Functional analysis of an individual IFT protein: IFT46 is required for transport of outer dynein arms into flagella

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Introduction

Intraflagellar transport (IFT), which is the bidirectional movement of particles within flagella, is required for flagellar assembly. IFT particles are composed of ~16 proteins, which are organized into complexes A and B. We have cloned *Chlamydomonas reinhardtii* and mouse *IFT46*, and show that *IFT46* is a highly conserved complex B protein in both organisms. A *C. reinhardtii* insertional mutant null for *IFT46* has short, paralyzed flagella lacking dynein arms and with central pair defects. The mutant has greatly reduced levels of most complex B proteins, indicating that *IFT46* is necessary for complex B stability. A partial suppressor mutation restores flagellar length to the *ift46* mutant. *IFT46* is still absent, but levels of the other IFT particle proteins are largely restored, indicating that complex B is stabilized in the suppressed strain. Axonemal ultrastructure is restored, except that the outer arms are still missing, although outer arm subunits are present in the cytoplasm. Thus, *IFT46* is specifically required for transporting outer arms into the flagellum.

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**Abbreviation used in this paper: IFT, intraflagellar transport.**

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In *Chlamydomonas reinhardtii*, IFT172 interacts with EB1, which is located at the tip of the flagellum (Pedersen et al., 2003, 2005), and an IFT172 temperature-sensitive mutant is defective in IFT particle turnaround at the tip of the flagellum (Pedersen et al., 2005); based on these results, it was proposed that IFT172 is involved in regulating the transition between anterograde and retrograde IFT (Pedersen et al., 2005). In mammalian cells, IFT20 was found to be unique among IFT particle proteins examined in that it is localized to the Golgi apparatus, as well as the cilium, and moderate knockdown of IFT20 reduced the amount of the membrane protein polycystin-2 in the cilium (Follit et al., 2006), suggesting that IFT20 is involved in trafficking of ciliary membrane proteins. Other than this, nothing is known about the specific roles of the IFT particle proteins and how, or even whether, they interact with specific cargos.

To obtain more information on the function of a specific IFT particle protein, we have focused on IFT46, which was previously briefly reported to be a complex B protein in *C. reinhardtii* (Cole et al., 1998). We have cloned and characterized IFT46 from *C. reinhardtii* and mouse, and find that it is a homologue of DYF-6, a protein very recently reported to undergo IFT in *Caenorhabditis elegans* and to result in truncated dendritic cilia when mutated in the worm (Bell et al., 2006). We also describe the phenotype of a *C. reinhardtii*-null mutant for IFT46, and of a suppressor of that mutant. The observations provide new insights into the role of IFT46 in IFT particle stability and transport of a specific IFT cargo. Portions of this work were previously reported in abstract form (Hou et al., 2005).

### Results

#### Cloning of *C. reinhardtii* IFT46

The gene and cDNA encoding *C. reinhardtii* IFT46 were cloned as described in Materials and methods. The cDNA (accession no. DQ787426) contains a 1,035-nt ORF predicted to encode a 37.9-kD protein (Fig. 1 A) with a pI of 4.61. The cDNA has a stop codon 18 nt upstream of the predicted start codon, and a polyA consensus sequence at nt 1,703–1,707. ESTs have a polyA tail 12–14 nt downstream of the polyA consensus sequence. Therefore, the ORF is complete. No structural domains or motifs were identified within the sequence.

IFT46 was initially identified as an IFT complex B protein, based on its cosedimentation with other complex B proteins.
in sucrose gradients (Cole et al., 1998). Characterization of our cloned protein indicates that it behaves exactly as expected of a 46-kd complex B protein, as follows: a) six unique peptides corresponding to the cloned protein were identified in the membrane plus matrix fraction of the flagellar proteome, but no peptides from it were found in any other fraction, which is a distribution typical for IFT particle proteins but unusual for non-IFT proteins (Pazour et al., 2005); b) using real-time PCR, we found that expression of the protein is up-regulated 10.4 ± 2.03-fold (SEM) upon deflagellation, which is characteristic of flagellar proteins, including other complex B proteins (Pazour et al., 2005); c) an antibody to a peptide contained in the cloned protein was generated and shown to react specifically with a single protein of Mr, ~46,000 in Western blots of whole cell lysates (Fig. 1 B); d) immunofluorescence microscopy with the antibody as probe showed that the majority of the cloned protein is located in the basal body region, with a lesser amount in puncta along the length of the flagella (Fig. 1 C), is a distribution identical to that of other IFT particle proteins (Cole et al., 1998; Deane et al., 2001); moreover, the protein colocalized with complex B protein IFT172, but not complex A protein IFT139 (see the section Complex A and B proteins are located in distinct compartments in the basal body region; Fig. 6 B); and e) when the flagellar membrane plus matrix fraction was analyzed by sucrose density gradient centrifugation, the cloned protein co-migrated precisely with IFT81, a complex B protein, when the flagellar membrane minus matrix fraction was analyzed by sucrose density gradient centrifugation, the cloned protein co-migrated precisely with IFT81, a complex B protein, and confirmed that IFT46 is a complex B protein.

**IFT46 is highly conserved**

Database searches revealed that IFT46 is conserved across organisms that have cilia, including Danio rerio (XP_694278; BLAST E, 1e-47), Apis melifera (XP_396519; BLAST E, 1e-47), Drosophila melanogaster (NP_609890; BLAST E, 1e-17), Mus musculus (NP_076320; BLAST E, 2e-61), and Homo sapiens (CAB66868; BLAST E, 8e-62). The protein is also homologous to C. elegans Dyr-6 (NP_741887; BLAST E, 9e-34), which was recently reported to undergo IFT in dendritic cilia when fused to GFP (Bell et al., 2006). No similar sequence was found in nonciliated organisms, including Saccharomyces cerevisiae and Arabidopsis thaliana.

The middle portions of the C. reinhardtii and mammalian proteins are highly similar (51% identity, 72% similarity; Fig. 1 A), making it likely that they are orthologous proteins. To test this, the putative mouse orthologue was Flag tagged and expressed in IMCD3 cells, a mouse kidney cell line. Immunofluorescence microscopy revealed that the Flag-tagged protein localized specifically to primary cilia (Fig. 2 A). To determine if the mammalian protein was part of IFT complex B, lysates were prepared from IMCD3 cells expressing either IFT46-Flag, IFT20-Flag (positive control), or GFP-Flag (negative control) and immunoprecipitated with an anti-Flag antibody. In each case, the Flag-tagged proteins were highly enriched in the immunoprecipitates (Fig. 2 B, top). Western blots showed that complex B proteins IFT88 and IFT57, but not complex A protein IFT140 or a control protein, were coimmunoprecipitated from lysates of the IFT46-Flag–expressing cells (Fig. 2 B, bottom). Similarly, in the positive control, IFT88 and IFT57, but not IFT140, were coimmunoprecipitated. No IFT proteins were coimmunoprecipitated from the lysates of cells expressing GFP-Flag. Therefore, mammalian IFT46 localizes to cilia and is tightly associated with complex B proteins, but not with complex A proteins.

**IFT46 is necessary for flagellar assembly**

To investigate the role of IFT46 in intraflagellar transport, we screened a collection of C. reinhardtii insertional mutants by Southern blotting and identified one strain, T8a44-11, with a defect in the IFT46 gene. Analysis by PCR showed that the mutant allele, which we term ift46-1, has a deletion or disruption somewhere between the fourth and the seventh exon of the IFT46 gene (Fig. 3, A and B). This mutant has short, stumpy flagella.

Strain T8a44-11 was backcrossed to wild-type cells, and a progeny, YH6, which lacked the pJ mutation carried by the parental strain, was selected for detailed characterization. As in T8a44-11, the IFT46 gene in YH6 is disrupted, as shown by Southern blotting (Fig. 3 C, lane 2). No IFT46 can be detected in lysates of YH6 cells (Fig. 3 D, lane 2), indicating that IFT46 is not expressed in YH6 cells. Thus, the mutant allele is a null allele (see also the section The 3' end of the IFT46 gene is
transcribed in Sup1441 cells). Like T8a44-11, YH6 cells have short, stumpy flagella that barely extend beyond the flagellar collar (Fig. 4). The flagella are nonmotile.

To confirm that the mutant phenotype of YH6 was caused by the disruption of the IFT46 gene, YH6 cells were transformed with a 4.8-kb fragment containing only the wild-type IFT46 gene (Fig. 3 A). Numerous wild-type swimmers with full-length flagella were recovered. Southern blotting revealed that the exogenous IFT46 gene had integrated into the genome at different sites in several of these rescued strains (Fig. 3 C, lanes 3–9), confirming that the rescued strains were independently derived. Therefore, restoration of motility was caused by incorporation of the transgene, and not caused by disruption of some other gene. Western blotting confirmed that expression of IFT46 was restored in the transformants (Fig. 3 D, lanes 3–9). These results demonstrate that the short flagella phenotype of YH6 is caused by the absence of IFT46. Hereafter, this strain will be referred to as the ift46 mutant.

The ift46 mutant has unique defects in its axoneme

Although very short, ift46 flagella are longer than those of mutants with defects in the complex B proteins IFT88 (Pazour et al., 2000) and IFT52 (Brazelton et al., 2001), which do not form flagella beyond the transition region. Because flagella are formed in the ift46 mutant, we were able to compare them with flagella from wild-type and rescued cells by EM to identify flagellar defects associated with loss of IFT46. Serial sections of wild-type flagella have shown that the outer doublet microtubules are connected by rodlike “peripheral links” in the most proximal part of the flagella (Fig. 4 A, a); the rows of dynein arms begin at a level slightly more distal, but still within the flagellar collar (Fig. 4 A, b; Hoops and Witman, 1983). The ift46 flagella have nine outer doublet microtubules and frequently extend to the limits of the flagellar collar or beyond (Fig. 4 A, f–p), but we never observed dynein arms in longitudinal or cross sections of these axonemes. In addition, the mutant flagella lack the projections into the lumens of the B-tubule (Hoops and Witman, 1983) and frequently have defects in the central pair of microtubules (Fig. 4 A, f–k). In contrast to mutants with defects in the retrograde IFT motor (Pazour et al., 1999; Porter et al., 1999; Hou et al., 2004), few, if any, IFT particles accumulate in the ift46 mutant flagella. It is important to note that the flagella from the rescued cells (Fig. 4 A, d and e) have typical wild-type morphology with normal inner and outer dynein arms and central pair microtubules; this confirms that

Figure 3. The nonmotile phenotype of YH6 is caused by a null mutation in the IFT46 gene. (A) IFT46 gene structure. There are two PstI sites (P) within the IFT46 gene. Three primer sets used for PCR to map the mutation region in the mutant are indicated by arrowheads. Regions corresponding to the ~4.8-kb genomic fragment used for rescue experiments, the cDNA probe used for screening the mutant collection, and the genomic DNA probe used for Southern blotting also are shown. (B) PCR results using primers to different regions of the IFT46 gene showed that strain T8a4-11 is defective in the middle portion of the gene. (C and D) The nonmotile phenotype of YH6, which is an offspring of a cross between T8a4-11 and wild-type cells, was rescued by transforming the mutant cells with the wild-type IFT46 gene. Genomic DNAs from wild-type cells, YH6, and rescued cells were cut by PstI and analyzed by Southern blotting using an IFT46 genomic DNA probe (C). The rescued cells (6R29 through 6R38) have the 1.5-kb fragment originating from the transgene (the 1.9-kb fragment is missing because it was not present in its entirety in the transgene) and two hybridizing bands (∗) originating from the mutated ift46 gene. They also have other hybridizing bands, indicating that the IFT46 transgenes were incorporated at different sites. Western blots of whole cell lysates (D) show that YH6 cells lack the IFT46 protein and that the rescued cells express IFT46 protein. The same blot was stripped and probed with an anti-tubulin antibody as control (bottom).
the ultrastructural defects seen in the mutant are caused by loss of IFT46.

To determine whether the dynein arm deficiency in the ift46 mutant is caused by degradation of dyneins within the cell body, by an inability to transport dyneins into the flagella, or by an inability to assemble them onto the axonemes, we analyzed whole cell lysates and flagella from ift46 and wild-type cells by Western blotting (Fig. 4 B). The cell lysates of the mutant contained normal levels of the outer arm dynein intermediate chain IC2 and the inner arm dynein intermediate chain IC138. Therefore, the dyneins are present in the mutant cells. However, both IC2 and IC138 were completely absent from the ift46 mutant flagella, indicating that the dyneins are not transported into the flagella. In contrast, DC2, which is a component of the outer dynein arm docking complex that is transported into the wild-type flagellum and assembled onto the doublets independently of the outer dynein arm (Wakabayashi et al., 2001), is transported into the ift46 flagella. The presence of DC2 in the flagella provides additional evidence that the lack of dynein arms is not simply because of the short length of the mutant flagella or to a general failure to transport proteins into the flagellum. These data confirm that the ultrastructural findings that the ift46 mutant has a defect in transporting dynein arms into the flagella.

**IFT complex B is unstable in the absence of IFT46**

To investigate the role of IFT46 in IFT complex assembly, we examined the cellular levels of IFT complex B and A proteins in cell lysates of wild-type and ift46 cells (Fig. 5, lanes WT and ift46). When normalized with tubulin, the levels of complex B proteins IFT20, IFT57, IFT72, and IFT81 were greatly decreased in the mutant cells relative to the wild-type cells. The only complex B protein not reduced in the absence of IFT46 was IFT172, the level of which was the same as or greater than in wild-type
cells, depending on the preparation, suggesting that the level of IFT172 is controlled independently from that of the other complex B proteins. In contrast to the decrease in most complex B proteins seen in the ift46 mutant, the levels of complex A proteins IFT139 and IFT140 were greatly increased in ift46 cells relative to wild-type cells.

To examine if these differences in protein levels were caused by changes in synthesis or stability, we used real-time RT-PCR to measure transcript levels for several complex A and B proteins in wild-type and ift46 cells. Transcript levels in the mutant were increased by ~2.8- and ~2.0-fold for complex A proteins IFT140 and IFT139, and by ~1.8- and ~1.6-fold for complex B proteins IFT81 and IFT72, respectively. Therefore, the mutant responds to its defect by increasing the mRNA levels of at least these complex A and B proteins. The increase in complex A proteins in the mutant presumably reflects this increase in mRNA abundance. However, because the levels of most complex B proteins are drastically decreased in the mutant, even though complex B mRNA levels in general appear to be increased, it is likely that these proteins are specifically degraded in the absence of IFT46.

**Complex A and B proteins are located in distinct compartments in the basal body region**

To determine if the absence of IFT46 and the accompanying large decrease in most other complex B proteins affected the transport of IFT172 or complex A into or out of the flagellum, we used immunofluorescence microscopy to examine ift46 cells that were double labeled with antibodies to tubulin and IFT172 or IFT139 (Fig. 6 A). In both cases, the IFT particle proteins were concentrated around the basal bodies and in the short flagella. Thus, both proteins are transported into the flagella in the absence of IFT46. Surprisingly, however, the distributions of IFT172 and IFT139 differed from each other in the cell body, with that of IFT172 (Fig. 6 A, a–d) appearing to have almost no overlap with that of IFT139 (Fig. 6 A, e–h), which was more anterior and often concentrated into two distinct lobes.

To clarify whether this difference in distribution was normal or caused by loss of IFT46, wild-type cells were double labeled with antibodies to IFT46 and IFT172 or IFT139. In most cases, IFT46 and IFT172 coloculated precisely with each other in the peribasal body region (Fig. 6 B, a–c), which is consistent with the other evidence that IFT46 is a complex B protein. In contrast, although IFT139 colocolated with IFT46 at the extreme apical end of the cell, the labeling of IFT46 almost always extended more posteriorly than that of IFT139 (Fig. 6 B, d–f). This is the first observation that complex A and B proteins differ in their distribution, and indicates that the complexes, or at least a subset of them, are not physically associated in the cell body. This, together with the results for the ift46 mutant, also shows that in the absence of IFT46, the colocalization of IFT172 with complex A proteins at the extreme apical end of the cell is lost.

Our observation that IFT172 was transported into the short flagella of the ift46 mutant (Fig. 6 A) raised the question of whether IFT172 was being transported into the flagella independently of other complex B proteins or in association with incomplete complex B particles, possibly assembled from the small amount of complex B proteins still present in the mutant. To address this question, we used immunofluorescence microscopy to examine the distribution of another complex B protein, IFT57, the levels of which are greatly reduced in the mutant. Like IFT172, the residual IFT57 was transported into the short flagella of the ift46 mutant (Fig. 6 C). These results support the hypothesis that a small number of incomplete complex B particles assemble from the residual complex B proteins and are capable of being transported into the flagellum in the absence of IFT46. The resulting low level of IFT may account for the ability of the ift46 cells to assemble their short flagella.

**Loss of IFT46 is specifically correlated with loss of the outer dynein arm in a partially suppressed strain**

Ift46 cells are completely nonmotile. However, on one occasion, swimming cells were observed in an unaerated, stationary phase culture of ift46 cells. Cells from this culture were cloned, and a partially suppressed strain, Supift461, was isolated. Supift461 cells are usually nonmotile when grown in M media with aeration, but are stimulated to form flagella of variable length (Fig. 7) and swim with a slow jerky movement in the absence of aeration. The suppressed phenotype is the result of a rare spontaneous mutation that allows transcription of the 3′ end of the IFT46 gene (see next section).

To elucidate the effect of the partial suppressor mutation on IFT46 and other IFT particle proteins, the levels of the
proteins in stimulated Sup_{if46}1, wild-type, and if46 cells were compared by Western blotting. In the Sup_{if46}1 cells, complex B proteins IFT20, IFT57, IFT72, and IFT81 were increased to a level between those of if46 and wild-type cells (Fig. 5), whereas the levels of the complex A proteins IFT139 and IFT140 were decreased to a level between those of if46 and wild type. Importantly, IFT46 is still undetected in the suppressed strain. This result indicates that the partial suppression of if46 involves an increased stability of IFT complex B in the absence of full-length IFT46. It is possible that a C-terminal fragment of IFT46 is expressed in Sup_{if46}1 cells and incorporated into complex B, thereby stabilizing it. Such a fragment would not be detected by our antibody to the N terminus of IFT46.

The slow, jerky swimming of Sup_{if46}1 is typical of outer dynein arm mutants. Therefore, we used immunofluorescence microscopy to check for the presence of outer and inner dynein arms in Sup_{if46}1 flagella. No outer arm dynein was detected using an antibody to the α heavy chain of outer arm dynein (Fig. 7 A, a–i). In contrast, labeling of Sup_{if46}1 flagella by an antibody to inner arm dynein I1 intermediate chain IC138 was normal (Fig. 7 A, j–r). These results show that transport into the flagellum of inner arm dynein I1, but not outer arm dynein, is restored in the suppressed strain.

To determine the extent to which the ultrastructural defects of if46 were restored in the partially suppressed strain, Sup_{if46}1 cells and flagella were examined by electron microscopy (Fig. 7 B). The inner arms, radial spokes, and central microtubules were present and appeared normal. However, no outer dynein arms were observed. Therefore, the suppressor strain assembles flagella that lack the outer dynein arm but appear normal in every other way. Western blotting showed that the levels of both outer arm dynein and outer dynein arm docking complex proteins, as

![Image of Western blotting results](https://example.com/ift46_result.png)
represented by IC2 and DC2, respectively, were normal in Supift461 cells (Fig. 5). Thus, the inability to transport and assemble outer arms in the flagella is not simply caused by an absence of these components from the cell cytoplasm. These results indicate that IFT46 is specifically needed to transport outer dynein arm components into the flagellum. The inner dynein arm and central pair defects observed in the ift46 mutant are likely attributable to a more general deficiency in IFT caused by the reduced number of complex B particles.

The 3′ end of the IFT46 gene is transcribed in Supift461 cells

Analysis by PCR revealed that the suppressor mutation involved a rearrangement or deletion somewhere in the region between the 3′ end of the inserted NIT1 gene and the seventh intron of the IFT46 gene (unpublished data). To determine if this mutation caused a change in the transcription of the IFT46 gene, wild-type, ift46, and Supift461 cells were examined by real-time PCR using primer pairs designed to assay for the presence of the 5′ end, middle, and 3′ end of the IFT46 mRNA (Fig. 8). In wild-type cells, all three regions were detected. In the ift46 mutant, only the 5′ end was detected, indicating that the 5′ end of the gene is transcribed, but a full-length mRNA is not made. Because our antibody to the N terminus of IFT46 did not detect a product, it appears that the truncated mRNA is not translated into a stable protein. This provides further evidence that ift46 is a null allele. In Supift461 cells, both the 5′ and the 3′ end, but not the middle, were reproducibly detected. Therefore, the suppressor mutation results in transcription, and possibly translation, of the 3′ end of the IFT46 gene. Our antibody would not detect a product containing the C-terminal end of IFT46, but lacking its N-terminal end. However, we can rule out the possibility that the suppressor mutation results in translation of the N-terminal part of IFT46 fused with the C-terminal part of IFT46, because our antibody did not detect any product in Supift461 cells. Transcripts encoding the 3′ end of the IFT46 gene were detected in Supift461 cells in both the presence and absence of aeration, so the suppressor mutation, not stress, causes transcription of the 3′ end of the gene.

Discussion

The C. reinhardtii IFT46 sequence, which is reported for the first time in this study, demonstrates that this protein, like other IFT particle proteins, is highly conserved among ciliated organisms. C. reinhardtii IFT46 was previously reported to cosediment with other IFT complex B proteins (Cole et al., 1998). We confirm that IFT46, in both C. reinhardtii and mammals, is a complex B protein based on cosedimentation, coimmunolocalization, and coimmunoprecipitation with other complex B, but not complex A, proteins. Our analysis of a C. reinhardtii ift46 mutant and a suppressed strain of the mutant indicate that IFT46 is necessary for complex B stability and is specifically required to transport outer dynein arm complexes into the flagellum.

Our sequencing of C. reinhardtii IFT46 also revealed that it is a homologue of C. elegans DYF-6 (Starich et al., 1995), the sequence of which was recently reported by Bell et al. (2006).
IFT46 is required for transport of outer arm dynein arms into flagella

In addition to being very short, ift46 flagella have defects in central pair and dynein arm assembly. Aspects of this phenotype are undoubtedly caused by the greatly reduced amount of complex B in the ift46 mutant. Because there is not enough IFT machinery to transport a full complement of axonemal proteins, the flagella are short and assembly of specific axonemal structures is affected.

However, our discovery of a suppressor mutation that stabilizes complex B in the absence of full-length IFT46 and subunits, as well as of the peripheral subunits other than IFT172. This is in contrast to the situation when another complex B core protein, IFT88, is disrupted; loss of this protein in an ift88 mutant had little or no effect on the levels of IFT172 and IFT81, but caused a significant decrease in IFT57 (Pazour et al., 2000). This difference suggests that although IFT46 and IFT88 may both be components of the complex B core, the former is essential for the core’s stability, whereas the latter is not. IFT46 is required for the stability of IFT81, and presumably IFT88, but the stability of IFT81 is not dependent on IFT88, in agreement with a model in which IFT81 and IFT88 are in different domains of the core (Lucker et al., 2005), and suggesting that the assembly or stability of both core domains is dependent on IFT46. Because IFT57 is a peripheral protein, it requires either an intact complex B core or direct interaction with IFT88 for its stability.

The ift46 mutant can form very short flagella with normal outer doublet microtubules, a phenotype that is distinct from that of the other published C. reinhardtii IFT complex B–null mutants, ift88 and ift52, which are bald with axonemal structures extending beyond the transition zone (Pazour et al., 2000; Brazelton et al., 2001). No information is available on how loss of IFT52 affects the other complex B proteins. However, one possible explanation for the difference between the ift46 and ift88 mutants is that the residual complex B proteins in both mutants form incomplete complex B particles, and that those formed in the absence of IFT46 have some functionality, whereas those formed in the absence of IFT88 are completely unable to form a flagellum. This could occur if IFT46 served primarily to transport a nonessential axonemal protein, such as outer arm dynein, but IFT88 was necessary for transport of a protein, such as tubulin, which is absolutely necessary for axonemal assembly.

It is of interest that the level of IFT172 in the ift46 mutant did not show the decrease observed for the other complex B proteins. IFT172 also differs from the other complex B proteins in that it readily dissociates from the rest of the complex B particle during sucrose gradient centrifugation (Fig. 1 D; Cole et al., 1998), and that it interacts with the C. reinhardtii microtubule end–binding protein CrEB1 in a manner that does not require association with the other complex B proteins (Pedersen et al., 2005). Thus, IFT172 is unique in that its cellular level is regulated independently of other complex B proteins, that it binds relatively weakly to complex B, and that it can interact with other proteins independently of complex B.

IF46 is important for the stability of complex B

In the C. reinhardtii mutant lacking IFT46, levels of both complex A and B mRNAs increased relative to their levels in wild-type cells. This strongly suggests that the genes encoding proteins of both complexes are constitutively induced when the cell cannot assemble flagella. The mutant exhibited a corresponding increase in levels of complex A proteins. However, levels of complex B proteins other than IFT172 decreased in the mutant, suggesting that these proteins are broken down in the absence of IFT46. These results indicate that a) in the absence of IFT46, complex B is unstable; b) stability of complex A proteins is not dependent on the presence of complex B; c) the normal 1:1 stoichiometry between complex A and complex B proteins (Cole et al., 1998) is uncoupled in the absence of IFT46; and d) flagella assembly requires complex B, even in the presence of increased amounts of complex A.

Biochemical analysis (Lucker et al., 2005) has shown that complex B is composed of a 500-kD “core” that includes IFT88, IFT81, IFT74/72, IFT52, IFT46, and IFT27, and four “peripheral” subunits including IFT172, IFT80, IFT57, and IFT20. (The term “core” here refers to a group of proteins that are tightly associated with one another, and has no implication in regard to whether the proteins are or are not exposed on the surface of the IFT particles.) Our finding that IFT46 is required for the stability of all complex B proteins tested except for IFT172 is consistent with this model. In the absence of IFT46, the complex B core is destabilized, leading to degradation of the core
restores flagellar assembly, including assembly of the central pair and the inner dynein arms, but does not restore outer dynein arm assembly, even though outer arm proteins are present in the cytoplasm. Strongly argues that IFT46 has a specific role in outer dynein arm transport. This is the first direct evidence that the outer dynein arms require IFT for transport into the flagellum, and the first evidence connecting a specific IFT particle protein with a specific cargo. Because the outer arm components are preassembled in the cytoplasm into complexes as large as 1.2 MD (Fowkes and Mitchell, 1998), it is likely that IFT is needed to move them efficiently into the flagellum and out to the flagellar tip, which is the site of axonemal assembly (Witman, 1975; Johnson and Rosenbaum, 1992).

Further work will be necessary to determine if IFT46 is involved directly in outer arm binding, or if loss of IFT46 causes a conformational change in the IFT particle that eliminates an outer arm binding site at some distance from IFT46. However, the fact that the suppressor mutant has a partially stabilized complex B but still fails to transport outer arms into the flagellum strongly supports the first possibility. The first possibility is further supported by the recent finding that the human homologue of ODA16, which is a C. reinhardtii flagellar protein that is not a component of dynein but is essential for outer arm transport into the flagellum (Ahmed and Mitchell, 2005), interacts with the mouse homologue of IFT46 in a yeast two-hybrid system, and thus may be an adaptor coupling IFT46 to the outer arm (Ahmed et al., 2006).

Our finding that IFT is involved in transport of outer arm complexes explains a previous observation that antibodies to complex B proteins IFT52 and IFT72 communoprecipitated subunits of the outer dynein arm from a flagellar membrane plus matrix fraction (Qin et al., 2004). An earlier study had reported that inner dynein arms, but not outer dynein arms, required the activity of FLA10, which is one motor subunit of the anterograde IFT motor kinesin-2, for transport into the flagellum (Pipeño et al., 1996). There are at least two possible explanations for the difference between these results and our own. First, as discussed by Qin et al. (2004), the earlier studies used a fla10 temperature-sensitive mutant and observations 45–75 min after shift to the restrictive temperature, which may not have been adequate for complete cessation of FLA10 activity. Second and more interestingly, it is possible that there is more than one kinesin for anterograde IFT in C. reinhardtii, as there is in C. elegans (Snow et al., 2004). Phylogenetic analysis on complete kinesin repertoire of a diversity of organisms revealed that some kinesin families are specific for ciliated species (Wickstead and Gull, 2006). The C. reinhardtii kinesin-2 motor subunits FLA10 and FLA8 and the central pair kinesin KLP1, as well as several novel kinesins, were grouped in these subfamilies; two of the latter (C_250150 in the kinesin-9 family, and C_710026 in the newly proposed kinesin-17 family) were each identified by multiple hits to a single peptide (shared with FLA8) in the C. reinhardtii flagellar proteome (Pazour et al., 2005; http://labs.umassmed.edu/chlamyfp/protector_login.php). It is possible that one of the novel kinesins is an IFT anterograde motor, and that it and kinesin-2 transport IFT particles linked to different cargos.

We also observed that the outer dynein arm docking complex, as represented by its DC2 subunit, was transported into the ift46 mutant flagella. The movement of the docking complex, but not the outer dynein arm, into ift46 flagella is consistent with previous results that the docking complex is preassembled in the cytoplasm as a distinct complex not associated with the outer arm (Wakabayashi et al., 2001), and that it is transported into the flagellum independently of the outer arm (Takada and Kamiya, 1994; Wirschell et al., 2004). DC2 was communoprecipitated by antibodies to IFT particle proteins (Qin et al., 2004), indicating that it interacts with the IFT machinery and probably is dependent on it for transport into the flagellum. Our results clearly show that the docking complex does not specifically require IFT46 for entry into the flagellum.

Complex A and complex B occur in distinct, but overlapping, compartments in the basal body region

Complexes A and B are associated with each other in large linear assemblages during transport within the flagellum (Qin et al., 2004), and it has been proposed that turnover of IFT particle proteins and motors at the tip of the flagellum involves the dissociation of complex A from complex B, followed by their reassociation before retrograde transport (Pedersen et al., 2006). However, virtually nothing was known about the interactions of the complexes at the base of the flagellum. Our immunofluorescence microscopy observations have revealed different patterns of localization for complex A and complex B proteins in the wild-type cell, with the former localized more apically in the peribasal body region. In contrast, the complex B proteins IFT172 and IFT46 usually colocalized precisely with each other. These results suggest that complex A and complex B separate from each other upon passage from the flagellum into the cytoplasm, are sorted into separate albeit overlapping compartments, and are subsequently reassembled before their transport into the flagellum, in a reversal of the process proposed to occur at the tip of the flagellum. The region of overlap at the apical end of the peribasal body region may correspond to the basal body transition fibers, which are proposed to be docking sites where the IFT particles are assembled or disassembled before entry into the flagellum or cytoplasm, respectively (Deane et al., 2001; Rosenbaum and Witman, 2002). Within the cell body of the ift46 mutant, the IFT172 in excess over other complex B proteins localizes primarily to the posterior peribasal body region and has little or no overlap with IFT139 in the anterior peribasal body region, indicating that IFT172 does not interact directly with complex A in the cell body.

Our immunofluorescence microscopy studies also showed that both complex A and residual complex B proteins are transported into the short flagella of the ift46 mutant, indicating that even in the absence of suppression, transport of the IFT complexes into the flagella does not require ift46.

Stability of complex B in Supift461 cells may be caused by expression of the C-terminus of IFT46

Our analysis of the Supift461 cells revealed that they differ from ift46 cells in that the suppressor mutation causes transcription of the 3’ end of the IFT46 gene. This could come about as a
result of an intragenic mutation that allows transcription of the 3′ end of the IFT46 gene from the NIT1 promoter present in the vector originally used to generate the ift46 insertional mutant. Irrespective of the mechanism, the results suggest that the C-terminal portion of IFT46 is expressed, possibly as part of a fusion protein with nitrate reductase (encoded by the NIT1 gene). This fragment may then be incorporated into complex B, stabilizing it.

Expression of the suppressed phenotype was observed only in Supift461 cells grown in the absence of aeration. A possible explanation for this is that under stress conditions (hypoxia), a chaperone is produced that helps stabilize complex B. ift46 cells do not form flagella in the absence of aeration, so this hypothetical chaperone does not stabilize complex B in the complete absence of IFT46. It may be that a stress-induced chaperone can stabilize complex B in the presence of a C-terminal fragment of IFT46, but not in the absence of the fragment.

Flagella are formed in Supift461 cells, but the flagella lack the outer dynein arms. Therefore, if complex B is indeed stabilized by a C-terminal fragment of IFT46 in Supift461 cells, this would imply that the N-terminal end of IFT46 is essential for transport of outer arms into the flagellum.

Cells can compensate for defects in IFT complex B
Our identification of a partial suppressor of the ift46 phenotype is the second report of suppression of the phenotype resulting from disruption of a complex B protein. Brown et al. (2003) identified a spontaneous partial suppressor of a null mutant of IFT52 in Tetrahymena thermophila. The T. thermophila ift52-null mutant has basal bodies that fail to form flagella or form short flagella that lack the central pair of microtubules, whereas a variable number of cells of the partially suppressed strain had slightly longer flagella, of which ~13% had a central pair of microtubules, depending on growth conditions. Just as the suppressed phenotype of C. reinhardtii Supift461 was stimulated by lack of aeration, the suppressed phenotype of the T. thermophila strain was stimulated by pericellular hypoxia; suppression of the T. thermophila strain was also stimulated by growth at abnormally low temperature. This suppression differed from that which we observed, in that it arose spontaneously with high frequency, whereas ours was a rare event that was observed only once in 2 yr of culturing the cells; however, in both cases, the phenotype was stable during vegetative growth. Therefore, the mechanism of suppression may be similar in both C. reinhardtii and T. thermophila. In our case, Western blotting showed that the IFT protein levels in the partially suppressed strain were restored to levels between those of wild-type cells and the ift46 mutant cells, indicating that restoration of the ability to form flagella was caused by stabilization of complex B in the absence of full-length IFT46.

Materials and methods

Cells and culture media
C. reinhardtii strains 137c (nit1, nit2, mt+), CC124 (nit1, nit2, mt−), and S1D2 were obtained from the Chlamydomonas Genetics Center (Duke University, Durham, NC). T8a4-11 [ift46::NIT1, nit1, pf1, mt+] was generated by K. Kozminski and J. Rosenbaum (Yale University, New Haven, CT) by transforming KK30A3 [nit1, Nit2, pf1, mt+] with the plasmid pMN24 linearized with EcoRI. YH6 (ift46::NIT1, PF1, mt−) is an offspring of a cross between T8a4-11 and CC124. Supift461 is a spontaneous partial suppressor for YH6. Cells were grown in M (Sager and Granick [1953] medium I altered to have 0.0022 M KH2PO4 and 0.00171 M K2HPO4, M-N [M medium without nitrogen], or IAP (Gorman and Levine, 1965) media. Mutant IMCD3 cells (CLONTECH Laboratories, Inc.) were grown as described in Folli et al. (2006).

Antibodies
The antibodies used are listed in Table S1 (available at http://www.jcb.org/cgi/content/full/jcb.200608041/DC1). The rabbit antibody to IFT46 was generated against a synthetic peptide corresponding to the protein’s N-terminal 19 amino acids (Pocono Rabbit Farm) and affinity purified using the same 19 amino-acid peptide.

C. reinhardtii IFT46 gene cloning
165 IFT particles were purified from C. reinhardtii flagella (Cole et al., 1998) and the protein particles separated by PAGE. A band corresponding to IFT46 was excised and microsequenced. Two peptides, VPRPTKPD-YLVK and KPKPPDKPAPVCGIDETFK, were obtained; these identified the protein C2130037 predicted by the C. reinhardtii genome (v. 2; http://genome.jgi-psf.org/crg-bin/searchGRdb-chlre2). Several EST clones in Genbank that contain these two peptides in their ORF were used to clone the IFT46 cDNA. A 4.8-kb fragment that contains only the full-length IFT46 gene was cloned from C. reinhardtii genomic DNA after its amplification by PCR with primers IFT46-5 and IFT46-6 (the sequences of all primers are given in Table S2, available at http://www.jcb.org/cgi/content/full/jcb.200608041/DC1) using ELongase Enzyme Mix (Invitrogen). The sequences of the 5′- and 3′-UTRs of the IFT46 cDNA were verified by sequencing the cloned IFT46 gene; the sequence of the coding region was verified by sequencing a PCR product from a cDNA library.

IFT46 homologues were identified by searching the translated nr database at http://www.ncbi.nlm.nih.gov/BLAST/. Sequences were analyzed as described in Hou et al. (2004).

DNA and RNA isolation and analysis
DNA was isolated from C. reinhardtii as described in Pazour et al. (1998). DNA gel electrophoresis was carried out by standard procedures (Sambrook et al., 1989). Southern blotting was performed using the DIG High Prime DNA Labeling and Detection Starter Kit II (Roche); instead of using the kit’s hybridization buffer, we used Church buffer (7% SDS, 1 mM EDTA, and 0.25 M Na2HPO4, pH 7.2; Church and Gilbert, 1984) and hybridized it at 65°C. IFT46 gene induction upon deflagellation was analyzed by real-time PCR, as described in Pazour et al. (2005), using primers IFT46-3 and 4. The ratio of the amount of IFT46 message after deflagellation to that before deflagellation was calculated for each trial. Three independent sets of mRNA were isolated and analyzed three times each.

To measure the mRNA levels of IFT140, IFT81, and IFT72, cDNAs were prepared from cells at the mid-log phase of growth, and quantitated by real-time PCR as described in Pazour et al. (2005) using the primer pairs IFT140F/IFT140R, IFT81F/IFT81R, or IFT72F2/IFT72R2. Two independent sets of mRNA were isolated and analyzed three times each.

To assay transcription of the IFT46 gene, cDNAs were prepared from wild-type cells and from ift46 and Supift461 cells with or without aeration. Real-time PCR was performed using primer pairs to the 5′ end of the gene IFT46-11/IFT46-2, middle part of the gene IFT46-9/IFT46-28, and 3′ end of the gene IFT46-5/IFT46-4. Samples were normalized using G protein β subunit (Pazour et al., 2005). The end products were examined on a 1.5% agarose gel. Three independent sets of mRNA were isolated and analyzed three times each.

A collection of insertionnal mutants having motility defects was screened for a defect in IFT46 by Southern blotting, using an 864-bp partial cDNA fragment amplified by PCR with primers IFT46-41 and IFT46-42 as a probe. The mutated region in the IFT46 gene in the mutant was located by PCR using primer pairs 1 (IFT46-1/IFT46-2), 2 (IFT46-9/IFT46-10), and 3 (IFT46-3/IFT46-4). Murine IFT46 and Flag-tagged proteins
The open reading frame of MmIFT46 was PCR amplified from mouse testis cDNA using primers mIFT46-1 and -2. The PCR product was digested with BsrBI, cloned into the BglII site of pGEX-KIF1 (1), and called pJAF116.24. pJAF113.1 was derived from p3XFLAG-myc-CMV-26 (Sigma-Aldrich) by
filling in the HindIII site to shift the polylinker by four nucleotides. pJAF161.24 encodes a fusion protein in which the 3′-Flag tag is fused to the N-terminal end of IFT6. pJAF16.1 encoding GFFFlag was constructed by moving the XbaI–EcoRI GFF-containing fragment from pEGFP N2 (CLONTECH Laboratories, Inc.) into pJAF16.1. pJAF134.3 encoding MintFT20-Flag was described by Follit et al. (2006).

Immunoprecipitations
IMCD3 cells that had been transfected with JAF161.24 (MintFT46-Flag), pJAF134.3 (MintFT20-Flag), or pJAF16.1 (GFP-Flag) were lysed in Cell lytic M (Sigma-Aldrich) containing 0.1% Tween 20 and 0.1% CHAPSO (Bio-Rad Laboratories). After incubation for 10 min at 4°C, the extract was clarified by centrifugation at 18,000 g and treated for 10 min with Sepharose-4B beads, which were removed by centrifugation through a Macro Spin Column (Harvard Apparatus). The treated extract was then incubated with anti-Flag M2-Agarose Affinity Gel (Sigma-Aldrich) for 1 h at 4°C. Unbound proteins were removed by washing the beads in Wash Buffer (Sigma-Aldrich) containing 1% Tween 20 and 150 mM NaCl, followed by washes in Wash Buffer alone. Bound proteins were eluted with 200 ng/ml 3′-Flag Peptide (Sigma-Aldrich) and analyzed by Western blotting, as described in Pazzouz et al. (1998).

Protein biochemistry
Preparation of C. reinhardtii whole-cell extracts, isolated flagella, and the flagellar membrane plus matrix fraction, as well as PAGE and Western blotting, were performed as described in Pazzouz et al. (1999). Sucrose gradient analysis was carried out as described by Hou et al. (2004).

Genetic analysis and transformation
mutant cells were cotransformed (Hou et al., 2004) with linearized plasmid pSP124S (Lumbrañas et al., 1998) and the cloned 4.8-kb fragment, which contains only the wild-type IFT64 gene.

Microscopy
C. reinhardtii cells were fixed in gluteraldehyde for EM (Hoops and Witman, 1983) and processed as described in Wilkerson et al. (1995). C. reinhardtii cells were fixed and stained for immunofluorescence microscopy by the alternate protocol of Cole et al. (1998), using Alexa Fluor 488– or 568–conjugated secondary antibodies (Invitrogen); images were acquired at room temperature with an AxioCam camera, AxioVision 3.1 software, and an Axioskop 2 plus microscope equipped with a 100×/1.4 NA oil DIC Plan-Apochromat objective (all from Carl Zeiss MicroImaging, Inc.) and epifluorescence. Mammalian cells were fixed in 2% paraformaldehyde and processed for immunofluorescence microscopy as described by Follit et al. (2006). Images were prepared for final publication using Photoshop 6.0 (Adobe).

Online supplemental material
Table S1 shows the antibodies used in this work. Table S2 shows the primer sequences used in this study. The online version of this article is available at http://www.jcb.org/cgi/content/full/jcb.200608041/DC1.

References


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