The IDA3 adapter, required for intraflagellar transport of I1 dynein, is regulated by ciliary length

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The IDA3 adapter, required for intraflagellar transport of I1 dynein, is regulated by ciliary length


INTRODUCTION

Cilia, also known as flagella, play essential roles in motility and cell signaling (Ostrowski et al., 2011; Viswanadha et al., 2017). Defective ciliary motility results in human disease, including primary cilia dyssmorphia (PCD) (Horani et al., 2016; Knowles et al., 2016). Defective motility can arise from the failure to assemble dynein arms (Kamiya and Yagi, 2014). Proper assembly of axonemal dynein arms requires not only the structural components, such as dynein heavy, intermediate, and light chains, but also factors extrinsic to the dynein for cytoplasmic assembly (Iomini et al., 2009; Kobayashi and Takeda, 2012), intraflagellar transport (IFT) (Hou et al., 2007; Ahmed et al., 2008; Viswanadha et al., 2014; Desai et al., 2015; Lechtreck, 2015; Hou and Witman, 2017; Taschner et al., 2017), and docking in the large 20S complex in the cytoplasm that is transported by IFT to the tip of the cilium for assembly in the axoneme (Viswanadha et al., 2014). How I1 interacts with IFT remains unknown. While tubulin binds IFT directly through IFT81/IFT74 (Bhogaraju et al., 2014; Craft et al., 2015; Kubo et al., 2016; Taschner et al., 2016; Hou and Witman, 2017), the outer dynein arm (ODA) requires the specialized adapter protein ODA16 to interact with IFT46 for efficient transport (Ahmed et al., 2008; Hou and Witman, 2017; Taschner et al., 2017). Whether I1 or other inner dynein arms require specialized adapters to bind IFT remains unknown.

Here we focus on the IFT transport of the inner dynein arm I1/f (Kamiya and Yagi, 2014; King, 2016). I1 dynein is assembled into a large 20S complex in the cytoplasm that is transported by IFT to the tip of the cilium for assembly in the axoneme (Viswanadha et al., 2014). How I1 interacts with IFT remains unknown. While tubulin binds IFT directly through IFT81/IFT74 (Bhogaraju et al., 2014; Craft et al., 2015; Kubo et al., 2016; Taschner et al., 2016; Hou and Witman, 2017), the outer dynein arm (ODA) requires the specialized adapter protein ODA16 to interact with IFT46 for efficient transport (Ahmed et al., 2008; Hou and Witman, 2017; Taschner et al., 2017). Whether I1 or other inner dynein arms require specialized adapters to bind IFT remains unknown.

Through study of the Chlamydomonas I1 dynein mutant ida3, we show that the IDA3 protein is a specialized and transient IFT adapter required to load I1 dynein onto IFT for entry and transport in the...
growing cilium. Unlike the loading and transport of ODA16, which binds IFT regardless of cilium length (Ahmed et al., 2008), IDA3 loading and transport are regulated by changes in cilium length in a cilium autonomous manner, similar to the axonemal cargoes such as tubulin (Craft et al., 2015). Thus, IDA3 is unique in that it behaves similarly to an axonemal cargo of IFT, but neither binds the axoneme nor remains in the cilium once full length is achieved. We suggest that other axonemal complexes also require specialized and transient IFT adapters to precisely control entry and transport in the cilium.

RESULTS AND DISCUSSION

Inner dynein arm I1 is specifically missing in ida3 mutant axonemes

Although the 20S I1 complex forms in the ida3 cytoplasm, I1 dynein does not enter the cilium, preventing I1 incorporation into the axoneme (Kamiya et al., 1991; Viswanadha et al., 2014). We examined the structure of the ida3 axoneme by cryo-electron tomography and subtomogram averaging. Tomographic slices (Figure 1A, a–4) and isosurface renderings (Figure 1A, g–j) reveal that I1 dynein is missing in ida3 axonemes, except on rare occasions (Supplemental Figure S1A, a–e). Notably, all other axonemal structures assemble properly in the ida3 axoneme, as also seen by thin-section electron microscopy (Supplemental Figure S1B). Thus, like other I1 dynein mutants that include ida1, ida2, ida7, and bop5 (Wirschell et al., 2007; Heuser et al., 2012; Ishikawa, 2012; Kamiya and Yagi, 2014; King, 2016), only I1 dynein fails to assemble in ida3 axonemes. In contrast to other I1 mutants, all known I1 dynein subunits of the 20S I1 dynein complex assemble in the ida3 cytoplasm (Viswanadha et al., 2014). We postulated that IDA3 encodes a protein extrinsic to I1 dynein that is specifically required for ciliary entry and/or transport of I1 dynein by IFT.

A nonsense mutation in IDA3 results in loss of I1 dynein in the axoneme

The ida3 mutant was mapped to a small region on Chromosome 3 between markers 953 and 120055. This 369-kb region contains the centromere, and better resolution could not be obtained with additional markers. With 40x coverage of the ida3 genome, we identified only one SNP in the mapped region after filtering. This change is in Cre03.g205000, and there is a G-to-A transition that changes a tyrtophan codon (TGG) to a stop codon (TAG) at amino acid 22 (Figure 1B; Supplemental Figure S2 Table I). This mutation cosegregates with the slow-swimming phenotype in 75 meiotic progeny. Transformation of ida3 with an untagged IDA3 or IDA3 fused to 3xHA or NeonGreen (NG) rescued I1 assembly in the axoneme and the slow-swimming phenotype (Figure 1, C and D; Supplemental Figures S1B and S2 Table II). Reversion (Lin and Dutcher, 2015) of ida3 in the ida3; oda2 double mutant (defective in I1 and outer dynein arm assembly) rescues assembly of I1 dynein in the axoneme and paralysis of ida3; oda2 (Figure 1E; Supplemental Figure S2 Table III). Together, these data confirm that Cre03.g205000 (IDA3) is the defective gene in ida3.

IDA3 is transported by anterograde IFT within the regenerating cilium

The IDA3 gene encodes an ~115-kD coiled-coil protein that contains a CCDC24 domain (Pfam domain PF15669) in the N-terminal quarter of the protein (indicated by the bar, Figure 1B; Supplemental Figure S2, A and B), whereas the C-terminal half of IDA3 does not show conservation outside of green algae. Immuno blot analysis of cytoplasmic extract from ida3; IDA3::HA revealed that IDA3::HA is present in the cytoplasm of ciliated cells but not in axonemes (Figure 1, F and G).

Given the 205 I1 dynein does not enter the cilium in ida3 (Viswanadha et al., 2014), we predicted that IDA3 function would be tightly linked to I1 dynein transport into the cilium. To test this prediction, we analyzed matrix (soluble fraction of isolated cilia) (Cole et al., 1998; Craige et al., 2013) from full-length and regenerating ida3; IDA3::HA cilia. IDA3::HA, though absent in the matrix of full-length cilia, is present in the matrix of regenerating cilia, as are the intermediate chains IC140 and IC138 of I1 dynein (Figure 2, A and B). Thus, I1 only enters the cilium when IDA3 is present. Together, these data demonstrate that IDA3, though not an axonemal component, selectively enters cilia during regeneration and is essential for I1 entry into the cilium. IDA3 appears to be modified in the matrix of regenerating cilia, as indicated by the presence of two distinct IDA3 bands (arrowheads, Figure 2B). The nature of this modification remains unknown.

I1 dynein, marked by IC140::GFP, is transported by anterograde IFT (Supplemental Figure S3A). Given that IDA3 is essential for I1 assembly in the axoneme, we asked if IDA3 is also a cargo of IFT inside the cilium. Using live-cell total internal reflection fluorescence microscopy (TIRF) (Lechtreck, 2013), we imaged ida3; IDA3::NG cells with either full-length or regenerating cilia (Supplemental Movie 1). Similarly to bona fide axonemal proteins (Lechtreck et al., 2017), IFT transport of IDA3::NG in regenerating cilia is robust, whereas IDA3 transport in full-length cilia is rare (Figure 2, C and D). Approximately 90% of individual IDA3::NG particles are transported processively to the distal tip of the cilium at a velocity of 1.98 ± 0.37 μm/s, consistent with the speed of anterograde IFT in Chlamydomonas (Figure 2, Ea–G; Supplemental Figure S3, B–D). Occasionally, we observed stationary IDA3::NG (Figure 2Ed). This could result from stalling of IFT trains along the length of the axoneme, as recently described (Stepanek and Pigino, 2016), or by transient association with the axoneme. At the tip, multiple IDA3 proteins linger before diffusion begins (Supplemental Figure S3, B and C, white arrows). IDA3::NG then diffuses within the cilium ~ 88% of the time (Figure 2, Ec and H). Occasionally, retrograde IFT transports IDA3::NG at a velocity of 2.66 ± 1.2 μm/s (Figure 2, E(b) and H; Supplemental Figure S3D). One possibility is that diffusion of IDA3 through the cilium into the cell body controls the pool of IDA3 available for I1 transport (Chien et al., 2017; Wingfield et al., 2017).

IDA3 transport by anterograde IFT is dependent on ciliary length

To further explore the link between IDA3 and ciliary growth, we quantified the number of IDA3::NG particles that enter the cilium as it lengths. Similarly to axonemal cargoes of IFT (Wren et al., 2013; Craft et al., 2015), the number of IDA3 particles transported per minute decreases as the cilium lengthens (Figure 3A). Thus, IDA3 is the first identified nonaxonemal cargo of IFT whose transport frequency is regulated by ciliary length. It is possible that the transport of IDA3, in addition to axonemal cargoes of IFT, may be regulated by mechanisms that control cilium length (Chien et al., 2017; Ishikawa and Marshall, 2017). The quantity of cargo transported by IFT at any given time may also be regulated by ciliary length.

We next asked whether IDA3 would selectively enter the growing cilium in a cell that had one growing and one full-length cilium. ida3; IDA3::NG cells with one regenerating (short) cilium and one full-length (long) cilium were imaged by TIRF (Supplemental Movie S2; Craft et al., 2015). Anterograde IFT transport, dwell at the tip of the cilium, and diffusion of IDA3::NG were observed only in the regenerating cilium (Figure 3, B and C). These data confirm that
IDA3 selectively enters the growing cilium and indicate that transport of the IDA3 is regulated independently within each of the two cilia in a single Chlamydomonas cell. This behavior is reminiscent of the regulation of tubulin–IFT interaction (Craft et al., 2015). How the cell selectively targets IDA3 into the growing cilium remains unknown.
Given the specificity of IDA3 for I1 dynein, we predicted that the need to assemble I1 dynein in the axoneme prompts IDA3 entry/transport in the growing cilium. To test this, we mated ida3 x ida3; IDA3::HA to generate dikaryons with four cilia: two full-length cilia with I1 docked in the axoneme and two full-length cilia lacking I1 dynein (Figure 3D). TIRF imaging revealed that IDA3::NG rarely enters any of the four cilia, consistent with the infrequent transport of IDA3 in full-length cilia (Figure 3E). Hence, it is changes in ciliary length, and not the need to assemble I1 dynein in the axoneme, that cue increased IDA3 transport. However, infrequent transport of IDA3 and I1 is eventually sufficient to rescue I1 dynein assembly and motility in the full-length axoneme (Viswanadha et al., 2014).

Stable binding of IDA3 to IFT requires I1 dynein

We investigated whether IDA3 transport by IFT also requires I1 dynein. We isolated the triple mutant ida7; ida3, IDA3::NG, which carries a mutation in the IC140 gene (Perrone et al., 1998) that prevents cytoplasmic assembly of the 20S I1 dynein (Viswanadha et al., 2014), but carries wild-type IDA3::NG. IDA3::NG is expressed and is stable in this ida7 background (see Viswanadha et al., 2014). TIRF imaging revealed that IDA3::NG is transported by IFT in growing cilia even in the absence of I1 dynein (Figure 4, A–C; Supplemental Movie S3). However, in the wild type, IDA3 is typically transported without interruption from the base to the ciliary tip, whereas in the absence of I1, IDA3::NG transport is less processive (Figure 4D; Supplemental Movie S3). For example, in wild-type cilia, 74% of the transports are processive from base to tip, whereas, in the ida7 background, only 30% of transport is continuous from base to tip (n = 80 and 61 transports, respectively). As a consequence of increased dissociation of IDA3 from IFT, IDA3::NG diffusion is prominent in growing ida7; ida3; IDA3::NG cilia (Figure 4A). Thus, IDA3 is transported by IFT in the absence of I1, but the I1–IFT interaction appears to be more transient, suggesting that I1 dynein stabilizes the IDA3–IFT interaction. Given that I1 dynein does not bind IFT in the absence of IDA3, we suggest that IDA3 bound to IFT renders IFT competent to bind and transport I1 dynein. In turn, I1 dynein possibly stabilizes IDA3 interaction with IFT.

IDA3 interacts biochemically with IC140 in the matrix of regenerating cilia

Considering that IDA3 permits entry/transport of I1 dynein in the cilium, we predicted that IDA3 and I1 dynein interact while in transit...
ODA16 binds IFT regardless of cilium length (Ahmed et al., 2008). Thus, ODA16 behaves as an IFT component, while IDA3 behaves as a cilium length–dependent cargo of IFT. Considering the contrast in IDA3 and ODA16 behavior, it may be necessary to redefine the in vivo properties that define an adapter to IFT as compared with a genuine IFT component. Predictably, other large axonemal components (other inner dynein arms, the radial spokes, or N-DRC) may require their own highly specialized and transient adapters to attach to IFT.

FIGURE 3: IDA3 transport by anterograde IFT is regulated by cilium length. (A) The frequency of IDA3::NG anterograde transport events compared with cilium length. As the length of the cilium increases, the quantity of IDA3::NG transported by anterograde IFT decreases. (B) Still frames and kymograms of IDA3::NG transport in ida3; IDA3::NG cilia of long-short (LS) cells. Frequent anterograde IFT transport of IDA3::NG only occurs in the regenerating cilium (open arrowheads). Bar = 2 s and 2 μm. (C) Quantification of IDA3::NG transport frequency in the short and long cilia of LS cells (n = 10 cells). Error bars = SD. (D) Schematic representation of dikaryon rescue experiment that results in ida3 x ida3; IDA3::NG zygotes. Orange dots indicate I1 docked in axoneme. Red dashes indicated IDA3 transport by IFT. (E) Bright field (a, d), TIRF images (b, e), and corresponding kymograms (c, f) of ida3; IDA3::NG x wild-type dikaryon (a–c) and ida3; IDA3::NG x ida3 dikaryons (d–f). IDA3::NG transport is rare in all four full-length cilia, regardless of I1 absence in the axoneme. Bar = 2 s and 2 μm.

to the ciliary tip. Immunoprecipitation of IDA3:HA from the matrix of regenerating ida3; IDA3::HA cilia revealed the presence of both IDA3:HA and IC140 in pull down (Figure 5A). IDA3:HA was also detected in complementary pull downs of IC140::SNAP from the regenerating matrix of the quadruple mutant ida7; IC140::SNAP; ida3; IDA3::HA cilia (Figure 5B). Together these data suggest co-transport of IDA3 and I1 dynein to the tip of the growing cilium (Figure 5C). While a modified form of IDA3::HA exists in the matrix of regenerating cilia (Figure 2B), only one of the two bands is pulled down in our interaction studies (Figure 5, A and B). Whether the IDA3 modification regulates IDA3-I1 dynein interaction remains to be determined.

Summary and conclusions

IFT adapters are defined as proteins present on IFT machinery that are not integral to the overall assembly and function of IFT. To date, ODA16, required for efficient transport of ODA, is one of the best-described IFT adapters (Ahmed et al., 2008; Hou and Witman, 2017; Taschner et al., 2017). Although both ODA16 and IDA3 are needed to assemble specific axonemal components, IDA3 predominantly binds IFT during ciliary assembly, while ODA16 binds IFT regardless of cilium length (Ahmed et al., 2008). Thus, ODA16 behaves as an IFT component, while IDA3 behaves as a cilium length–dependent cargo of IFT. Considering the contrast in IDA3 and ODA16 behavior, it may be necessary to redefine the in vivo properties that define an adapter to IFT as compared with a genuine IFT component. Predictably, other large axonemal components (other inner dynein arms, the radial spokes, or N-DRC) may require their own highly specialized and transient adapters to attach to IFT.

IFT transport of I1 dynein is dependent on the adapter IDA3, and in the absence of IDA3, I1 fails to enter the cilium. The requirement for IFT-mediated I1 dynein entry supports the notion that axonemal components destined to enter the cilium do so based on their ability to bind IFT. Analogously to adapters for cytoplasmic dynein–cargo interaction (e.g., Redwine et al., 2017), adapters may play an essential role in allowing the ~22 IFT core proteins to bind hundreds of different axonemal proteins and protein complexes (Taschner and Lorentzen, 2016; Lechtreck et al., 2017). IDA3 is highly specific for I1 dynein (Figure 1A; Supplemental Figure S1B). Thus, highly specialized adapters, such as IDA3, may be the key to regulating IFT loading and to precisely adjusting the quantity of individual cargoes.
transported into the cilium at any given time. IDA3 attachment to IFT, like axonemal cargoes of IFT but unlike IFT proteins, responds to changes in cilium length. Further study will be required to determine how IDA3 loading and transport are regulated by changes in cilium length.

**MATERIALS AND METHODS**

**Strains and culture conditions**

*C. reinhardtii* strains used include wild type (CC-124, CC-125, CC-620, CC-621), ida3 (CC-2668), ida3; IDA3::NG cells, lacking 1 dynein, imaged by TIRF. (a) Still frame of regenerating ida7; ida3; IDA3::NG cells, and (b, c) kymograms of IDA3::NG transport in regenerating ida7; ida3; IDA3::NG cilia. IDA3::NG both undergoes anterograde IFT (white arrowheads) and diffuses (open arrowheads) in the absence of I1 dynein. (d) Kymogram of IDA3::NG diffusion in full-length ida7; ida3; IDA3::NG cilia. IDA3::NG processive motion is rarely observed. Bars = 2 s and 2 μm. (E) Still frames and kymogram of an ida7; ida3; IDA3::NG short-long cell. IDA3::NG transport is restricted to regenerating cilium. Bar = 2 s and 2 μm. (F) Quantification of IDA3::NG transport events per minute in long and regenerating ida7; ida3; IDA3::NG cilia. Error bars = SD. (G) Analysis of IDA3 transport efficiency in the presence and absence of I1. The lengths of IDA3::NG anterograde IFT tracks were compared with the length of the cilium in ida3; IDA3::NG (n = 96) and ida7; ida3; IDA3::NG (n = 74) cilia. IDA3::NG transport is less processive in the absence of I1. A two-tailed unpaired t test confirms a significant difference in the length of anterograde IFT tracks in ida3; IDA3::NG and ida7; ida3; IDA3::NG cells (P < 0.0001). Error bars = SD.

**Generation of ida7; IC140::SNAP**

A GFP-tagged IC140 construct, containing the APHVIII selection cassette (Sizova et al., 1996), was generated from clone pCP3 (Perrone et al., 1998). The APHVIII cassette was inserted into pCP3 with Smal and Kpnl to produce the plasmid IC140::GFP-APHVIII. The 3.28-kb Nru–EcoRI fragment from IC140::GFP-APHVIII was excised and subcloned into plasmid pSE280 to produce pCS5.1. A 2.068-kb Nru-RsrII fragment containing the SNAP tag in place of GFP in exon 2 was synthesized and cloned into the pUC57-Kan vector (Genscript) to make clone pCS17. The Nru-RsrII fragment from pCS17 was excised and subcloned into the pCS5.1 plasmid to produce pCS18. A 2.71-kb Pspl-XcoRI fragment from pCS18 was subcloned into the IC140::GFP-APHVIII clone to produce pCS20, which contains the IC140 gene fused to SNAP in exon 2. Plasmid pCS20 was used to transform the ida7 strain using the glass bead method (Kindle, 1990). Paromomycin-resistant colonies were selected and examined for assembly of the SNAP::IC140 fusion protein in axonemes and for motility. Several transformants were selected that displayed wild type–like motility.

**Generation of oda6; ida7; IC140::GFP**

To visualize the IC140 movement in cilia, a rescued strain of oda6; ida7 expressing exogenous IC140::GFP molecules was generated (oda6; ida7R::GFP) and used for the TIRF analyses. To generate the oda6; ida7R::GFP strain, oda6; ida7 mutants were transformed with the vector pCP3-GFP-APHVIII, which had the pBlueScript backbone and contained an XbaI-Smal Chlamydomonas genomic fragment covering all the IC140 genomic region with a GFP inserted in either the first or second exon of the IC140 gene. pCP3-GFP-APHVIII also had the APHVIII-gene cassette, which confers paromomycin resistance to transformants. Transformation was carried out by the electroporation method with successful rescue of ida7 with either the GFP DNA tag in exon 1 (pCP3-GFP(1)-ApHVIII) or 2 (pCP3-GFP(2)-ApHVIII) of the IC140 gene. For TIRF microscopy we used IC140 with the GFP inserted in exon 1. We also used TIRF microscopy to observe I1 dynein transport analyzed ida7; IC140::GFP obtained from Oda et al. (2015).

**Constructing double, triple, and quadruple mutants**

Strains (e.g., ida3; oda2, ida7; ida3; IDA3-N, and ida3; IDA3-HA; ida7; IC140::SNAP) were crossed by standard protocols (Dutcher, 1995). To generate the ida3; oda2 mutant, cells were treated with dbCAMP and IBMX (Pasquale and Goodenough, 1987) for 30 min to allow mating of a strain with short or no flagella. Markers were determined by PCR with the following primers: ida7 via pMM24 sequence (AAT ACG CAA ACC GCC TCT T and TGG CGT AAT CAT CAG AGC), ida3::HA (ATC GAT CCG GAC GAG GCG ACC C and GTG GTG AGC TAG TCC AGC AG), and IDA3::SNAP via the
to mixing the gametes of each cell type (Harris, 2009), and the zygotes with full-length, steady-state cilia were observed by TIRF microscopy.

Molecular mapping and whole-genome sequencing

Strain CC-2668 (ida3) was backcrossed to wild-type cells (CC-125) five times.

The backcrossed ida3 strain was crossed to CC-1952 (S1C5) and 230 progeny were used in mapping. Crude DNA preparation, PCR, and enzymatic digestion of DNA from individual progeny were performed as previously described (Lin and Dutcher, 2015). The single ida3 progeny was subjected to whole genome sequencing (Lin et al., 2013; Lin and Dutcher, 2015). The NCBI accession number for the raw sequencing reads of ida3 is SRX525037. We had 40x coverage of the Chlamydomonas genome (Lin et al., 2013). The ida3 nonsense mutation was confirmed in both ida3 and ida3; oda2 by PCR (Primers: ACT TGC TTT CTC ACG GCA CT and CCA TGA GAC TCC TTC CGT GT) and Sanger sequencing.

Reversion analysis

UV light at 750 μJ was used to mutagenize ida3; oda2 (Lin and Dutcher, 2015). UV-mutagenized ida3; oda2 plates were incubated in the dark overnight. After 1–2 d, cells were scraped into a tube containing 20 ml of R liquid medium. After 1.5 d, the top 5 ml of the medium was moved to a new tube. The medium was transferred once every 3 d until swimmers were observed. ida3; oda2 swimmers were visually scored for motility rescue and were analyzed by immunoblot for rescue of the intermediate chains IC140/IC138 as a marker for I1 dynein assembly in the axoneme. Sanger sequencing confirmed the intragenic reversion within ida3 of the ida3; oda2 cells exhibiting a rescue phenotype (Supplemental Figure S2, Table III).

Cloning of IDA3 and transformation and rescue of ida3 mutants

All cloning and tagging of IDA3 was completed at the custom cloning core facility at Emory University. Briefly, the IDA3 gene (4.2 kb) was PCR-amplified from the BAC (4E5) clone containing the Cre03. g205000 gene. Chlamydomonas codon–optimized p3xHA (Silflow et al., 2001) or NeonGreen (Craft et al., 2015; Harris et al., 2016) were inserted into either the N-terminus or C-terminus of IDA3 or embedded within the first or second exon of the IDA3 gene (Supplemental Figure S2, Table III). All IDA3-tagged constructs were inserted into the PUCBM20 vector containing a Chlamydomonas Hygromycin B selection marker (pHyg3) (Berthold et al., 2002). The resulting constructs were transformed into the ida3 mutant by electroporation and placed on TAP+Hygromycin plates (final concentration at 10 μg/ml) for selection of single colonies expressing Hygromycin resistance. Surviving colonies were visually scored for motility rescue of wild-type speed and isolated axonemes from each colony were analyzed by immunoblot for rescue of IC140/IC138 as a marker for I1 dynein assembly in the axoneme.

Preparation of matrix fractions

C. reinhardtii cells grown on constant light in L medium were collected by centrifugation and resuspended in chilled deciliation buffer (10 mM Tris, pH 7.5, 5% sucrose, 1 mM CaCl2) and kept on ice. C. reinhardtii cells were deciliated by pH shock (Alford et al., 2013; Hunter et al., 2016). Cells were resuspended in room temperature L medium and aerated for 35 min at room temperature on constant light to regenerate cilia to approximately half length (Hunter et al., 2016). Regeneration of cilia was observed by phase contrast microscopy. Cells were collected by centrifugation

![ID3 interacts with IC140 of the I1 dynein complex](image-url)
(3000 rpm for 5 min) and again resuspended in chilled deciliation buffer. A second deciliation was induced on ice by pH shock and flagella were collected by subsequent centrifugation.

To isolate the matrix fraction, cilia were resuspended in HMDE + 25 mM NaCl (10 mM HEPES, 5 mM MgSO₄, 1 mM EDTA [dithiothreitol], 0.5 mM EDTA, 25 mM NaCl, protease inhibitors, pH 7.4). EDTA was omitted from HMDE + 25 mM NaCl buffer for all SNAP pull-down experiments. Cilia were flash frozen in liquid nitrogen and thawed at room temperature prior to centrifugation to remove remaining axonemes and membranes from the matrix fraction (Cole et al., 1998; Luckner et al., 2005; Pazour et al., 2005; Craige et al., 2013). Matrix fractions were either stored at 4°C prior to use in immunoprecipitation/pull-down analyses or denatured with Laemmli sample buffer for immunoblot analysis. For matrix fractions of full-length cilia, the regeneration step was omitted, and cilia were isolated by pH shock and centrifugation prior to matrix isolation through identical freeze-thaw methods.

Antibodies and immunoblot analyses

SDS–PAGE and immunoblotting were performed using standard procedures. Primary antibodies used in this study include mouse monoclonal antibody (mAb) against HA (Clone 12CA5; Roche, Mannheim, Germany) and IFT57 (Cole et al., 1998; Hou et al., 2007). Rabbit polyclonal antibodies include IC140 (Yang and Sale, 1998), IC138 (Hendrickson et al., 2004), and RSP3 (Wischell et al., 2008). The secondary antibodies goat anti-mouse (#1706516) and goat anti-rabbit (#1706515) were purchased from Biorad.

Isolation of axonemes

Cells were grown to mid–log phase and deciliated either by pH shock (Lefebvre, 1995; Hunter et al., 2016) or by treating the cells with dibucaine (Witman, 1986). After centrifugation to separate cilia from cell bodies, the cilia were demembranated by final 1% Nonidet P-40 (EMD Millipore, Darmstadt, Germany) and IFT57 (Cole et al., 1998; Hou et al., 2007). Rabbit polyclonal antibodies include IC140 (Yang and Sale, 1998), IC138 (Hendrickson et al., 2004), and RSP3 (Wischell et al., 2008). The secondary antibodies goat anti-mouse (#1706516) and goat anti-rabbit (#1706515) were purchased from Biorad.

Isolation of cytoplasmic extracts

Glass beads were used to lyse cells cultured for 3 d (Ahmed et al., 2008). Broken cells were clarified by centrifugation at 10,000 rpm in a Sorval SA600 rotor for 10 min. The supernatant was then further clarified at 22,500 rpm for 2 h (Type-40 fixed angle rotor, Beckman Coulter). Clarified supernatant was collected and denatured with 1 mM SrCl₂, 10 mM HEPES buffer (ph 7.4) and the pH lowered to 4.5 by adding 0.5 M acetate acid. After 80 s, the pH value was brought back to 7.4 by adding 1 M KOH. After detachment of the cilia from the cell bodies the following solution was added to the buffer: 5 mM MgSO₄, 1 mM EGTA (ethylene glycol-bis[β-amino ethyl ether]-N,N,N’,N”-tetraacetic acid), 0.1 mM EDTA, and 100 µl protease inhibitor cocktails (Sigma-Aldrich). Cilia were washed two times over a 20% sucrose cushion and then demembranated with 0.1% IGEPAL CA-630 (Sigma-Aldrich). Axonemes were collected by centrifugation at 10,000 × g for 10 min and resuspended in HMEEK buffer (30 mM HEPES, 25 mM KCl, 5 mM MgSO₄, 0.1 mM EDTA, and 0.2 mM EGTA). Cilia isolation and all steps thereafter were performed on ice or at 4°C.

Cryo–sample preparation, cryo–electron tomography, and image processing. Freshly prepared axonemes were plunge-frozen on glow discharged (for 30 s at ~35 mA) grids with holey carbon film (copper; R2/2; 200 meshes; Quantifoil Micro Tools GmbH, Jena, Germany) using a homemade plunge freezer to achieve sample vitrification, as previously described (Heuser et al., 2009). In brief, 3 µl of axoneme sample was applied to the grid and gently mixed with 1 µl of 10x concentrated 10-nm colloidal gold solution. The gold particles were precoated with 5% (wt/vol) BSA (bovine serum albumen) solution to help prevent their aggregation. Sample grids were stored in liquid nitrogen until used.

Vitrified axonemes were imaged on a Tecnai F30 transmission electron microscope (Thermo-Fisher/FEI) operated at 300 kV. Tilt series (from –60° to 60°; 1.5°–2.5° tilting increments) were recorded with a 2k × 2k charge-coupled device camera (Gatan, Pleasanton, CA) after energy filtering (Gatan) in zero-loss mode (20 eV slit width). Using the low dose mode in the microscope control and data acquisition software SerialEM (Mastronarde, 2005) the total electron dose per tilt series was limited to ~100 e/A² to avoid radiation damage. A magnification of 13,500 (pixel size of 1 nm) and a defocus of ~8 µm were used for imaging.

For image processing, the tilt series images were aligned using the 10 nm gold as fiducial markers. Both alignment and tomogram reconstruction by weighted back-projection were performed using the IMOD software package (Kremer et al., 1996). The axonemal 96 nm repeats were picked from the raw tomograms, aligned and subtomogram averaged using the PEET software (Nicastro et al., 2006). Three-dimensional (3D) visualization of the averaged structures by isosurface rendering was performed with UCSF Chimera package (Petterson et al., 2004). Automated classification analyses of the 11 inner dynein arm were carried out with a PCA (principal component analysis) clustering approach (Heumann et al., 2011).

TIRF microscopy

For TIRF imaging, we used an Eclipse Ti-U microscope (Nikon) equipped with a 60× NA1.49 TIRF objective and through-the-objective TIRF illumination provided by a 40-mW 488-nm diode laser (Spectraphysics) (Lechtreck, 2013). Excitation and emission were filtered using the Nikon GFP/mCherry TIRF filter and the emission was separated using an image splitting device (Photometrics DualView2 with filter cube 11-EM). Observation chambers for live cell imaging were assembled by inverting a 22 × 22 mm No. 1.5 cover glass with ~10 µl of 5 mM HEPES, pH 7.3, 6.25 mM EGTA onto an equal volume of cells in M medium at a 24 × 60 mm No. 1.5 cover
glass. Images were recorded at 10 fps using an IXON3 (Andor) and the NIS-Elements Advanced Research software (Nikon). FLII (ImageJ plug-in bundle; National Institutes of Health) was used to generate kymograms (Lechtreck, 2016). Individual frames were copied into Photoshop (Adobe) and adjusted for contrast and brightness; figures were assembled in Illustrator (CS6 version 16.0.3, Adobe). To generate videos, stacks were saved in avi format. For photobleaching of the entire cilia, the intensity of the 488-nm laser was increased to 10% or more for 4–12 s (Wingfield et al., 2017).

To examine regenerating cilia, cells were deflagellated by a pH shock, washed into fresh M medium, and incubated with agitation in bright light. To delay regeneration, cells were stored on ice until needed. For long–short experiments, cells were passaged four to six times through a 26G × 1/2 needle using a 1-ml syringe. This treatment resulted in a small percentage (~1%) of long-zero cells that were imaged using TIRF microscopy after flagellar regeneration was allowed for ~10–20 min.

Immunoprecipitation of IDA3::HA
All immunoprecipitation experiments were performed in matrix fractions isolated from regenerating cilia (as described above). To perform HA immunoprecipitation analyses, matrix fractions were isolated from regenerating cilia of ida3 (CC-2688) and ida3; IDA3::HA strains. Immunoprecipitation (IP) buffer consists of 10 mM HEPES (pH 7.4), 5 mM MgSO₄, 1 mM DTT, 0.1 mM EDTA, 25 mM KCl, 75 mM NaCl, and 0.05% Triton X-100. Part of each matrix fraction was denatured with Laemmli sample buffer for analysis of input by immunoblotting. The rest of the matrix fraction was preincubated with protein A agarose beads (Invitrogen) for 1 h at 4°C with slight agitation to preclarify it. Prior to immunoprecipitation, 3F10-crosslinked beads (Roche) were blocked with 3% BSA in IP buffer by rocking for 1 h at 4°C. Precleared matrix fractions and preblocked 3F10-crosslinked beads were collected by centrifugation and combined for immunoprecipitation overnight at 4°C with slight agitation. Immunoprecipitates were washed with IP buffer the next day and denatured with 2× Laemmli sample buffer. Input samples and immunoprecipitates were resolved by SDS–PAGE and analyzed by immunoblotting.

SNAP affinity purification
Matrix fractions were prepared by freeze–thaw, stored at 4°C, and supplemented with 0.5% Triton X-100 prior to use. For affinity purification, we used a modified protocol from Zlatic et al. (Zlatic et al., 2013). SNAP magnetic beads (Cat. No. S9145S; New England Biolabs) were prepared as follows: for each strain, 40 μl of the SNAP magnetic beads were spun down at room temperature using a bench-top minicentrifuge at top speed (14,000 × g) for 1 min. The clarified supernatant was removed and the beads were incubated overnight in an end-over-end rotator at 4°C in a buffer containing 3% BSA, 10 mM HEPES, 5 mM MgSO₄, 1 mM DTT, 25 mM NaCl, and protease inhibitors at pH 7.4. Fresh DTT and protease inhibitors were added to the buffer solution every day prior to use. The next day, the beads were washed twice in a buffer containing 10 mM HEPES, 5 mM MgSO₄, 1 mM DTT, 0.5 mM EDTA, 25 mM NaCl, 0.5% Triton X-100, and protease inhibitors at pH 7.4 using the magnetic holder. Matrix fractions were then added to the SNAP beads and the mixture was incubated at 4°C in an end-over-end rotor overnight. The magnetic beads were then washed six times in a buffer containing 10 mM HEPES, 5 mM MgSO₄, 1 mM DTT, 0.5 mM EDTA, 25 mM NaCl, 0.5% Triton X-100, and protease inhibitors at pH 7.4. The beads were then resuspended in 2× Laemmli sample buffer and denatured at 95°C for 5 min for immunoblot analysis.

Analysis of processive IDA3 movement in ida7; ida3; IDA3::NG
TIRF microscopy was used to visualize IDA3 transport in regenerating ida3; IDA3::NG and ida7; ida3; IDA3::NG cells. Both cell types were imaged when cilia were approximately the same length (roughly 7–9 μm). Subsequent kymograms were generated. The length of the cilium and the length of anterograde IFT tracks were measured using ImageJ Software (National Institutes of Health). Any kymograms in which the tip of the cilium could not be clearly distinguished were excluded from the analysis. The ratio of anterograde IFT track length to cilium length was then determined.

Statistical analysis
To determine whether a statistical difference between anterograde IFT (or retrograde transport) vs. diffusion of IDA3 exists, a two-tailed binomial test was performed in Graphpad software (www.graphpad.com) as described before (Lechtreck, 2013). To determine whether a statistical difference exists between IDA3 IFT transport in the presence or absence of t1, a two-tailed unpaired t test was performed in Graphpad software. The graphs were drawn with Adobe Illustrator and Excel.

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