Supplemental material JCB

Oda et al., http://www.jcb.org/cgi/content/full/jcb.201312014/DC1

Figure S1. Averaged tomograms of DMT used for Student's *t* test. Related to Fig. 2. (A and B) Individual averaged tomograms of the wild-type and streptavidin–cytochrome *c*-labeled BCCP-RSP mutant axonemes. Bars, 20 nm. (C) Relationship between the label densities of *rsp3C* (red) and the neighboring RS on the adjacent DMT. Bar, 10 nm. (D and E) Fourier shell correlation curves of the averaged DMT (D) and CP (E) tomograms. The intersection between each curve and the horizontal line at 0.5 was taken as the effective resolution. The effective resolutions of all the structures were \sim 7 nm. WT, wild type.

Figure S2. Effect of streptavidin on the motor activity of dyneins. Related to Fig. 3. (A) Binding of Alexa Fluor–conjugated streptavidin to *rsp4C* axonemes was quantified by measuring the intensity of the fluorescent signals. Binding of streptavidin appears to saturate at 20 µg/ml. The binding ratio of streptavidin at the concentration of \overline{C}_{50} is \sim 5% of the maximum. Means \pm SEM were calculated from 10 axonemes. (B and C) Sliding disintegration assays of intact axonemes. Axonemes were incubated with streptavidin (Str) or BSA, and microtubule sliding was induced with ATP and trypsin treatment. Sliding events per axoneme were counted and presented as histograms. (B) 1 mM ATP; (C) 50 µM ATP. *rsp3C* axonemes showed complete inhibition of sliding in the presence of streptavidin even with 50 µM ATP. Each of the frequencies was determined by observation of >100 axonemes. WT, wild type.

Figure S3. The swimming paths of wild-type and *pf6 rsp4C* cells. Related to Fig. 4. Images were recorded using an inverted microscope (IX70; Olympus) and a CCD camera (ORCA-R2; Hamamatsu Photonics). The trajectories of the swimming cells were detected using an ImageJ plugin, Particle Tracker (Sbalzarini and Koumoutsakos, 2005). WT, wild type. Bar, 50 µm.

Table S1. Summary of the strains used in this study

Table S1. Summary of the strains used in this study *(Continued)*

Strain	Description	Swimming speed	Beat frequency	References
$pf18$ $pf1$ -rsp3-c-bccp $pf18$ $\mathsf{r}\mathsf{p}\mathsf{s}\mathsf{3}\mathsf{C}$	Paralyzed flagella, similar to pf18			This study
$pf18pf14$ -rsp4-c-bccp $pf18$ $rsp4C^b$	Paralyzed flagella, similar to pf18	–		This study
$pf18$ pf26-rsp6-c-bccp (pf18 $rsp6C^b$	Paralyzed flagella, similar to pf18			This study

Minus signs indicate these are unmeasurable due to the immotility of the cells.
^aSensitive (insensitive) to streptavidin means that the demembranated cells of the strain show (or do not show) streptavidin-dependent inhib

Table S2. The ATPase activities and sliding speed of axonemes

Strains and treatments	ATPase activity ^a	Sliding speed ^b	
		μ m/s	
WT + BSA	0.49 ± 0.03	19.9 ± 2.6	
WT + streptavidin	0.48 ± 0.01	19.2 ± 3.1	
$rsp3C + BSA$	0.44 ± 0.02	18.8 ± 2.5	
$rsp3C + streptavidin$	0.44 ± 0.01	No sliding	
rsp3N + BSA	0.44 ± 0.04	20.1 ± 4.1	
$rsp3N + streptavidin$	0.43 ± 0.03	19.3 ± 3.5	
rsp4C + BSA	0.44 ± 0.03	18.3 ± 2.1	
$rsp4C + streptavidin$	0.47 ± 0.04	17.9 ± 4.5	
$rsp4N + BSA$	0.43 ± 0.05	19.2 ± 1.2	
rsp4N + streptavidin	0.42 ± 0.05	18.8 ± 3.3	
$rsp6C + BSA$	0.46 ± 0.03	16.7 ± 4.8	
$rsp6C + streptavidin$	0.45 ± 0.02	15.9 ± 3.7	
rspóN + BSA	0.49 ± 0.03	18.5 ± 4.4	
$rsp6N + streptavidin$	0.44 ± 0.05	18.0 ± 3.2	
$rsp11C + BSA$	0.45 ± 0.03	19.8 ± 4.0	
$rsp11C + streptavidin$	0.46 ± 0.05	19.1 ± 2.2	

The means ± SEM were calculated from 10 and 20 measurements for ATPase

activities and sliding speeds, respectively. WT, wild type.
ªThe unit of ATPase activity is micromoles P_i/minute/milligram of axoneme.
^bSliding speed of DMTs slid out of disintegrated axonemes.

Video 1. Streptavidin-dependent inhibition of motility in *rsp4* tag mutant cells. Related to Fig. 3. Swimming of demembranated, ATP-reactivated *rsp4C*, *rsp4N*, *oda1 rsp4C*, and *ida3 rsp4C* cells was observed using a dark-field microscope (BX51; Olympus). Image sequences were recorded using a high speed CCD camera (MC1362; Mikrotron) at 30 frames per second (fps; *rsp4C* and *rsp4N*) or 10 fps (*oda1 rsp4C* and *ida3 rsp4C*) and shown at 30 fps. Demembranated cells were incubated with 1 mM ATP and 2 µg/ml BSA or streptavidin for 1 min before recording.

Video 2. Suppression of the motility defect in the *pf6* mutant by *rsp4C*. Related to Fig. 4. Impaired motility of *pf6* mutant and the recovered motility of *pf6 rsp4C* live cells were recorded using an inverted microscope (IX70; Olympus). Image sequences were recorded using a high speed CCD camera (MC1362; Mikrotron) at 30 fps and shown at 30 fps.

Video 3. ODA is required for suppression of the motility defect in *pf6* mutant by *rsp4C-GFP.* Related to Fig. 4. Motility of *pf6 oda/ida* double mutants and *pf6 oda/ida rsp4C-GFP* quadruple mutants was recorded using an inverted microscope (IX70; Olympus). Image sequences were recorded using a high speed CCD camera (MC1362; Mikrotron) at 10 fps and shown at 30 fps.

References

- Adams, G.M.W., B. Huang, G. Piperno, and D.J.L. Luck. 1981. Central-pair microtubular complex of *Chlamydomonas* flagella: polypeptide composition as revealed by analysis of mutants. *J. Cell Biol.* 91:69–76. http://dx.doi.org/10.1083/jcb.91.1.69
- Dutcher, S.K., B. Huang, and D.J. Luck. 1984. Genetic dissection of the central pair microtubules of the flagella of *Chlamydomonas reinhardtii*. *J. Cell Biol.* 98:229– 236. http://dx.doi.org/10.1083/jcb.98.1.229
- Huang, B., G. Piperno, Z. Ramanis, and D.J. Luck. 1981. Radial spokes of *Chlamydomonas* flagella: genetic analysis of assembly and function. *J. Cell Biol.* 88:80–88. http://dx.doi.org/10.1083/jcb.88.1.80
- Kamiya, R. 1988. Mutations at twelve independent loci result in absence of outer dynein arms in *Chlamydomonas reinhardtii*. *J. Cell Biol.* 107:2253–2258. http:// dx.doi.org/10.1083/jcb.107.6.2253
- Kamiya, R., E. Kurimoto, and E. Muto. 1991. Two types of *Chlamydomonas* flagellar mutants missing different components of inner-arm dynein. *J. Cell Biol.* 112:441– 447. http://dx.doi.org/10.1083/jcb.112.3.441
- Kato, T., O. Kagami, T. Yagi, and R. Kamiya. 1993. Isolation of two species of *Chlamydomonas reinhardtii* flagellar mutants, ida5 and ida6, that lack a newly identified heavy chain of the inner dynein arm. *Cell Struct. Funct.* 18:371–377. http://dx.doi.org/10.1247/csf.18.371
- Mitchell, D.R., and W.S. Sale. 1999. Characterization of a *Chlamydomonas* insertional mutant that disrupts flagellar central pair microtubule-associated structures. *J. Cell Biol.* 144:293–304. http://dx.doi.org/10.1083/jcb.144.2.293
- Piperno, G., B. Huang, and D.J. Luck. 1977. Two-dimensional analysis of flagellar proteins from wild-type and paralyzed mutants of *Chlamydomonas reinhardtii. Proc. Natl. Acad. Sci. USA*. 74:1600–1604. http://dx.doi.org/10.1073/pnas.74.4.1600
- Rupp, G., E. O'Toole, and M.E. Porter. 2001. The *Chlamydomonas* PF6 locus encodes a large alanine/proline-rich polypeptide that is required for assembly of a central pair projection and regulates flagellar motility. *Mol. Biol. Cell*. 12:739–751. http://dx.doi.org/10.1091/mbc.12.3.739
- Sbalzarini, I.F., and P. Koumoutsakos. 2005. Feature point tracking and trajectory analysis for video imaging in cell biology. *J. Struct. Biol.* 151:182–195. http://dx.doi. org/10.1016/j.jsb.2005.06.002
- Takada, S., C.G. Wilkerson, K. Wakabayashi, R. Kamiya, and G.B. Witman. 2002. The outer dynein arm-docking complex: composition and characterization of a subunit (oda1) necessary for outer arm assembly. *Mol. Biol. Cell*. 13:1015–1029. http://dx.doi.org/10.1091/mbc.01-04-0201
- Witman, G.B., J. Plummer, and G. Sander. 1978. *Chlamydomonas* flagellar mutants lacking radial spokes and central tubules. Structure, composition, and function of specific axonemal components. *J. Cell Biol.* 76:729–747. http://dx.doi.org/10.1083/jcb.76.3.729
- Yang, C., and P. Yang. 2006. The flagellar motility of *Chlamydomonas* pf25 mutant lacking an AKAP-binding protein is overtly sensitive to medium conditions. *Mol. Biol. Cell*. 17:227–238. http://dx.doi.org/10.1091/mbc.E05-07-0630