Regulation of flagellar motility by the conserved flagellar protein CG34110/Ccdc135/FAP50

Yong Yang
Wayne State University

Let us know how access to this document benefits you.
Follow this and additional works at: https://escholarship.umassmed.edu/cellbiology_pp

Repository Citation

This material is brought to you by eScholarship@UMMS. It has been accepted for inclusion in Cell and Developmental Biology Publications by an authorized administrator of eScholarship@UMMS. For more information, please contact Lisa.Palmer@umassmed.edu.
Regulation of flagellar motility by the conserved flagellar protein CG34110/Ccdc135/FAP50

Yong Yang1, Deborah A. Cochran2, Mary D. Gargano3, Iryna King4, Nayef K. Samhat4, Benjamin P. Burger5, Katherine R. Sabourin4, Yuqing Hou5, Junya Awata6, David A.D. Parry7, Wallace F. Marshall8, George B. Witman9, and Xiangyi Lu3

1Institute of Environmental Health Sciences and Department of Biochemistry and Molecular Biology, Wayne State University, Detroit, MI 48201; 2Department of Cell Biology, University of Massachusetts Medical School, Worcester, MA 01655; 3Institute of Fundamental Sciences and the Riddet Institute, Massey University, Palmerston North 4442, New Zealand; 4Department of Biochemistry and Biophysics, University of California at San Francisco, San Francisco, CA 94143

ABSTRACT Eukaryotic cilia and flagella are vital sensory and motile organelles. The calcium channel PKD2 mediates sensory perception on cilia and flagella, and defects in this can contribute to ciliopathic diseases. Signaling from Pkd2-dependent Ca2+ rise in the cilium to downstream effectors may require intermediary proteins that are largely unknown. To identify these proteins, we carried out genetic screens for mutations affecting Drosophila melanogaster sperm storage, a process mediated by Drosophila Pkd2. Here we show that a new mutation lost boys (lobo) encodes a conserved flagellar protein CG34110, which corresponds to vertebrate Ccdc135 (E = 6e-78) highly expressed in ciliated respiratory epithelia and sperm, and to FAP50 (E = 1e-28) in the Chlamydomonas reinhardtii flagellar proteome. CG34110 localizes along the fly sperm flagellum. FAP50 is tightly associated with the outer doublet microtubules of the axoneme and appears not to be a component of the central pair, radial spokes, dynein arms, or structures defined by the mbo waveform mutants. Phenotypic analyses indicate that both Pkd2 and lobo specifically affect sperm movement into the female storage receptacle. We hypothesize that the CG34110/Ccdc135/FAP50 family of conserved flagellar proteins functions within the axoneme to mediate Pkd2-dependent processes in the sperm flagellum and other motile cilia.

INTRODUCTION Cilia and flagella are evolutionarily homologous cell organelles, with ciliary being a generic term for either a motile or nonmotile axoneme-containing protrusion and a flagellum being a motile cilium used for locomotion (Mitchell, 2007; Satir et al., 2008). Recent studies have shown that most cells have one or more cilia that mediate sensory perception and fluid homeostasis necessary for normal development and physiology of living systems (Baker and Beales, 2009; Mirzadeh et al., 2010; Vogel et al., 2010; Wilson et al., 2010). Ciliary dysfunction results in a variety of ciliopathic diseases, including many that are caused by abnormal motility of motile cilia (Baker and Beales, 2009). During evolution, ciliary motility-dependent functions have expanded beyond swimming, food gathering, and parasitism in unicellular organisms to many more complex fluid-driven cellular processes in vertebrates, including humans. For example, the nodal cilia generate a directional flow that provides positional cues to the surrounding cells, leading to left–right body asymmetry in the developing embryos. Disruption of the nodal flow leads to situs inversus with mispositioning and malformation of internal organs (Okada et al., 1999). The motile cilia of ependymal cells generate a flow of cerebrospinal fluid that plays roles in neuronal migration to the olfactory lobes (Sawamoto et al., 2006). Disruption of the cerebrospinal fluid flow affects the neuronal migration and also causes fluid retention and hydrocephalus (Sawamoto et al., 2006; Lechtreck et al., 2008; Wilson et al., 2010). In the reproductive tract, abnormal motility of motile cilia may cause ectopic pregnancy (Lyons et al., 2006). Abnormal motility of the airway cilia leads to...
inefficient mucociliary clearance and respiratory problems (Braiman and Priel, 2008). To accomplish these diverse physiological roles, motile cilia and flagella exhibit a large repertoire of waveforms and are capable of versatile motility changes in response to the external environment (Gibbons, 1981).

A well-known mechanism for eliciting motility changes is alteration of intraflagellar Ca$^{2+}$ concentrations (Kaupp et al., 2008; King, 2010). This has been shown for ciliary reversal in Paramecium (Naito and Kaneko, 1972), reversal of flagellar bending chirality in various sperm (Ishijima and Hamaguchi, 1993; Kaupp et al., 2008), sperm hyperactivation and chemotaxis (Publicover et al., 2008), and wave-form conversion from the asymmetric ciliary form to the symmetric flagellar form in the green alga Chlamydomonas reinhardtii (Schmidt and Eckert, 1976; Bessen et al., 1980). Aside from inducing alternative waveforms, intraflagellar calcium can also reverse the flagellar wave propagation direction along the longitudinal axis of the axoneme (Sugrue et al., 1988; Ishijima et al., 1994). Whereas flagellar waves of most protozoa and spermatozoa start at the base and propagate toward the tip, some species, such as the Tephritid fly and the marine invertebrates Myzostomum and Turritella, have flagella that can propagate waves in both axial directions (Baccetti et al., 1989; Ishijima et al., 1994, 1999). Trypanosomes are unicellular parasites that use their singular flagella for movement in host tissues. Trypanosome flagella are unique in that they routinely propagate tip-to-base waves, which generate a flagellum-tip-leading, forward movement (Walker, 1961; Sugrue et al., 1988; Hill, 2003). However, in response to lights or obstacles, trypanosoma flagella initiate short bursts of base-to-tip waves that generate a backward movement. Flagellar waveform conversion or reversal of wave direction provides a means of backing up, reorienting the cell, and avoiding obstacles in physiological settings.

The axoneme of nearly all motile cilia and flagella has the canonical “9+2” structure (Porter and Sale, 2000; Heuser et al., 2009). The cylindrical wall of the axoneme consists of nine outer doublet microtubules (ODs) that enclose a central pair (CP) of singlet microtubules in the center, extending from the basal body to the distal tip. Serving as interconnecting structures between the ODs and the CP are radial spokes, which are anchored along the lengths of each of the nine ODs and project toward the CP. The radial spokes are known to interact with regulatory proteins located on the CP and to relay signals back to the dynein motors that are anchored on the ODs (Smith, 2002b; Smith and Yang, 2004; Mitchell, 2004). The isolated demembranated axonemes of C. reinhardtii and Crithidia oncopelti have been shown to execute reversible waveform conversion and wave direction reversal, respectively, when reactivated in solutions of varying free Ca$^{2+}$ concentrations (Bessen et al., 1980; Sugrue et al., 1988). This indicates that the mediators for waveform conversion and wave direction reversal are located on the axoneme. Many calcium-sensing proteins are integrated within the CP, radial spokes, and dynein motors (Smith, 2002a; Smith and Yang, 2004; Dynek and Smith, 2007). Although less is known about calcium-sensing or responding proteins on the ODs, three C. reinhardtii mbo (move backward only) mutations result in the loss of six to eight OD-associated polypeptides, and these mutant flagella are unable to execute waveform conversion (Segal et al., 1984). The cloned mbo2 locus encodes a conserved coiled-coil protein on the ODs with yet undefined functions in other organisms (Tam and Lefebvre, 2002).

The PKD2 family of calcium channels has been shown to function in motile as well as immotile cilia. Mutations in vertebrate PKD2 lead to renal cystic growth (Wu et al., 1998) and defects in left–right body asymmetry (Pennekamp et al., 2002) due to dysruptions of fluid sensation by the kidney and nodal cilia, respectively. The mating defect of Caenorhabditis elegans Pkd2 is due to the loss of mechanosensation by the ciliated sensory neurons that mediate vulva location during mating (Barr and Sternberg, 1999). A working model applicable to these situations is that mechanical depression/bending of cilia opens the PKD2 channels on the ciliary membranes, which results in calcium influx into the cilia; this eventually leads to signal transduction and physiological changes in the cell body. It is unclear whether this ciliary bending model applies to C. reinhardtii and Drosophila where Pkd2 functions on flagella that are constantly beating (Gao et al., 2003; Watnick et al., 2003; Huang et al., 2007).

The C. reinhardtii PKD2 (CrPKD2) is required for flagellar adhesion-mediated mating (Huang et al., 2007). RNAi knockdown of CrPKD2 does not interfere with flagellar adhesion between the (+) and (−) gametes, but does block downstream signaling, resulting in the reduction of gamete fusion and formation of diploid cells (Huang et al., 2007). Studies have shown that, in this pathway, CrPKD2 functions downstream of flagellar adhesion but upstream of a flagellar protein tyrosine kinase, which leads to downstream activation of the cGMP-dependent protein kinase CrPKG (Wang et al., 2006) and an adenylate cyclase that produces cAMP (Wang and Snell, 2003). cAMP appears to be the critical second messenger because exogenously supplied cAMP is sufficient to induce gamete fusion, by-passing the steps of CrPKD2, CrPKG, and the adenylate cyclase. CrPKD2 is also present in flagella of vegetative cells, and so it is likely to have additional functions in other signaling pathways, possibly including control of flagellar motility (Huang et al., 2007).

The Drosophila Pkd2 is highly enriched on the sperm flagellum (Gao et al., 2003), and its expression in S2 Drosophila tissue culture cells generates cation channel activities similar to those of mammalian PKD2 (Venglarik et al., 2004). As a normal reproductive process, Drosophila sperm in the uterus travel into a long and narrow seminal receptacle (SR) tubule that has a closed end. Sperm are stored in the distal half of the SR for weeks, and during this period, they gradually exit out of the SR to fertilize the egg (Bloch Qazi and Wolfner, 2006). Mutant sperm lacking wild-type Pkd2 show grossly normal motility but are unable to move efficiently into the SR (Watnick et al., 2003; Gao et al., 2004). This leads to a working model that Drosophila sperm storage is induced by an SR entry signal that activates Pkd2, leading to calcium influx into the sperm and thereby producing the specific swimming behavior necessary for SR entry. Here, we report the identification of CG34110, another flagellar protein required for the Drosophila sperm to enter the SR tubule. Loss-of-function CG34110 results in specific sperm motility defects that are essentially the same as those of the Pkd2 mutant. CG34110 has unequivocal orthologues in organisms possessing motile cilia and flagella, but is absent in organisms that do not have cilia and in C. elegans, which does not have motile cilia. Biochemical analyses indicate that the C. reinhardtii orthologue FAP50 (Pazour et al., 2005) is an OD-associated protein unaffected in all three mbo mutants.

**RESULTS**

**lobo is a new locus required for sperm storage**

There are two types of sperm storage organs in female Drosophila: one coiled SR tubule and two mushroom-shaped spermathecae (Figure 1A). We initially identified a recessive storage-defective mutation and mapped its meiotic position to ~990 kb distal to a P element insertion PXP(9)30711. The P element insertion was removed by recombination, resulting in a “clean” storage-defective locus named lost boys (lobo) (see Materials and Methods). The wild-type sperm entered the storage organs (Figure 1B), whereas few sperm from the lobo homozygous males entered the storage organs (Figure 1C). This phenotype is similar to the characterized

---

*Volume 22  April 1, 2011*  
*Regulation of flagellar motility*  
| 977 |
phenotype of Pkd2 on the second chromosome. The lobo locus is clearly a distinct locus because it is on the right arm of the third chromosome (3R).

To identify the responsible gene, genetic complementation tests were carried out between lobo and genomic deletions distal to P{XP}kal. The lobo locus was found to fall within the Df(3R)Exel6201 deletion but outside of the distal flanking deletion Df(3R)Exel9056. This suggested that the responsible gene lies within the 59 kb of DNA at coordinates 3R:20963561..21022720. To verify the deletion breakpoints, the (deletion+/+) DNA samples were isolated and used to hybridize to long oligonucleotide microarrays and compared with (+/+7) DNA samples in parallel. The microarray data indicated that Df(3R)Exel9056 did not obviously delete any genes, whereas Df(3R)Exel6201 deleted five annotated genes (CG13652, CG13651, CG34110, CG13653, and CG11849); only one of these, CG34110, is highly expressed in the male testis (Chintapalli et al., 2007).

Consistent with CG34110 being the responsible gene, lobo failed to complement CG34110MB00722, which contains a Minos transposon insertion. Excision of CG34110MB00722, via Minos transposase-induced transposon excision (Metaxakis et al., 2005), led to a reversion of the phenotype back to wild type, suggesting that the Minos insertion was causing the storage defect. DNA sequencing indicated that the Minos transposon inserts at E_{378}^{GTTGTGACTCA} and produces a 378-amino-acid (aa) truncated polypeptide of the full-length CG34110 protein of 897 aa. In addition, lobo is a 7-base pairs (bp) deletion (ctgcact) in exon 6 of CG34110, which produces a 567-aa truncated polypeptide. Thus lobo is referred to as CG34110^{mob}.

To further verify that CG34110 is the responsible gene, antipeptide antibodies were produced and targeted to recognize two nonoverlapping regions of CG34110. Both antibodies were found to bind to a protein of ~167 kDa (arrowhead in Figure 2A) on Western blots of protein samples derived from wild-type testes (Figure 2A, lane 2) and mature sperm (Figure 2A, lane 5). The band was not detectable in samples from wild-type adult females (Figure 2A, lane 1) and testes from CG34110^{mob} or CG34110^{mob} homozygous males (Figure 2A, lanes 3 and 4). During the course of this study, we isolated the CG34110^{mob} allele by chemical mutagenesis in an F_{3}ogenic screen. Thus the CG34110 locus is defined by three independently derived loss-of-function alleles (Q46, lobo, MB00722) with severity close to that of the gene deletion Df(3R)Exel6201 (Figure 2B).

**CG34110 is a highly conserved flagellar protein**

A reduction of sperm storage could be caused by a defect in the sperm or a defect in the seminal fluid proteins that are known to influence the efficiency of sperm storage (Neubaum and Wolfrner, 1999). To localize CG34110 expression, immunostaining was done with the male reproductive tract, including the accessory gland and ejaculatory duct (ED), but only the testis and sperm showed positive protein staining. As all sperm proteins are produced during spermatogenesis in the testis, CG34110 is likely to assemble and function in the sperm, which is supported by CG34110 immunofluorescence along the sperm flagellum (Figure 2C). The CG34110 staining appears as regular puncta along the flagellum; based on the 9-μm sperm head in the same image, the periodicity of the puncta is >10x greater than that of the 96-nm repeats of inner dynein arm complexes along the axoneme (Piperno et al., 1990).

To define the extent of functional conservation, Blastp searches were conducted and showed that, with a probability value of 2e-70
to 6e-78, CG34110 has an unequivocal vertebrate orthologue Ccdc135 (synonymous with Gm770 [McClintock et al., 2008], SRG-L, and SRG-S [Guo et al., 2004; Ma et al., 2006]). Ccdc135 is conserved in human, mouse, rat, chicken, and zebrafish, but not C. elegans, rice, and Arabidopsis. The alignment between CG34110 and Cdc135 shows extensive sequence conservation throughout the entire polypeptide (~29% identity, ~46% similarity, Supplemental Figure 1). Expression report from Unigene (http://www.ncbi.nlm.nih.gov/unigene) indicates that Ccdc135 is highly expressed in the nasopharynx, which includes respiratory epithelial cells with motile cilia, and in the tests. Gm770 was previously predicted to have a high probability of ciliary function based on differential expression in tissues containing motile cilia (McClintock et al., 2008).

Ccdc135 was predicted by others (Ma et al., 2006) to contain a transmembrane domain and possibly enzymatic activity. These features, however, could not be confirmed upon careful inspection of Ccdc135 or CG34110. Protein domain searches were carried out with current programs on the ExPasy Proteomics Server. CG34110 does not contain recognizable calcium- or calmodulin-binding motifs. The only protein structural features we could identify are four regions (aa153–173, aa436–460, aa633–652, and aa787–807; Supplemental Figure 2) that each contain three heptad repeats. Such heptad repeats with apolar residues separated alternately by three and four residues are frequently involved in the formation of alpha-helical coiled coils or alpha-helical bundles (Parry et al., 2008). In this case, the repeats lack oppositely charged residues in positions necessary for forming interchain ionic interactions that are often seen with two- and three-stranded coiled coils. This indicates a greater probability of forming alpha-helical bundles, probably four-stranded for CG34110, rather than a coiled coil structure.

**FAP50 is associated with the outer doublets**

Blast searches indicate that CG34110 is a mutual best fit to a C. reinhardtii flagellar-associated protein, FAP50, that was identified by more than 30 peptide hits in the published C. reinhardtii flagellar proteome (Pazour et al., 2005). The peptides from FAP50 were found exclusively in fractions derived from the axoneme, suggesting that FAP50 is an axonal component. To confirm this and to locate FAP50 more precisely within the axoneme, we made a peptide antibody to FAP50. The antibody reacted with three bands in Western blots of isolated flagella, one of which (Figure 3A, arrowhead) is in the region of the gel from which virtually all of the FAP50 peptides originated in the proteomic analysis (Pazour et al., 2005). This protein was highly enriched in flagella versus whole cells (Figure 3B), indicating that FAP50 is likely to function specifically in the flagellum. In Western blots of flagellar fractions (Figure 3B), FAP50 was found almost exclusively in the 0.6 M KCl-extracted axonemes (EX-AX), which lacks inner and outer dynein arms and many CP proteins. Extraction of the axoneme by 0.6 M KCl solubilizes almost all outer dynein arms and substantial amounts of most inner dynein arm components (Pfister et al., 1982; King et al., 1986; Kagami and Kamiya, 1990, 1992; Pazour et al., 2005; Yagi et al., 2009) (Supplemental Table 2). Therefore FAP50 appears to be specifically associated with the ODs but not with their dynein arms. This is consistent with a previous result that FAP50 is present in the flagellar axoneme of a mutant lacking the outer dynein arms (Pazour et al., 2005). To learn more about the location of FAP50 within the axoneme, we compared isolated flagella of wild type, the mutant pf18 which lacks the CP, and the mutant pf14 which lacks the radial spokes. FAP50 was present at wild-type levels in the flagella of both pf18 and pf14 mutants (Figure 3C). Therefore FAP50 is a component of the ODs but appears not to be a subunit of the dynein arms, the radial spokes, or the CP.

In C. reinhardtii, three independent mutations (mbo1, mbo2, and mbo3) result in a phenotype in which the flagella propagate only the symmetrical waveform used for backward swimming and are unable to form the asymmetrical waveform used for forward swimming (Segal et al., 1984). The mbo mutant flagella lack six to eight proteins normally present in wild-type flagella. The mutations also correlate with loss of a beak-like projection in the lumens of a subset of the ODs. Because the proteins missing in the mbo mutants are involved in waveform control and may be localized to the ODs, we investigated whether FAP50 is defective in these mutants. All three mbo mutants had normal levels of FAP50 (Figure 3D), indicating that FAP50 is not one of the constellation of six to eight proteins associated with the move-backward-only phenotype.
**FIGURE 4:** Movement of sperm from the SV into the ED in the male. The sperm heads and tails were marked with GFP, and the images were obtained by GFP imaging. (A, B) Video snap views from Supplemental Movie 1, which captured sequential events occurring in the reproductive tract of a wild-type male within 1–4 min following its copulation with a wild-type female. The sperm exited out of the bilateral SV through a converging tube (CT, arrow) and entered the ED. Sperm heads were visible as GFP specks (arrowheads) at the leading edges of the moving front (MF). (C, D) Still images obtained from fast-freezing copulating wild-type (C) and lobo mutant males (D, CG34110MB00722/CG34110lobo). Scale bars are all 0.1 mm.

**lobo does not affect sperm exit movement from the seminal vesicle**

To elucidate the function of CG34110 and compare its mutant phenotype with that of the Pkd2 mutant, sperm heads and tails were marked with Protamine-GFP and Dj-GFP transgenes (Santel et al., 1997; Ratke et al., 2007), and movement was examined by fluorescence microscopy. During copulation, the male and female reproductive tracts join together, forming a continuous conduit for the sperm to travel from the male into the female. The first narrow tubule in the sperm conduit connects the bilateral male seminal vesicles (SVs), where mature sperm are stored, to the outgoing ED. Shortly after mating commences, the exit tubules of the SVs open and sperm heads (short specks, arrowheads in Figure 4) lead the way out of the SVs through a connecting tube (CT; Figure 4A) and enter the ED (Supplemental Movie 1). Because the ED (its distal end is broken off in Figure 4C) has a length similar to that of the sperm, the sperm heads captured in Figure 4 are leading ends of the sperm. Approximately 200 sperm heads passed through the CT to enter the ED while the sperm moving front (MF) advanced up to the anterior ~1/8 of the ED length (Figure 4B); the tail ends of these sperm have not entered the ED at this time based on length measurement of the flagellar portion that was inside the ED.

To confirm the head-leading orientation, the coupling flies were fast-frozen and the male ED was imaged (Figure 4, C and D). These still images validated the video observation and provided numerical data that 96% (n = 215) of the wild-type sperm found in the ED have the head-leading orientation. The mutant alleles analyzed (Pkd2<sup>ko67</sup> [Gao et al., 2004], Pkd2<sup>1</sup> [Watnick et al., 2003], CG34110<sup>MB00722</sup>, and CG34110<sup>lobo</sup>) are near complete loss-of-function mutations with little residual male fertility (Figure 2B). The majority of the Pkd2 mutant sperm (96% for Pkd2<sup>ko67/1</sup>, n = 103; 96% for Pkd2<sup>ko67/KO67</sup>, n = 68; 98% for Pkd2<sup>ko67/Df(2L)prd1.7 n = 116</sup>) and the lobo mutant sperm (98% for CG34110<sup>lobo/MB00722</sup>, n = 257) also exited the CT with head-leading orientation (Figure 4D). Consistent with this, the amount of sperm inseminated into the uterus is similar for wild-type, Pkd2, and lobo males (Figure 1) (Gao et al., 2003; Watnick et al., 2003).

**lobo affects sperm entry movement into the female seminal receptacle**

In the uterus, flagella of wild-type sperm move with circular-shaped bends and the sperm head is dragged behind the flagellum (Figure 5A and Supplemental Movie 2). From the uterus, ~5–10% of the wild-type sperm enter the female SR tubule (an average of 330 sperm out of 4000–6000 in the ejaculate; Supplemental Table 1). The maximum number of sperm in the SR was reported to be 400 (Manier et al., 2010). The proximal half SR (PSR; 1 mm long, ~19 μm wide) is slightly narrower than the distal half SR (DSR; 1 mm long, ~24 μm wide). The PSR serves as the passageway for the sperm to go in or out of the DSR, whereas the DSR is the site of sperm storage (Figure 5, J and K). Wild-type sperm pass through the PSR in bundles (Figure 5B), as shown by the exposed parallel sperm flagella at the region where the PSR tubular wall was teased open (Figure 5C). The sperm in the exposed flagellar bundles have a tail-leading orientation (Figure 5C, arrowheads). To determine the initial sperm entry orientation, still images were obtained from copulating flies that were fast-frozen at an early stage of sperm storage (15 min from mating onset), and the orientations of individual sperm that had entered the PSR were observed. The tail end of the wild-type sperm was found to enter the PSR first (Figure 5D), and the sperm went through the PSR tubule without making turns (Supplemental Movie 3). Quantification showed that the tail-leading orientation occurred at a frequency of 80% (20/25 sperm), whereas the head-leading orientation (2/25 sperm) and flagella with one hairpin-shaped fold (3/25 sperm, similar to Figure 5F) were found in only a minority of the sperm. The explanation for the minority head-leading and folded sperm is uncertain, but they may represent transitional forms of sperm during their normal conversion from the folded form in the uterus to the extended parallel form at the initiation of PSR entry (see Discussion).

In contrast to wild-type sperm, the lobo mutant sperm (CG34110<sup>MB00722/lobo</sup>) show increased frequencies of head-leading orientation during PSR entry and excessive flagellar folding in the PSR lumen. Still images were obtained for the lobo mutant in the same manner as for wild type. This showed that the head-leading entry orientation was increased from the 8% wild-type baseline to 55% (18/33 sperm) for the lobo mutant such that multiple lobo mutant sperm heads were found to enter the PSR simultaneously (Figure 5E), which was not observed for wild-type sperm. In addition, the folded flagellar configuration was increased from the 12% wild-type baseline to 24% (8/33 sperm) for the lobo mutant. Although flagella with one hairpin-like fold (similar to Figure 5F) were occasionally observed for the wild-type sperm, only the mutant sperm showed excessive folding into tangles (Figure 5G). Many tangled flagella were found in freshly dissected PSRs at later hours when sperm storage had stopped as indicated by the extrusion of inseminated sperm out of the uterus. This suggests that the tangled flagella were trapped in the PSR and unable to move into the DSR. The
Comparisons of Pkd2 and lobo single mutants with the double mutant

To determine possible differences between Pkd2 and lobo, the numbers of sperm that entered the DSR were determined for Pkd2 and lobo single mutants and the double mutant. Like the single mutants, the double-mutant male produced a large number of motile sperm that entered the uterus (Figure 5L), suggesting that motility required for sperm transfer from male to female was grossly normal. In contrast to wild-type males, which consistently lead to ~275–404 sperm in the DSR (Supplemental Table 1), the numbers of the mutant sperm that enter the DSR varied greatly on an individual basis, from male to male or from one mating to the next mating of the same male. The overall storage patterns were determined by examining 100–150 individual males (Figure 6). The percentages for each storage class are zero sperm (30.1%), 1–5 sperm (55.3%), 6–10 sperm (9.7%), 11–15 sperm (2.9%), and 16–20 sperm (1.9%) for Pkd2KO67/ko67 (average 2.8 sperm stored per female per mating [sp/f/m]). Similar patterns were observed for Pkd2ko67/MB06703 (average 5.5 sp/f/m), CG34110MB00722/lobo (average 4.0 sp/f/m), and the double mutant (Pkd2ko67/MB06703; CG34110MB00722/lobo, average 2.4 sp/f/m), with the highest numbers of sperm stored to be 21, 22, and 24 for the respective genotypes (Figure 6). These patterns of sperm storage suggest that successful entrance into the DSR is stochastic. Possibly, the mutant sperm enter the DSR if they, by chance, do not get stuck in the PSR lumen. Although the double mutant showed a more severe phenotype than either of the single mutants in the combination, the differences were very small (~3 sperm or ~1% of the wild-type average of 330 sperm). Such small differences are normally observed for males of different genetic backgrounds.
process results in the extrusion of unstored sperm out of the uterus (Figure 5K). Aside from egg laying, a recent study showed that the unstored sperm are ejected out of the uterus before the first egg is laid and 84% of the females no longer contain unstored sperm 5 h after mating (Manier et al., 2010). To determine whether the stored double-mutant sperm could exit the DSR and fertilize the egg, we did time-course counts of the F1 progeny produced. When wild-type females were mated with the double-mutant males, the eggs laid in the first 6 h after mating accounted for 0–6.8% of the total F1 progeny produced, leading to the possibility that as many as 93% of the F1 progeny could be fertilized by the double-mutant sperm that entered the DSR. We also examined F1 production by the females that had already laid eggs. At 8 h after mating, many mated females (n = 30) had laid 1–12 fertilized eggs (n = 113 F1); these females were found to produce an additional 91 progeny afterward (45% of the total F1 produced). The females that had already laid 4–12 eggs were found to produce an additional 2–9 F1 progeny that were fertilized by the double-mutant sperm.

We also examined the movement orientation of the sperm that exit the PSR by imaging the PSRs obtained from females fast-frozen at 24 h after mating. Wild-type sperm travel out of the PSR with a head-leading orientation (Figure 5K; head-leading in 30/30 sperm). The lobo mutant sperm also showed head-leading orientation (Figure 5J; head-leading in 23/24; tangled flagella in 1/24). Many Drosophila species have long sperm; while their heads enter the egg, their tail tips hang outside of the egg shell in at least four species analyzed, including D. melanogaster (Karr and Pitnick, 1996). Thus the head-leading SR exit orientation that we observed probably readies the sperm for a head-in-first fertilization of the egg.

FIGURE 6: Comparison of sperm counts in the DSR with the progeny produced for the Pkd2 and lobo single mutants and the double mutant. The x axis indicates sperm counts; “In” for the number of sperm stored in the DSR per female per mating and “Out” for the number of viable F1 progeny produced per female per mating. Each data point was obtained from one wild-type female (collected as virgin) after mating with one mutant male. The four male mutant genotypes are (A) Pkd2(Ko67/Ko67), (B) Pkd2(Ko67/Mb06703), (C) CG3110(lobo/Mb00722), and (D) Pkd2(Ko67/Mb06703), CG3110(lobo/Mb00722) (also carrying one copy of Protamine-GFP). The y axis represents the percentages of the “In” or “Out” in the tested populations (n). All progeny were checked for the expected genotype to make sure that they were fathered by the experimental males. The wild-type male consistently stores an average of 330 sperm (range 275–404, Supplemental Table1).

DISCUSSION

This study reports a novel motility function for the conserved flagellar protein CG34110/Cdc135/FAP50 through genetic analysis of a Drosophila sperm storage–deleterious mutation lobo, which encodes CG34110. The study encompasses the initial genetic screen for lobo, molecular identification of the culprit gene, and detailed motility analyses that show that the Pkd2 and lobo single mutants and the double-mutant sperm have essentially the same motility phenotypes. The biochemical analyses presented here together with the published flagellar proteomic study clearly demonstrate that the C. reinhardtii orthologue FAP50 (Pazour et al, 2005) is associated with ODs of the flagellar axoneme. In a Clustal analysis of the proteome data, FAP50 grouped closely with many OD-associated proteins (Pazour et al., 2005), including RIB43a, a component of the tektin ribbon filament on the ODs (Norlander et al., 2000). This is consistent with Western blot results of normal FAP50 abundance in C. reinhardtii mutant flagella lacking the CP and radial spoke structures. Furthermore FAP50 protein levels on the axoneme were unaffected by 0.6 KCl extraction that removes almost all outer and inner dynein microtubules of the axoneme. Therefore FAP50 may represent a novel regulatory protein located on the OD microtubules of the axoneme.

A second intriguing finding is that the fly sperm appears to move with either head- or tail-leading orientation. The majority of sperm exit the SV with a head-leading orientation (Supplemental Movie 1), whereas the majority of sperm in the uterus move with the head dragging behind the flagellum (Supplemental Movie 2). Such an ability to move in both axial directions has only been shown in a few organisms (see Introduction), but this is not unexpected for
superlong sperm that have to move within the narrow confines of the male or female reproductive tract. Sperm movement is powered by bending of the flagellum. The flagellar bends push against the surrounding medium, thereby generating the force for forward movement. When a symmetrically bending flagellum switches to asymmetrical bends, this effectively alters the vector of the force generated. This is how most types of sperm make turns during chemotaxis or obstacle avoidance. However, because the fly sperm is as long as the SR tubule and the tubule has a length-to-width ratio of 100:1, asymmetric flagellar bending would unlikely be effective in the narrow confines of the SR tubule. The acquisition of bidirectional movement capability by the *Drosophila* sperm could be an adaptation of the long sperm to the narrow tubular structures of the reproductive tract since this provides an alternative strategy for backing up and obstacle avoidance. It would be interesting to determine whether long sperm in other insect species have evolved bidirectional movement capability. Interadaptive changes between the sperm and the female SR have been shown in experiments where selection for females with longer SRs results in longer sperm in the selection population in as little as 30–40 generations (Miller and Pitnick, 2002).

It is interesting that the fly sperm seems to adopt preferentially one of the two possible orientations for specific movements within the reproductive tract. This is also an expected finding because, if bidirectional movements are not tightly regulated, it would lead to frequent directional reversal and the sperm would end up staying at the same place. Due to the large number of sperm in the reproductive tract, we cannot be sure that each and every individual sperm is moving with one orientation at a given time or condition. However, this does not present a critical issue because, having a bidirectional movement capability, the sperm is likely to be able to reverse its movement orientation when situations call for it. In trypanosomes, which also have a bidirectional movement capability, basal levels of orientation reversal are observed in the absence of encounters with obstacles (Sugrue et al., 1988). To our knowledge, absolute uniformity of sperm behavior is difficult to find and variability occurs in many situations. Sperm motility is known to vary depending on sperm maturation and competency (Immler, 2008; Werner and Simmons, 2008). A general phenomenon related to sperm in a variety of chemotaxis settings is that only a small fraction (usually <10% of the sperm) responds to physiological signals (reviewed in Kaupp et al., 2008; Eisenbach and Giojalas, 2006). We determined that 5–10% of the sperm in the uterus enter the DSR. The sperm in the uterus are moving with circularly bending flagella (Figure 5A), whereas sperm moving within the PSR lumen are mostly parallel to each other (Figure 5C). The PSR-entry-responding sperm from the crowded sperm mass in the uterus may carry along the nonresponding sperm that are folded, leading to our observation of some sperm that are folded or have a head-leading orientation at the PSR opening. Some of the folded flagella we saw in the PSR could correspond to sperm in normal transition from the folded to the extended parallel form according to a working model of *Drosophila* sperm storage (Yang and Lu, 2011). As shown in Supplemental Movie 3, the wild-type sperm can go all the way through the PSR to enter the DSR without making any turns. This is at least one of the modes that the sperm move into the DSR.

In a previous study, gross sperm motility such as beat frequency was not obviously affected in the *Pkd2* mutant sperm that were taken out of the male SV and analyzed in vitro (Watnick et al., 2003). To elucidate the *Pkd2* and *lobo* motility function, here we took an in vivo approach. The data showed that *Pkd2* and *lobo* single mutants and the double mutant exhibit essentially the same spectrum of phenotypes. The motility required for the sperm to enter the SR tubule is severely impaired, whereas the motility required for sperm transfer from male to female is grossly normal. Both the single- and double-mutant males can father viable progeny to a degree comparable to the number of mutant sperm that enter the DSR, suggesting that the motility required for fertilization is unlikely to be affected. The observed differential motility effect is likely to reflect the true functions of *Pkd2* and *CG34110* because the analyzed mutant alleles exhibit phenotypic severity close to that of gene deletions. Based on the established flagellar propulsion theory and hydrodynamic principles (Brokaw, 2006), the bidirectional sperm movement is the consequence of flagellar wave propagation in either base-to-tip or tip-to-base direction. The folded or parallel flagellar configuration reflects the waveform the sperm is propagating. Our analyses suggest that successful sperm storage requires a waveform compatible with forming linear arrays of flagellar bundles, and it also requires preferential wave propagation from one of the ends (in this case, the tail end) so that the sperm can travel into the DSR. Without wild-type *Pkd2* or *CG34110* activity, the mutant sperm enter the PSR with the wrong or random orientation, and the sperm tend to be trapped in the lumen with abnormal flagellar folding. These phenotypes could be interpreted as failure of waveform conversion and inappropriate switching between head-leading and tail-leading swimming modes. Waveform conversion and regulation of wave propagation could be two aspects of a single process that is regulated by *Pkd2* and *CG34110*.

Currently, very little is known about how the direction of flagellar wave propagation is controlled, yet this is important for all flagella because an unstable direction of wave propagation would result in unproductive locomotion. Our characterization of in vivo sperm behavior in *Drosophila* and the roles of *Pkd2* and *CG34110* provide a new opportunity to address mechanisms of wave propagation and waveform conversion. Furthermore, *CG34110* has highly conserved orthologues in species containing motile cilia, but homologous genes are absent in species without cilia (rice and *Arabidopsis*) and in *C. elegans*, which does not have motile cilia. Future identification of mutations in *Ccdc135* and *FAP50* should shed light on the precise roles of these conserved flagellar proteins. At the present time, we favor a working hypothesis that *Pkd2* and *CG34110* function in a common signaling pathway: *Pkd2* at the level of the flagellar membrane and *CG34110* on the axoneme. No calcium- or calmodulin-binding domains are found in *CG34110/Ccdc135/FAP50*, suggesting that there are intermediary components in the pathway. Identification of the intermediary components will be necessary to fully understand the *Pkd2* to *CG34110/Ccdc135/FAP50* signaling pathway.

**MATERIALS AND METHODS**

**The sperm storage assay**
The sperm storage phenotype can be assayed by direct observation of sperm presence in the female SR. The males to be tested were collected and aged in isolation (1–4 d) before mating with females of the genotype *y*¹ *w*¹, which has good female fertility. The *y*¹ *w*¹ females were collected as virgins and aged for at least 2 d before mating with the males. Thirty minutes after mating, the SR tubule with the uterus was removed by dissection. The SR from a female mated with a wild-type male looks opaque-white due to sperm loading in the DSR. In contrast, the SR from a female mated with a storage-defective mutant male looks transparent due to the lack of sperm in the DSR. The number of sperm in the storage was determined by counting Protamine-GFP (Rathke et al., 2007) marked sperm heads in the DSR at 4 and 20 h after mating; similar values were taken out of the male SV and analyzed in vitro (Watnick et al., 2003). To elucidate the *Pkd2* and *lobo* motility function, here we took an in vivo approach. The data showed that *Pkd2* and *lobo* single mutants and the double mutant exhibit essentially the same spectrum of
were obtained at both time points for the wild-type sperm (Supplementary Table 1). Thus the mutant sperm in the DSR were counted at 4 h after mating.

The male fertility assay
The sperm storage phenotype can also be assayed by the viable progeny produced per female per mating because the stored sperm is the main source for fertilization, whereas unstored sperm are extruded out of the uterus within 5 h after mating or as soon as the first egg is laid. Collected y°f female virgins were aged for 3 d in culture vials with added live dry yeast to enhance egg production. The vials holding the female virgins were checked for the presence of larvae before the females were used for the assay. If larvae were found, it meant that some of the females were not virgins and these flies were discarded. The male was separated away from the female immediately after mating, the mated female was allowed to lay eggs, and the viable progeny were counted when they formed pupae on the wall of the culture vial. To examine the temporal pattern of fertility, the mated female was kept in a culture vial for the first 6 or 8 h after mating and then transferred to a new vial for the remaining 10 d. Vials that had no progeny were checked for the presence of eggs. If no eggs were laid, that vial was not included in the tabulation of male fertility because the lack of progeny was the female’s fault. Later, the progeny were checked for the expected genotype to make sure that they were fathered by the experimental males.

Genetic identification and mapping of the first CG34110^lobo allele

Pck2 mutations result in a severe reduction of sperm accumulation in the female sperm storage organs (Gao et al., 2003). To identify new components of the pathway, we screened Bloomington Drosophila stock collections of viable mutations on the third chromosome for reduced sperm storage by the sperm storage assay described above. Information for Bloomington stocks is available from FlyBase (http://flybase.org). The first CG34110 allele was identified in Bloomington stock #19168 (w^118; P(XP)kal-1^D037966). Only the P(XP)kal-1^D037966 homozygous male showed the sperm storage defect, whereas the heterozygote male was wild type in terms of sperm storage. This suggested that the storage defect was caused by a recessive lesion on the P(XP)kal-1^D037966 chromosome. Such a recessive lesion could be caused by the P(XP)kal-1^D037966 insertion or by an unrelated (background) mutation on the same chromosome. To distinguish between these two possibilities, the P(XP)kal-1^D037966 insertion was excised via the P element transposase (Δ2–3). The recessive sperm storage defect remained following the precise excision of P(XP)kal-1^D037966. Thus the sperm storage lesion was due to a separate mutation but located on the P(XP)kal-1^D037966 chromosome.

To map the storage-defective lesion, meiotic recombination was carried out between P(XP)kal-1^D037966 and its proximal marker P(GT1) CG5346(D02475) (#12694) or its distal markers P(EP)farkytEY2476 (#17132) and P(SUP)Par-PigroK07717 (#14322). Individual recombinants were tested for the presence of the storage defective lesion in order to calculate its DNA coordinate. The tabulated results showed that the lesion was located ∼990 kb distal to P(XP)kal-1^D037966. The above meiotic recombination analysis also showed that the P(XP)kal-1^D037966 chromosome actually carried two genetic lesions, both independently causing male infertility, but only one located at 3R:20963561...21022720 was causing the sperm storage defect. The other lesion was located at the tip of 3R, which was removed from the P(XP)kal-1^D037966 chromosome by recombination to produce a “clean” sperm storage defective mutation, which we named the lost boys (lobo) allele, CG34110^lobo. CG34110^lobo fails to complement CG34110^MBOO722, CG34110^246 (described later), and Df(3R)Exel6201, but complements the adjacent deletion Df(3R)Exel9056, for wild-type sperm storage.

Reversion of CG34110^MBOO722 by the Minos transposase
CG34110^MBOO722 (#22880) was identified to be allelic to CG34110^lobo by genetic complementation test, and it contains an engineered transposon Mi[ET1] from the Minos transposable element (Metaxakis et al., 2005). To prove that the insertion is causing the sperm storage defect, Minos transposase was introduced into the male germline from P(nsl[LM1]22.4(#24613)). The excision of Mi[ET1], as shown by the loss of the GFP eye marker it carried, reverted the defective sperm storage phenotype back to wild type, indicating that CG34110^MBOO722 is a bona fide allele of CG34110^lobo.

Genetic screen for an additional CG34110 allele

Because CG34110 is located at (3R:20963561...21022720), a nearby P element insertion P(EPgy2)mld1^Y12290 (3R:20448650; #21378), which inserted a wild-type sperm storage phenotype and carried a red eye marker, was used to tag the starting chromosome for mutagenesis. Briefly, males carrying the tagged chromosome (w°; Tag/TM3) were treated with 20 mM EMS for 12 h as described (Zhang et al., 1999), and then crossed to female virgins carrying two third chromosome balancers, w°; TM2/TM6 (referred to as T/T), to ensure the stable transmission of all newly introduced mutations (*) in a balanced genotype of w°; Tag/T. To identify a new CG34110 allele, individual (w°; Tag/*T) males were crossed to w°; CG34110^lobo/T female virgins, and the male offspring (Tag/* CG34110^lobo) were tested in the sperm storage assay described above. One new allele of CG34110^246 was identified by screening ~1320 individual mutagenized stocks. The CG34110^246 allele produced the storage defect over CG34110^lobo, CG34110^MBOO722, or Df(3R)Exel6201.

DNA sequencing

Genomic DNA samples were isolated from homozygous mutant males (CG34110^MBOO722 or CG34110^lobo), and regions containing exons were amplified by PCR, cloned into pGEM, and sequenced. The primers Lobo1F and Lobo2R amplified exons 1–2 (885 bp); Lobo3F and Lobo4R amplified exons 3–4 (922 bp); Lobo5F and Lobo6R amplified exons 5–7 (895 bp); and Lobo7F and Lobo8R amplified exons 8–10 (946 bp). Primer sequences are as follows:

<table>
<thead>
<tr>
<th>Primer Name</th>
<th>Sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lobo1F</td>
<td>5′-CTA-ATT-AGA-ATT-AGG-AAA-GTT-TTT-TTA-GAC-3′</td>
</tr>
<tr>
<td>Lobo2R</td>
<td>5′-GCT-CGG-AAC-ATA-AGA-ATA-ATG-GAT-ATG-TG-3′</td>
</tr>
<tr>
<td>Lobo3F</td>
<td>5′-ggt-agt-taa-tcc-agt-ttt-gtc-t-3′</td>
</tr>
<tr>
<td>Lobo4F</td>
<td>5′-AGG-AGC-CGA-TGC-AAT-CCA-GGT-GCT-TCT-3′</td>
</tr>
<tr>
<td>Lobo5F</td>
<td>5′-gaa-qca-ctt-gtg-cat-cgg-ctt-ctc-3′</td>
</tr>
<tr>
<td>Lobo6F</td>
<td>5′-GCC-TTG-AGG-AGA-ATA-TTG-AGG-ATA-CTT-GTG-3′</td>
</tr>
<tr>
<td>Lobo7F</td>
<td>5′-cag-aca-agt-att-aaa-tct-ctc-ggc-3′</td>
</tr>
<tr>
<td>Lobo8R</td>
<td>5′-GCG-AGC-ATA-TCT-TGA-TTA-CGG-AGA-ATG-3′</td>
</tr>
</tbody>
</table>

Antibody production, purification, and uses

Anti-CG34110^61-874 and anti-CG34110^382-842 were produced by immunizing rabbits with synthetic peptides derived from the CG34110 sequence, CHEESQKKYEVKNS-amide (8861–874) and CENOPFN-YDYKRLVQ-amide (#828–842), respectively. Anti-FAP50^825-940 was produced by immunizing rabbits with the synthetic peptide CRRDKLERRYPQK-k-amide (#925–940) of FAP50 from C. reinhardtii. Peptide design and immunizing procedures were performed by YenZym Antibodies (San Francisco, CA). The rabbit antisera were purified using affinity resin coupled with the immunizing peptides, by means of a step-wise elution protocol as published (Gao et al.,
2003, 2004). The anti-CG34110 antibodies were used at 0.4 μg/ml for Western blotting (Lot 679A1) and 1 μg/ml for sperm staining. The anti-FAP50 antibody was used at a 1:4000 dilution (Lot 681A1F-1, salt fraction).

**Immunofluorescence microscopy**

Mature *Drosophila* sperm from a freshly dissected male SV were spread onto poly-l-lysine-coated glass slides with forceps, covered with a coverslip, and dropped into liquid N₂. After a brief moment in liquid N₂, the coverslip was removed and sperm on the slide were fixed in acetone (−20°C) and methanol (−20°C), successively, for 5 min each, followed by air drying for another 5 min. This fixation protocol (from R. Kamiya) splays the outer doublets of the flagellar axoneme, leading to the exposure of the CG34110 epitope for antibody recognition. Fixation of sperm with 4% formaldehyde did not work for this antigen. Following air drying, the slide was rehydrated in PBT and treated with Image-iT FX Signal Enhancer (Molecular Probes, Eugene, OR) for 30 min, then processed for immunostaining as published (Gao et al., 2003). The anti-CG34110 antibody was either anti-CG34110 861–874 or anti-CG34110 828–842 (1 μg/ml), and the secondary antibody was Alexa Fluor 594 goat anti-rabbit immunoglobulin (Ig) (H+L) conjugate (A-11037; Molecular Probes). The blocking solution was StartingBlock blocking buffer from Pierce (Rockford, IL).

**Characterization of sperm orientation in the reproductive tract**

Sperm orientation in the reproductive tract was imaged by using the GFP markers Protamine-GFP (Rathke et al., 2007) and Dj-GFP (Gao et al., 2003; Santel et al., 1997) (obtained from B.T. Wakimoto and R. Renkawitz-Pohl) that label the sperm head and tail, respectively. Images were captured on a Nikon multizoom AZ100 microscope with a magnification range of 10x–320x using the Nikon NIS-Elements imaging software. The microscope was fitted with a Nikon Intensilight 130W High-Pressure Mercury Lamp, a GFP HC HiSN Zero Shift Filter set with excitation wavelength (450–490 nm), dichroic mirror (495 nm), and emission filter (500–550 nm), and a Photometrics CoolSnap EZ 12-Bit Cooled CCD monochrome camera.

To visualize sperm in the male or female reproductive tract, sperm movement was induced by male–female conjugation, which results in the movement of sperm from the male SV, where mature sperm are stored, to the male ED and then to the uterus of the con-jugating female. The sperm in the uterus then move into the 2-mm-long female SR tubule and eventually return back out of the SR for fertilization. To observe specific stages in this sequence of events, liquid N₂ or dry ice was used to freeze the conjugating pair of flies at various times following copulation. To set up mating, one mating before the females were fast-frozen for imaging. In our experiments, the females generally start to lay fertilized eggs between 5 and 6 h after mating. Many eggs produced in the first 24 h hatched, indicating that the 24-h time point was appropriate for observing the SR exit movement of sperm.

To observe sperm movement inside the uterus, the inseminated uterus was dissected out of the female between 10 and 30 min following mating completion. Sperm are extremely sensitive to mechanical stimulation. We avoided poking the uterine wall as this was found to stop all sperm movement inside the uterus. Video was captured by the Nikon NIS-Elements software using the “continuous” mode (see Supplemental Movie legend for video speed).

To observe sperm movement inside the DSR, the uterus from a mated female was mounted on a slide. Without further manipulation, the DSR is already exposed and ready for imaging. For wild-type sperm, the large number of sperm stored prohibits a clear observation of sperm movement in the DSR. To overcome this, successive mating of one male with multiple females was used to reduce the sperm number in the receptacle.

**Isolation, fractionation, and Western blotting of *C. reinhardtii* flagella**

*C. reinhardtii* strains 137c (wild type), pf14, pf18, mbo1 (CC2679), mbo2 (CC3664), and mbo3 (CC2378) were grown as described (Witman, 1986). For comparison of these strains, flagella and axonemes were isolated as described (Witman, 1986) with the following modifications. For comparison of wild type and the mbo mutants, EGTA instead of Na₂EDTA was used in the HMDE solution and a 1:100 dilution of Plant Protease Inhibitor Cocktail (Sigma P9599, St. Louis, MO) was added to the solution. The same method was used for the comparison of wild type, pf14, and pf18, except that dithiothreitol (DTT) was excluded from the HMDS solution and the protease inhibitor was omitted from the HMDE solution.

For the analysis of wild-type flagellar fractions, cells from a 4-L culture (midlog phase) were resuspended in ~100 ml of 10 mM HEPES, pH 7.0. The cells were deflagellated by adding 0.5 M acetic acid to pH 4.5; 30 s later, 0.5 M KOH was added to bring the pH back to 7.0. The cells were placed on ice immediately after deflagellation and then 1 M MgSO₄, 1 M DTT, 50% sucrose, 0.5 M EDTA, 100 mM phenylmethylsulfonyl fluoride (PMSF), and 1 M HEPES at pH 7.0 were added in that order to yield final concentrations of 5 mM MgSO₄, 1 mM DTT, 5% sucrose, 0.25 mM EDTA, 1 mM PMSF, and 10 mM HEPES. A 150-ml cell suspension in 250-ml tubes was underlain with 50 ml of 25% sucrose in HMDE (10 mM HEPES, 5 mM...
MgSO₄, 1 mM DTT, 0.25 mM EDTA) and centrifuged at 853 × g for 5 min at 4°C. The supernatant was collected and the flagella harvested by centrifugation at 11,950 × g for 10 min at 4°C. Flagellar fractionation was as previously described (Pazour et al., 1999), except that Plant Protease Inhibitor Cocktail (Sigma P9599, used 1:100) was added to the flagella and all extraction solutions immediately prior to demembranation.

SDS-PAGE and Western blotting were as previously described (Pazour et al., 1999). In addition to anti-FAP50 (see above), antibodies used to probe Western blots were rabbit polyclonal anti-IFT46 (Hou et al., 2007) and mouse monoclonal anti-IC2 (King et al., 1985).

ACKNOWLEDGMENTS

This research is funded by NIH DK071073 and PKD Research Foundation to X.L., and by NIH GM030626 and funds from the Robert W. Booth Endowment to G.B.W.; G.B.W. is a member of the Mass U Mass DERC (DK32520). W.F.M. acknowledges support from the W.M. Keck Foundation. We thank R. Kamiya for sharing flagellar staining protocol, E. Spana at Duke Model System Genomics for microarray experiments, T. McClintock for information on GM770, B.T. Wakimoto and R. Renkawitz-Pohl for sperm GFP reporters, the Bloomington Drosophila Stock Center for fly stocks, R. Patten and R. Lillich for Nikon microscopic imaging, and D. Neumann for video processing. The Microscopy and Imaging Resources Laboratory is supported, in part, by NIH Center Grants P30ES06639 to the Institute of Environmental Health Sciences, P30CA22453 to the Karmas Cancer Institute, and U54RR020843 to the Center for Proteolytic Pathways, the Burnham Institute and the Perinatology Research Branch of the NICHD, Way State University.

REFERENCES


