently, the sample was loaded on a trap column (C18 PepMap 100, 300 $\mu\text{m} \times 5\text{ mm}$, 5 mm particle size, 100 $\text{\AA}$ pore size; Thermo Scientific) and desalted for 5 min using TFA (0.05% v/v) / acetonitrile (2% v/v) in ultrapure water with a flow rate of 10 $\mu\text{L min}^{-1}$. Following, peptides were separated on a separation column (Acclaim PepMap100 C18, 75 mm i.d., 2 mm particle size, 100 $\text{\AA}$ pore size; Thermo Scientific) with a length of 50 cm. General mass spectrometric (MS) parameters are listed in Table S2 (Supporting Information).

Method Details—Adhesion Analysis: Cells were harvested at 1000 RCF for 30 s and subsequently resuspended in fresh TAP or HEPES/NMG buffer consisting of HEPES (5 mM), KCl (1 mM), HCl (1 mM), EGTA (200 μM) and pH adjusted to 7.4 with N-methyl-D-glucamine. Reconstituted cells were following transferred to ibidi polymer channel slides with a height of 0.4 mm. To give cells time to adhere and recover from centrifugation, mounted channels were incubated for 10 min before connecting them to the ibidi pump system and transfer to the microscopy chamber. The unidirectional flow was applied as soon as recording was started with 0.8 frames/sec using the 488 nm laser at 0.5% power as light source and a 40x magnification. Cells measured in TAP medium were analyzed at a constant flow rate of 3.77 mL min^{-1} . Cells measured in HEPES/NMG devoid of calcium were subjected to computer-controlled stepwise increasing pump pressure every 30 s.

Pump pressure [mbar]	Flowrate [mL min^{-1}]	Duration [s]
5	3.77	25
10	7.38	30
20	14.18	30
40	26.28	30
60	36.72	30
80	45.83	30
95	51.94	∞

Method Details—TIRF Microscopy: TIRF microscopy was applied to assess gliding behavior of *C. reinhardtii* strains expressing fluorescently tagged IFT46. Therefore, cell densities were adjusted to $10^5\text{ cells mL}^{-1}$ in TAP. Samples were loaded to a glass bottom microscopy chamber and refreshed every 20 min while imaging. TIRF microscopy was performed at room temperature with a Nikon Eclipse Ti and a 100x objective. IFT46::YFP/mNG was excited at 488 nm and fluorescence was recorded with an iXon Ultra EMCCD camera (Andor). For analysis, images were captured with NIS-Elements software over 30 s at 10 fps.

Method Details—Spinning-Disk Microscopy: Cells were deposited on a cover slide in a custom holder and imaged on an Olympus IX83 platform using an Olympus 100x/1.4 U Plan SApo Oil immersion objective and a Yokogawa CSU-W1 spinning disk scan head with two attached Andor iXon Ultra 888 cameras resulting in images with a pixel size of 79 nm. Z-stacks were acquired using a piezo-driven Prior Pro Scan III stage.

Method Details—Microsphere Binding Assay: An equal number of cells of CC-124 *fmg1b-fmg1a* and CC-124 *FMG1A-mScarlet-FMG1B-mNeonGreen* were merged and washed twice in TAP-medium before an excess amount of thoroughly TAP-washed polystyrene microspheres (0.2 μm) were added to the cell suspension. After 15 min of incubation under gentle agitation in light, samples were fixed with glutaraldehyde (0.2% v/v) and directly subjected to microscopic analysis.

Method Details—Single Particle Analysis: FMG1B was purified by affinity chromatography using an FPLC system (Cytiva AktaPure). Specifically, cilia were isolated from 20 L of *fmg1-a* bubbling culture in 14h/10h light/dark to ensure the presence of only one isoform. Cells were concentrated for 10 min at 1200 RCF in at F8S-6x1000y rotor and resuspended in roughly 50 mL of HEPES (10 mM) per liter of culture, then pooled and centrifuged again for 10 min at 1200 RCF before resuspending to a total of 1.5 L with HEPES (10 mM) supplemented with CaCl_2 (300 μM). Decantation was induced by adding acetic acid (11.25 mL, 1 M) while stirring, followed by neutralization with NaOH (11.25 mL, 1 M), sucrose as osmolyte (150 mL, 50% w/v), MgSO_4 (6 mL, 1 M), EDTA (1.5 mL, 500 mM) and PMSF (10 mL, 100 mM). Cells were then spun out in two centrifugation steps of 10 min at 1400 RCF and the supernatant containing the cilia was collected. Isolated cilia were then concentrated by centrifugation at 30 kRCF for 30 min at 4°C and resuspended in ConA binding buffer (HEPES (10 mM) pH 7.2, NaCl (500 mM), MnCl_2 (1 mM), CaCl_2 (1 mM)) to a total of 8 mL, followed by membrane lysis with 0.1% final concentration IGEPAL CA-630. The lysate was clarified by 10 min of centrifugation at 16 kRCF in 2 mL tubes, followed by passing through a 0.22 μm syringe filter. The clarified lysate was loaded onto a 1 mL ConA sepharose 4B (Cytiva) column at 0.2 mL min^{-1} , washed with 20 mL of binding buffer + 0.1% IGEPAL followed by elution with a gradient of binding buffer mixed with 0M-1M sucrose over 20 mL at 1 mL min^{-1} . The purified FMG1B was then concentrated to 1 mL at $\approx 2\text{ mg mL}^{-1}$. To polish and passivate the protein, a Superose 6 column equilibrated in imaging buffer (10 mM HEPES, 300 mM NaCl) was loaded with 1 mL of imaging buffer + 10 mg of Amphipol A8-35, followed directly by adding 500 μL of FMG1B. Peak fractions were collected and concentrated to 500 μL at 0.8 mg mL^{-1} , then immediately plunged frozen on Quantifoil 1.2/1.3 grids at 1x, 2x, and 4x dilution on a Leica GP2.

The 4x diluted samples were screened on a Glacios and then imaged on a Krios G4 equipped with a Falcon4 camera. A total of 8010 images were acquired at $0.955\text{ \AA px}^{-1}$ with a total dose of $70\text{ e}^{-}\text{\AA}^{-2}$. Single particle processing was performed in CryoSPARC^[33] unless otherwise noted. Raw EER movies were motion corrected, CTF estimated by patch CTF, and particles were picked first by blob picking, classified, and used to train crYOLO^[34] for particle picking. Picked positions were then extracted again, classified over multiple rounds with solvent clamping and per-particle scaling and an initial model was estimated de-novo. Non-uniform refinement of 3.6 M particles yielded a density with 3.2 $\text{\AA}$ global FSC resolution, but due to the high flexibility of the structure, the local resolution of certain parts was much lower. 3Dflex refinement^[35] was performed with a manual segmentation using nine latent dimensions and resulted in a more uniform refinement. This volume was used as a reference for piecewise local refinement in 7 sub-volumes which were then combined into a final map with FSC resolution between 2.8 and 3.4 $\text{\AA}$.

An initial guess for the peptide model was generated using AlphaFold3. The result was locally well predicted but had an incorrect macro-structure. The initial prediction was manually manipulated to closely resemble the cryoEM density map in ChimeraX,^[36] then relaxed under the density by coarse grain molecular dynamics using IModFit.^[11] Finally, the model was fine-tuned on a per-residue basis by GPU assisted real-time molecular dynamics in ChimeraX using ISOLDE.^[12]

Method Details—Cryo-Electron Tomography: Chlamydomonas cells were frozen directly on the grid by applying a cell suspension and blotting away the excess before plunging into liquid ethane on a Leica GP2 plunge freezer. Grids were screened for cilia in open holes and acquired dose-symmetrically from -60 to 60 degrees in 2-degree increments. Images were acquired using a Krios G4 with a Falcon 4 camera at $3.06\text{ \AA px}^{-1}$ or $3.78\text{ \AA px}^{-1}$, 2.8 s exposure at a dose rate of $1.018\text{ e}^{-}\text{\AA}^{-2}\text{ s}^{-1}$ for a total of $2.85\text{ e}^{-}\text{\AA}^{-2}$ per image.

Pre-processing and tomogram reconstruction were done with the help of TOMOMAN. Raw EER files were motion-corrected in Relion, followed by CTF estimation with CTFFIND4 and finally automatic reconstruction at 4x binning with IMOD. For visualization purposes, tomograms were filtered with IsoNet^[37] deconvolution with a deconvolution strength and snrfalloff of 1. For tomogram segmentation (Figure 1C), the glycocalyx was masked by fitting the membrane along the cilium with custom python software with a closed spline which was then offset by a defined amount to get a mask containing the glycocalyx. Using this mask, densities and orientations matching a downscaled single-particle map of FMG1B were identified by template matching using GAPSTOP^[38] with GPU acceleration. Resulting peaks were filtered by filling in the predicted densities in a simulated tomogram while excluding particles with lower cross-correlation that would result in significant overlap. Resulting FMG1 positions were inspected in ChimeraX/ArtiaX^[39] and finally imported into Blender 4.1 where microtubules and membranes were manually modelled based on tomography slices.

Quantification and Statistical Analysis—Gliding Velocity and Distance: Obtained TIRF videos were evaluated by use of Fiji ImageJ^[40] KymographBuilder to determine gliding velocities and distances as described by Lechtreck et al.^[41] All gliding events (velocity > 0 $\mu\text{m s}^{-1}$) were included. Gliding velocities of 40 cells (161 gliding events) in *ift46::NIT IFT46-mNG* and 42 cells (219 gliding events) in *fmg1b-fmg1a ift46::NIT IFT46-mNG* were obtained and merged from three biological replicates. In total 60 gliding distances (20 per strain and replicate) were evaluated using ImageJ^[40] measure. Man–Whitney–U test was performed for statistical evaluation using OriginLabs Pro.

Quantification and Statistical Analysis—Adhesion Strength Comparison: Obtained videos were analyzed using Fiji ImageJ^[40] Frames were transformed into binary images and normalized intensity was plotted over time. Three biological replicates were performed. Data is shown as mean $\pm$ standard deviation. Student t-test was performed at time points 50, 100, 150, and 200 s using OriginLabs Pro.

Quantification and Statistical Analysis—Mass Spectrometry: For label-free protein quantification, if not further stated samples were measured in biological quadruplicates using standard, data-dependent acquisition. Protein identification and quantification were performed using Fragpipe default LFQ settings excluding MBR and allowing unique and razor peptides for quantification. LFQ data (combined_proteins.tsv) was analyzed using fragpipe-analyst developers version^[42] using MaxLFQ Intensity. Variance stabilizing normalization was allowed. Imputation was performed using Perseus imputation and False discovery rate (FDR) correction was carried out using the Benjamini–Hochberg method. Quantification based on single peptide identifications as well as proteins identified in less than 70% of replicates per group were excluded. N-glycopeptide identification and validation from ISF-MS/MS runs were performed using Ursgal as described elsewhere.^[43] Disulfide peptide identification and validation were performed using MaxQuant v2.0.3.1. N-terminal acetylation and methionine oxidation as well as carbamidomethylation of cysteines were allowed as variable modifications. Cysteine–Cysteine (–2.016 Da) was implemented as a potential cross-link.

Supporting Information

Supporting Information is available from the Wiley Online Library or from the author.

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Conflict of Interest

The authors declare no conflict of interest.

Author Contributions

L.M.H., A.P.N., G.P., and M.H. performed conceptualization. L.M.H. and A.P.N. performed methodology, visualization, and formal analysis, and wrote, reviewed, and edited the original draft. L.M.H., A.P.N., F.M., M. S., and H.E.F. performed investigation. L.M.H., A.P.N., G.P. and, M.H. performed reviewed and edited data curation. A.P.N., G.P. and, M.H. performed funding acquisition. J.R., A.v.A., G.P. and, M.H. performed resources. G.P. and M.H. performed supervision.

Data Availability Statement

All data reported in this paper will be shared by the corresponding authors upon request. Original gel images of all main figures are provided as supplementary data. The mass spectrometry proteomics was deposited to the ProteomeXchange Consortium via the PRIDE Ref. [44] partner repository with the dataset identifier PXD055593. TIRF and confocal microscopy data used in this paper have been deposited to Zenodo (doi:10.5281/zenodo.14892409). FMG1B peptide models have been deposited to RCSB PDB with the identifier 9GOS and single particle density maps have been deposited at EMDB with identifiers EMD-51499 (composite map), EMD-51661 (low-resolution consensus map) and focused refinements: EMD-51649, EMD-51650, EMD-51654, EMD-51655, EMD-51657 and EMD-51658. Code used to analyze cryo tomography data is included in supplemental data file S1. Any additional information required to re-analyze the data reported in this paper is available from the corresponding authors.

Keywords

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