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Primary Cilium Disassembly in Mammalian Cells

Occurs Predominantly by Whole-Cilium Shedding

Mary Mirvis[1], Kathleen Siemers[1,2], W. James Nelson[1,2], and Tim Stearns[2,3]

[1]Departments of [1]Molecular and Cellular Physiology, [2]Biology, and [3]Genetics,

Stanford University, Stanford, CA, 94305

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Corresponding author:

Tim Stearns

Dept. of Biology

Stanford University

Stanford, CA 94305-5020

(650) 725-6934

stearns@stanford.edu

Abstract

The primary cilium is a central signaling hub in cell proliferation and differentiation, and is built

and disassembled every cell cycle in most animal cells. Disassembly is critically important:

misregulation or delay of disassembly leads to cell cycle defects. The physical means by which

cilia are disassembled are poorly understood, and thought to involve resorption of disassembled

components into the cell body. To investigate cilium disassembly in mammalian cells, we used

rapid live-cell imaging to comprehensively characterize individual disassembly events. The

predominant mode of disassembly was rapid cilium loss via deciliation, in which the membrane

and axoneme of the cilium was shed from the cell. Gradual resorption was also observed, as well

as events in which a period of gradual resorption ended with rapid deciliation. Deciliation

resulted in intact shed cilia that could be recovered from culture medium and contained both

membrane and axoneme proteins. We modulated levels of katanin and intracellular calcium, two

putative regulators of deciliation, and found that excess katanin promotes disassembly by

deciliation, independently of calcium. Together, these results demonstrate that mammalian

ciliary disassembly involves a tunable decision between deciliation and resorption.

Introduction

Cilia are present throughout all branches of the eukarya, and are adapted to facilitate interactions between cells and their surrounding environment through the transduction of molecular and mechanical signals, and the ability to generate motion (1–3). All cilia share a core architecture consisting of a basal body (centriole), a core of stable microtubule doublets (axoneme), and a distinct ciliary membrane (4–6). In many cases, including vertebrate primary cilia and *Chlamydomonas* motile cilia, the presence of a cilium is closely linked with the cell cycle, generally forming in interphase (G0) and disassembling prior to mitosis (6–12). Misregulation or delay in primary cilia disassembly leads to defects in cell cycle progression, which underlie aberrant developmental and homeostatic phenotypes in ciliopathies and many cancers (7,13–26).

Despite recent progress in the identification of molecular players and pathways regulating primary cilia disassembly (12,22,24,27–36), the physical mechanisms by which mammalian cilia are ultimately lost have not been identified. In *Chlamydomonas*, cilia have been reported to be resorbed into the cell body preceding cell division with rates of approximately 0.3-0.7 μm/min. (26,27,32,35–45). Alternatively, under conditions of stress or pharmacological induction, comparatively rapid removal of cilia , defined as the concurrent release of membrane and axoneme from the cell body, has been described in many species as deciliation, ciliary excision, shedding, deflagellation, or flagellar autotomy (46–53). Whether deciliation occurs as part of normal primary cilium behavior, and contributes to cell cycle-linked disassembly, is unknown. In this work, we use rapid long-term live cell imaging to determine whether either of these physical mechanisms (resorption or deciliation) contributes significantly to mammalian cell cycle-associated cilia loss. Ours is the first comprehensive study of mammalian primary cilium disassembly events to determine the dynamics and underlying physical means of ciliary loss.

Results

Ciliary structures in cells undergoing serum-induced cilium disassembly

To assess the physical processes underlying ciliary disassembly, we observed ciliary morphology

in a population of mammalian cells entering the cell cycle and undergoing ciliary disassembly. We

manipulated serum level in the culture medium to synchronize the disassembly of primary cilia

(24,54) in IMCD3 cells expressing SSTR3::GFP (55), a fluorescent plasma membrane marker that

is concentrated in the ciliary membrane (Fig. 1A, S1A). The majority of serum-starved cells (60

+/- 9.09%) were ciliated. Serum stimulation for 6 h resulted in a decrease in the fraction of cells

with a cilium (30 +/- 0.4%) to levels comparable to asynchronously cycling cells (Fig. 1B). Serum-

induced ciliary disassembly has been shown to require the function of HDAC6, a deacetylase of

microtubules and cortactin [refs]. Cells treated with 2 μM tubacin, an HDAC6 inhibitor, failed to

undergo serum-induced ciliary loss (Fig. 1B) (24,56,57). Mitotic cells accumulated following

serum stimulation (Fig. SlB), but were inhibited or delayed in tubacin-treated cells (Fig. S1B),

consistent with a requirement for ciliary disassembly prior to mitotic entry (10,11,58–60). Thus,

serum stimulation induces synchronous, cell cycle-linked ciliary disassembly in these cells.

Fig 1. Serum stimulation of IMCD3 cells reveals non-canonical ciliary structures. Serum

starved IMCD3-SSTR3::GFP cells were stimulated with 10% serum in order to synchronize

ciliary disassembly. A, C-E) Cells were fixed at indicated time points after serum addition and

immunostained for pericentrin to mark the basal body (PCNT, white) and acetylated tubulin to

mark the axoneme (acTub, red). A) Morphology of a normal, intact cilium in a starved cell. B)

The population of ciliated cells quantified over a serum stimulation time course. Asynchronous

(Async) and serum starved (Stv) controls were included at 0 hr and 6 hr. Cells treated in parallel

with 2 µM tubacin. C-E) Non-canonical ciliary structures identified in serum stimulated cell

populations. C) Discontinuous acTub staining, in this case accompanied by narrowing of the

membrane. D) A ciliary stub, marked by punctate acTub and SSTR3 fluorescence. E) Full-length

axoneme marked by acTub, lacking corresponding SSTR3::GFP signal. F-G) Stacked plots of

cilia morphologies observed during serum stimulation in (F) DMSO and (G) tubacin-treated

cells. Quantifications are based on means of 3 independent experiments with 150-200 cells

analyzed per condition per replicate. Error bars – S.E.M. Statistical significance was assessed by

unpaired t-test, *$p<0.05$, **$p<0.01$, ***$p<0.001$.

Seeking a more systematic understanding of disassembly behaviors, we next

characterized cilia morphology in cells undergoing ciliary disassembly during the 6-hr serum

stimulation time course. We identified three types of cilium structures as likely disassembly

intermediates in fixed cells expressing SSTR3::GFP (Fig. 1C-G): 1) a discontinuous axoneme,

marked by a gap in acTub staining in all z-planes, ("Discontinuous acTub", Fig. 1C); 2) a ciliary

stub, characterized by a short (<1 μm) cilium positive for both acTub and SSTR3 membrane

fluorescence ("acTub+ SSTR3+ Stub", Fig. 1D); and 3) an axoneme marked by linear acTub

fluorescence (>1 μm), but lacking corresponding membrane SSTR3 fluorescence ("acTub+

SSTR3-", Fig. 1E). All intermediate structures were rare in serum-starved cells, but at 2-3 h after

serum-stimulation they comprised the majority of detectable cilia (Fig. 1F). Tubacin treatment

prevented the enrichment of all three structures in serum-stimulated cells (Fig. 1G), indicating

that these structures are most likely representative of disassembling cilia. These results suggest

that the mechanism of ciliary disassembly might be variable even within a single cell population,

and we next sought to use live cell imaging to observe the dynamics of cilia disassembly.

Rapid deciliation is the predominant mode of ciliary disassembly

To observe the spatio-temporal features of cilium disassembly directly, we generated IMCD3-

SSTR3::GFP cells which stably co-expressed a basal body marker (mCherry-PACT) (see

Materials & Methods). Live cells were imaged immediately following serum stimulation with full

confocal stacks acquired continuously for 6-12 h at 90 sec intervals. Apically-facing cilia were

selected for analysis, to avoid artifacts caused by deformations of basally-facing cilia by the glass

imaging dish. Observations of serum-starved cells were used as controls for ciliary behaviors not

associated with disassembly (Fig. 2A.1, Fig. S2A).

Figure 2. Live-cell analysis of cilia disassembly reveal highly heterogeneous dynamics. A)

Still images and raw length curves representing dynamics of individual cilia disassembly events.

Length measurements based on SSTR3::GFP fluorescence. Scale bar 5 μm. A.1) Control serum

starved cilium measured over 12 hr period undergoes slight length change of 1.66 μm at a rate of

0.003 μm/min. A.2) Gradual disassembly with a rate of 0.016 μm/min. A.3) Instant disassembly,

with an approximate minimum rate of 4.72 μm/min. A.4) Combined disassembly, consisting of an

initial stage of gradual shortening at a rate of 0.029 μm/min, followed by instant loss at a minimum

rate of 5.69 μm/min. B-E) Semi-automated analysis of disassembly events. B) Criteria for defining

gradual, instant, and combined behaviors. See text and Fig. S2 for more details. C-E) Cumulative

normalized length vs. time curves for all (C) *gradual*, (D) *instant*, and (E) *combined* disassembly

events. Open circles indicate individual event start points. F) Disassembly rates within dynamic

groups. Significance was determined by unpaired t-test, *p<0.05, **p<0.01, ***p<0.001. Error

bars – S.D. H) Relative frequency of disassembly behaviors (n=70).

Video sequences of disassembling cilia revealed a striking range of disassembly behaviors

(Fig. 2A and Movies S1-4). We grouped these behaviors into three categories: *gradual* - cilium

length reduction over at least two consecutive time points resulting in terminal cilium loss (e.g.,

Fig. 2A.2, 0.02 μm/min; $T_{start} \neq T_{final-1}$, see Fig. S2); *instant* - a single discrete cilium loss event

within a single imaging frame, i.e. 30-90 sec (e.g., Fig. 2A.3, ≥4.72 μm/min $L_{final-1} > 1.5$ μm); and

combined – a period of *gradual* disassembly directly followed by *instant* loss (e.g., Fig. 2A.4,

gradual phase (0.03 μm/min;), preceding rapid loss within 46 seconds, ≥5.69 μm/min).. To reduce

bias in our cumulative analysis, we developed an algorithm to normalize ciliary length fluctuations

to controls, identify a disassembly start point, and assign each event to one of the three categories

described above (Fig. 2B & S2, Materials & Methods). Disassembly curves were normalized by

time (to 1000 arbitrary units) and ciliary length (to the maximum length of each cilium) (Fig. 2C-

E). The *gradual* averaged curve shows early ciliary shortening with event start points distributed

along the curve, followed by a period of consistent shortening in the last ~150 normalized time

units as the slope of the curve increases (Fig. 2C). The *instant* averaged curve appears nearly

horizontal until the last point; start points were nearly all clustered in the last ~10 time units (Fig.

2D). The *combined* averaged curve features a period of slight slope characteristic of *gradual*

dynamics followed by an *instant* cilia loss event, with start points distributed along the curve (Fig.

2E).

Ciliary disassembly rates spanned several orders of magnitude ($10^{-3} – 10^1$ μm/min (Fig.

2F)), demonstrating the dynamic heterogeneity of the process. The slowest *gradual* disassembly

154 events were on the order of several hours, while the fastest *instant* events (10^1 μm/min) represented

155 behaviors in which an entire cilium was lost in less than 90 seconds. Within the *combined* category,

156 the rate of the first *gradual* step (0.08 μm/min ± 0.26) and second *instant* step (3.41 μm/min ±

157 2.10) were not significantly different from those of the *gradual*-only (0.08 μm/min ± 0.11) and

158 *instant*-only (3.88 μm/min ± 1.80) rates, respectively (Fig. 2F). Further, the majority of ciliary

159 length (72.6 ± 4.5%) was lost during the *instant* stage. Thus, *combined* disassembly likely

160 represents both *gradual* and *instant* mechanisms occurring within one cilium disassembly event,

161 rather than an independent third behavior with biphasic dynamics.

162   Strikingly, we found that the *instant* and *combined* groups together comprised 83.1%

163 (n=70) of the observed disassembly events (Fig. 2G). Thus, events with *instant* dynamics, which

164 occur within seconds, are the predominant behavior for terminal ciliary loss. Rates of *gradual*

165 disassembly were heterogeneous, but roughly consistent with previously reported rates of

166 resorption (36,43,44), while *instant* dynamics were significantly more rapid than would be

167 expected for resorption. To test whether *instant* disassembly dynamics might be consistent with

168 deciliation, we examined the dynamics of deciliation induced by dibucaine, which likely raises

169 intracellular calcium (47,49,50,61). Dibucaine-induced deciliation had qualitative features and a

170 dynamic profile similar to serum-induced *instant* disassembly (Fig. S3 & 2A.2). Therefore, we

171 hypothesized that deciliation is the physical mechanism underlying *instant* cilia loss.

172   In a rare instance, we observed direct shedding of the entire visible cilium from the surface

173 of a serum-stimulated cell (Fig. 3A, Movie S5). The shed cilium in the z-stack shown in Fig. 3A

174 has a fragmented appearance. Due to the rapid time scale of the shedding event, the shed cilium

175 can travel a considerable distance (>1μm) in the time between individual z-slices (roughly 2.6 sec)

176 within the stack. As a result, the shift in apparent location of the same object in subsequent slices

causes the final imaged object to appear distorted – artificially elongated or with the appearance

of separated fragments. We note that the segments in such sequences were visualized as a co-

migrating cluster, rather than dispersing independently, consistent with the interpretation that they

are parts of one structure imaged at slightly different times. Therefore, we interpret the fragmented

appearance of the cilium in Fig. 3A as the result of motion of the imaged object during acquisition,

rather than a biological change in morphology, and hypothesize that these images represent a

deciliation event.

Figure 3. Observation and validation of whole-cilium shedding. A) Serum stimulated cell,

imaged at 54-second intervals. A short ciliary membrane (in white outline) is visibly shed from

the cell surface. Time labels are interval of stack-acquisition. bar, 5 μm. B) Partial ciliary shedding

in IMCD3-SSTR3::GFP cells transiently expressing mCherry-α-tubulin, imaged at 30 s-intervals.

Intact and shed portions of the cilium are demarcated with a white outline. Tubulin is visible in

shed fragments. Scale bar, 3 μm. C-E) Ciliary immune-capture. Serum stimulation media were

incubated on immobilized anti-SSTR3 antibody. Isolated cilia were observed by C-D) confocal

fluorescent microscopy (scale bar, 2 μm) and E) SEM. Scale bar, 500nm. C-D) Immune-captured

cilium from IMCD3-SSTR3::GFP cells transfected with mCherry-α-tubulin. D) Normalized

quantification of (C), defined as elongated SSTR3+ objects at least 1.5 μm in length. Tubacin

treatment reduces the prevalence of captured cilia. F-G) Filter-spin concentration of shed cilia.

Serum stimulation media from IMCD3 cells with no endogenous fluorescence was concentrated

either by (F) vacuum & centrifugation filtration for immunofluorescence or (G) centrifugation

pelleting for subsequent Western blot. Media from artificially deciliated cells were included as a

positive control. F) Filtration-concentrated samples were processed for immunofluorescence

against IFT88 and α-tubulin. Scale bar, 20 μm. Representative insets show full-length cilia:

6.82μm (deciliated), 5.94μm (starved), and 6.10μm (stimulated). G) Western blot of concentrated

material shows presence of ciliary markers at expected molecular weights: α-tubulin & acetylated

tubulin. Molecular weights are indicated (kDa). Asterisk (*) denotes position of a large BSA band

present in samples derived from serum-containing medium. Two replicates per condition are

shown as side-by-side bands.

The rapid nature of the deciliation event shown in Fig. 3A (<54 secs), and the diffusion of

the shed ciliary remnant(s) away from the site of origin is consistent with the *instant* loss dynamics

found in 83.1% of serum-induced disassembly events (Fig. 2G) and in dibucaine-treated cells (Fig.

S3). In addition, cilia shed under our culture conditions from cells expressing mCherry-α-tubulin

contained tubulin in shed ciliary fragments (Fig. 3B) suggesting that the axoneme is shed together

with the ciliary membrane. These results further support the hypothesis that *instant* cilium loss

represents ciliary disassembly via deciliation.

Recovery of whole cilia from culture media demonstrates that deciliation occurs during

ciliary disassembly

If deciliation is a major mode of cilium disassembly, we expect to be able to recover whole cilia

from culture medium. These cilia should be of plausible length for whole cilia (at least 1.5μm, see

Fig. S2), and contain membrane- and axoneme-specific components. We developed two methods

to enrich for ciliary fragments spontaneously released at low concentration from serum-stimulated

cells (Fig. 3C-G, S4). First, we used immuno-capture of fluorescently-labeled cilia to directly

visualize unperturbed ciliary fragments. Culture medium from serum-stimulated IMCD3::SSTR3-

GFP cells transiently expressing mCherry-α-tubulin was incubated on imaging dishes coated with

an antibody against the extracellular domain of SSTR3 (Fig. S4A). Samples were imaged, without

fixation, by fluorescence; we were indeed able to reproducibly identify cilia marked by both

SSTR3-GFP and mCherry-α-tubulin captured in this manner (Fig. 3C). We interpret that the

jagged appearance of the cilia is due to thermal motion of the sample during stack acquisition of

material that is not firmly fixed to the substrate. Compared to control serum-starved medium,

serum-stimulated medium yielded a 4-fold increase in captured cilia. In addition, pre-treatment

with tubacin decreased the number of captured cilia to control levels (Fig. 3D). Finally, we found

objects with dimensions consistent with intact shed cilia after fixation and imaging by scanning

electron microscopy (Fig 3E).

The cilia immune-capture method was limited by low yield and further sample loss due to

the instability of antibody-bound cilia, which hindered subsequent composition analysis by

immunofluorescence or biochemistry. Therefore, we used a complementary method to increase

yield, in which culture media were subjected to a series of filtration and centrifugation steps to

concentrate ciliary material approximately 500-fold (Fig. 3F-G, S4B). As a positive control,

serum-starved cells were artificially deciliated with high-calcium buffer (62) (see *Materials and*

Methods). Immunostaining for axoneme markers (IFT88, α-tubulin, and acetylated tubulin)

demonstrated increased abundance of ciliary structures, many with the dimensions (1.5-7 μm)

expected of whole cilia (Fig. 3F). Immunoblotting against IFT88, α-tubulin, and acetylated

tubulin further confirmed enrichment of ciliary proteins in the concentrated medium (Fig. 3G).

These results indicate that whole cilia, including membrane and axoneme components, are shed

during ciliary disassembly.

Together, these two independent ciliary isolation methods suggest that deciliation occurs

during serum-induced ciliary disassembly, and is the phenomenon likely underlying *instant*

ciliary disassembly dynamics.

p60 katanin overexpression promotes *instant* ciliary loss

We next sought to gain insight into the regulation of deciliation. Although this process has been

observed in several organisms (49,63–65), the underlying machinery and mechanism of

deciliation have been elusive. A central requirement for complete deciliation is the disruption of

axonemal microtubules at the ciliary base (44,51,66,67). The microtubule-severing enzyme

katanin has been proposed as a candidate for this function in *Chlamydomonas* and *Tetrahymena*,

and has also been shown to have a general regulatory relationship with primary cilia

(46,51,66,68–71). Katanin is also required for microtubule rearrangement in mitotic spindle

formation (69,70,72,73), but its role in primary cilia disassembly is poorly understood.

To examine the potential regulation of ciliary disassembly by katanin, we manipulated

katanin levels by depletion or overexpression. We found that functional depletion of the catalytic

subunit of katanin, p60 (KATNA1), by siRNA or expression of a catalytically inactive mutant

(74–76) caused inviability in IMCD3 cells (data not shown), consistent with its function in

mitosis. We then overexpressed p60 katanin by creating IMCD3 cells stably co-expressing

SSTR3-GFP and turboRFP-p60. Consistent with previous reports (46,70,74,75,77,78), we

observed diffuse localization of p60 in the cytoplasm in both tRFP- and tRFP-p60-expressing

cells. In addition, in about 30% of ciliated cells, p60 localized near the base of the primary cilium

(Fig. 4A). Cytoplasmic acetylated tubulin intensity was reduced in serum-starved and serum-

stimulated tRFP-p60 cells compared to the control (Fig. S6A-B), consistent with increased

severing and destabilization of microtubules caused by katanin overexpression (71,74,79). We

conclude that overexpressed katanin is functional.

Figure 4. tRFP-p60 overexpression reduces ciliary length, promotes *instant* disassembly,

and counteracts effects of [Ca$^{2+}_i$] modulation on cilia. A-D) IMCD3-SSTR3::GFP cells stably

expressing turboRFP (tRFP) or tRFP-p60 fusion. A) Serum starved tRFP and p60 cells were

fixed, and stained with a polyclonal antibody against p60. (green – SSTR3::GFP; red – tRFP;

white – total p60 stain). B) Percent ciliation calculated from fixed starved tRFP and tRFP-p60

cells. Data from at least 7 independent experiments. C) Cilia lengths measured from confocal

stacks of live cells. Data pooled from at least 3 independent experiments, at least 50 cilia per

experiment. Statistical significance from Mann-Whitney U test. D) Relative frequencies of

gradual, *instant*, and *combined* dynamic behaviors in tRFP and tRFP-p60 cells. Data pooled

from at least 4 independent experiments. E-F) Effects of BAPTA-AM on (E) ciliary abundance,

disassembly and (F) length. Cilia counts from fixed populations, normalized to respective DMSO

controls; length from live cells. tRFP and p60 cells were starved and pre-treated with DMSO, or

1 µM BAPTA-AM (30 min). E) BAPTA-AM pre-treated cells were subjected to serum

stimulation and fixed at indicated time points. Data from 3 independent experiments, at least 100

cells counted per condition. Statistical significance was determined by unpaired t-test. G) Model

for regulation of ciliary disassembly. Major regulators of ciliary disassembly function at two

decision points – whether (Decision 1) and how (Decision 2) to disassemble the cilium, which is

dominated by deciliation (orange), but also features resorption (blue), and combined resorption-

deciliation (green). Katanin (p60) and Ca^{2+} can promote deciliation at Decision 2 independently

and/or antagonistically. Regulators of disassembly may further contribute to either decision

indirectly via modulation of cytoskeletal rearrangement (magenta). See text for full description.

Next, we determined whether tRFP-p60 katanin expression influenced overall assembly

and disassembly of cilia. Total levels of ciliation in response to serum starvation (Fig. 4B) and

stimulation (Fig. S5C) were unaffected, however, ciliary length was significantly reduced in

tRFP-p60 cells (Fig. 4C). Furthermore, the extent of inhibition of ciliary disassembly via tubacin

(19,24,34,80) and cytochalasin D (4,81,82) was unaffected in tRFP-p60 cells (Fig. S5C).

Therefore, tRFP-p60 katanin expression influences ciliary structure, but is not sufficient to

induce ciliary disassembly in serum-starved cells, and any effect of expression likely occurs

downstream of HDAC6 activity.

We next asked whether tRFP-p60 expression affects ciliary disassembly dynamics in

serum-stimulated cells. In cells expressing only tRFP, terminal cilium loss by *instant* dynamics

comprised 86.7% of disassembly events (n=61, 33.3% *instant* and 53.3% *combined*), consistent

with our analysis in Figure 2G. However, in tRFP-p60-expressing cells, *gradual* disassembly was

virtually eliminated, while the frequency of *instant* disassembly increased, resulting in 98% of

disassembly events featuring *instant* terminal cilium loss (n=50, 50% *instant* and 48% *combined*)

(Fig. 4D). Thus, tRFP-p60 expression shifts the distribution of disassembly behaviors toward

instant ciliary loss dynamics. These results suggest that increased katanin activity is capable of

modulating ciliary disassembly behavior by promoting deciliation with *instant* dynamics, and that

the distribution of heterogeneous disassembly behaviors is tunable by mechanistic regulators.

Katanin p60 overexpression blocks the effects of Ca^{2+} modulation on ciliary disassembly

High intracellular calcium concentration ($[Ca^{2+}]_i$) can trigger deciliation, and many methods of

experimentally inducing deciliation do so by raising $[Ca^{2+}]_i$ ((46,47,49–51,61,62,83–88), also see

Figs. 3F-G & S3). p60-katanin function and Ca^{2+}_i are both necessary for experimentally-induced

deciliation in isolated flagella (46). Additionally, calcium-calmodulin signaling functions

upstream of AurA, a key regulator of ciliary disassembly upstream of HDAC6 (23,35,89),

suggesting a broader role for cytoplasmic calcium in regulating ciliary disassembly via all of the

behaviors we have identified. Thus, we hypothesized that calcium and katanin functions may

cooperate in serum-induced ciliary disassembly. We asked whether, in the presence of high

$[Ca^{2+}]_i$, the frequency of cilium loss would be exacerbated by expression of tRFP-p60. Cells were

serum-starved to promote ciliation, and then treated with small molecule drugs to modulate

$[Ca^{2+}]_i$ levels. In both tRFP- and tRFP-p60-expressing cells, raising $[Ca^{2+}]_i$ with either 1 μM

ionomycin (90) or 190 μM dibucaine, reduced ciliary abundance and length to a similar degree

(Fig. S5). Treating cells with 5 μM thapsigargin, which raises $[Ca^{2+}]_i$ by releasing ER stores

(42,65, 67), also reduced ciliation but not cilia length (50) in control tRFP-expressing cells.

Intriguingly, this effect was reversed in tRFP-p60-expressing cells, which exhibited a slight

increase in ciliation and cilia length in response to thapsigargin (Fig. S5C-D). Overall, tRFP-p60-

expressing cells did not exhibit elevated rates of ciliary loss induced by high $[Ca^{2+}]_i$.

Conversely, we asked what effects depletion of $[Ca2+]_i$ would have on ciliary

disassembly in tRFP- and tRFP-p60-expressing cells. BAPTA-AM, a cell-permeable Ca^{2+}

chelator (92), did not affect ciliary length in starved cells, but inhibited ciliary disassembly in

serum-stimulated tRFP cells, (Fig. 4E-F), consistently with published work (23). However,

disassembly was not impaired in serum-stimulated tRFP-p60 cells (Fig. 4E), and ciliary length

was reduced in starved cells (Fig. 4F). Therefore, tRFP-p60 katanin expression can overcome the

requirement for $[Ca^{2+}]_i$ in ciliary disassembly. We summarize these results in a schematic in Fig.

S6E. Overall, we found that overexpression of tRFP-p60 eliminated or reversed the effects of

both increasing $[Ca^{2+}]_i$ with thapsigargin (Fig. S6C-D) and reducing $[Ca^{2+}]_i$ with BAPTA-AM

(Fig. 4E-F). Taken together, these results indicate that $[Ca^{2+}]_i$ and katanin do not act

cooperatively to promote ciliary loss. Rather, the negative regulation of cilia by $[Ca^{2+}]_i$ appears to

be mitigated or reversed in the presence of excess p60 katanin.

Discussion

We comprehensively characterized the disassembly dynamics and behaviors of IMCD3

primary cilia, a process critical to tissue homeostasis and development in vertebrates. Here we

will first present a model for ciliary disassembly based on these data, and then discuss

implications of that model.

Our results suggest that there are at least two mechanisms of ciliary disassembly in

mammalian cells: resorption, in which the axoneme is depolymerized and ciliary contents are

incorporated into the cell, and deciliation, in which the axoneme is excised near its base. We

have incorporated these in a model (Fig. 4G) in which ciliary disassembly requires at least two

major decision points – Decision 1: when to disassemble the cilium; and Decision 2: when to

invoke instant deciliation during disassembly. Decision 1 is controlled by Aurora A, HDAC6,

and other elements (24,34,54,80,93). Decision 2, in IMCD3 cells, results in deciliation

immediately (*instant*), after a delay (*combined*), or not at all (*gradual*). We assume here that

resorption of the cilium, as occurs in *combined* and *gradual* events, is the default mode of

disassembly, and that rapid deciliation, when invoked, overrides the slower-acting resorption.

Thus, cilium disassembly is a tunable decision in at least two ways – when to remove the cilium,

and the mechanism by which that removal is accomplished, both of which are likely to differ in

different cell types and different contexts.

We manipulated the system in several ways and found that the activity of overexpressed

katanin biases disassembly events nearly exclusively toward deciliation, likely representing an

intervention at Decision 2. Whether and how katanin might sever axoneme microtubules in

deciliation, or whether it is indeed required for deciliation (94) remain critical outstanding

questions. Katanin may also indirectly influence cilia, perhaps by severing centrosomal

microtubules and interfering with ciliary protein trafficking (in line with a diffuse staining

pattern at the cilium base, Fig. 4A), or by modulating the available pool of cytoplasmic tubulin

(95,96). These hypotheses could help explain why tRFP-p60 expression negatively affects cilia

length but not formation.

Calcium is necessary for ciliary disassembly (23) and sufficient to drive deciliation

(63,64,85,97), likely acting at both Decisions 1 and 2. Although the role of calcium is likely

multifaceted, it seems that calcium and increased p60 katanin activity may function

independently, and also negatively interact at the Decision 2 nexus (Fig. 4E-F, S6C-E). Despite

the requirement for Ca^{2+} for disassembly (Decision 1) and deciliation (Decision 2) in normal

conditions, tRFP-p60 cells were able to undergo ciliary disassembly after $[Ca^{2+}]_I$ chelation, likely

via deciliation. This suggests the existence of a Ca^{2+}-independent deciliation pathway, as has

been suggested previously (64). Alternatively, overexpressed p60 may promote disassembly via

resorption or other means in the absence of $[Ca^{2+}]_i$. This relationship may be consistent with the

finding that calcium binding inactivates p60 severing activity *in vitro* (76). We speculate that the

activities of katanin and $[Ca^{2+}]_i$ in modulating ciliary behavior may depend on their relative

levels in the cell (Fig. S6E).

We emphasize that disassembly of the cilium, a major organelle of the cell, likely

involves a complex interplay between general ciliary trafficking and regulation, cytoskeletal

dynamics, and intracellular signaling ((4,9), Fig. 4G), and that our manipulations of calcium and

katanin are best viewed as initial probing into the molecular nature of these decisions. Further

work will be required to understand the molecular mechanisms and must take into account that

many key regulators of ciliary disassembly have additional roles in cytoskeletal regulation

(22,32,54) and other cellular functions, including calcium (98,99), AurA (100–102), HDAC6

(4,103–106), and katanin (69,73,107).

Ciliary disassembly behaviors varied both in the dynamics (10^{-3} to 10^{1} μm/min) and

physical process (resorption vs. deciliation). The co-existence of resorption and deciliation in

the same cilium (*combined* disassembly) is intriguing and may suggest independent or

differential regulation of the distal and proximal portions of the cilium (36). It might be, for

example, that structural features of the axoneme, such as doublet-singlet microtubule interface or

post-translational modifications, contribute to differential regulation of ciliary regions (108–

110). We were unable to observe the axoneme directly in our live cell imaging experiments,

however, in fixed serum-stimulated cells, we identified several non-canonical structures that hint

at the fate of the axoneme during ciliary disassembly. These included discontinuous axoneme

staining that might reflect partial breaks away from the base, short axoneme stubs that could

represent a remnant of a severed or resorbed cilium (111–113), and even axonemes without

corresponding ciliary membrane staining, possibly representing a portion of axoneme retracted

into the cell, as has been previously reported (39). While these interpretations are speculative due

to the markers used and the nature of static representations of this dynamic process, the relatively

low abundance of these structures in starved and tubacin-treated conditions indicates that they

may represent ciliary disassembly intermediates.

We observed deciliation as a means for cell cycle-linked ciliary disassembly, whereas

previous descriptions of such behavior in mammalian cells have only been under conditions of

experimentally induced stress (50,52). The morphology and composition of isolated cilia

confirmed two major points supporting the interpretation that the observed *instant* disassembly

events represent deciliation: 1) the entire ciliary membrane can be shed from cells as an intact

structure; and 2) shed ciliary membranes contain tubulin, suggesting that the axoneme is severed

and shed along with the ciliary membrane. Interestingly, release of a small membrane segment

from the ciliary tip, referred to as apical abscission, decapitation, or release of ciliary ectosomes,

has been described in several contexts (9,80,114–117), but it is unclear whether axoneme

components are present in these structures. Ciliary decapitation was previously reported as an

initiating step in the cilia disassembly process (80), as well as in assembling cilia (9). Although

we observed similar tip-shedding behaviors in IMCD3 cells (M. Mirvis, unpublished results),

their relationship to ciliary disassembly was not clear and they did not necessarily precede

disassembly events. It would be particularly interesting to test whether there is a mechanistic link

between these events by investigating whether PI(4,5)P$_2$- and F-actin-mediated membrane

constriction that drives decapitation (80) participates in deciliation from the ciliary base as

well.Finally, the implications of our findings for understanding cilia disassembly should be

considered in the context of the general features of cultured kidney-derived epithelial cells, in

comparison to and contrast with cilia in other experimental approaches, cell types, tissues, and

organisms. Although most cilia share a similar core ciliary structure and associated machinery,

differences in structure and function (i.e. primary vs. motile/specialized) and the relative size of

cilia to the cell body, are likely to be relevant to the mechanisms of ciliary assembly and

disassembly.

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Materials & Methods
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Cell Culture. IMCD3 cells were grown in DMEM-F12 medium with 10% fetal bovine serum

and 1% penicillin-streptomycin-kanamycin antibiotic cocktail. Cells were passaged every 2-3

days at a dilution of 1:10-1:20. Cells were tested for mycoplasma with Sigma LookOut

Mycoplasma PCR Detection Kit (Cat#MP0035) as directed by the manufacturer, and incidences

of mycoplasma contamination was treated with Mycoplasma Removal Agent (MP Biomedicals,

#093050044). Following decontamination, experiments that were potentially affected by

mycoplasma contamination were repeated at least three times to determine any difference in

results, and no significant differences were observed.

Serum Starvation and Stimulation. Cells were seeded in 24- or 6-well dishes with glass

coverslips for imaging following fixation, or 35 mm glass-bottomed MatTek dishes (#P35G-0-

10-C) for live imaging. 24-well dishes were seeded at a density of 1.5×10^4 cells and 6-well and

35 mm MatTek dishes at $1-1.5\times10^5$, to achieve 50-70% confluence next day. For serum-

starvation, cells were washed once with 0.2% DMEM-F12 + PSK, then grown in 0.2% DMEM-

F12 + PSK for 24 hr. Serum stimulation was by either re-addition of FBS directly to dishes to

10% final concentration, or replacement with 10% FBS DMEM-F12.

Antibodies. The following antibodies and dilutions were used. Acetylated tubulin mouse

monoclonal 6-11B-1 (1:1000 for IF & WB) (Sigma-Aldrich Cat# T7451); Pericentrin rabbit

polyclonal Poly19237 (1:500 for IF) (Covance Cat #PRB-432C, now BioLegend); Arl13b rabbit

polyclonal (1:250-1:500 for IF) (Proteintech Cat# 17711-1-AP); N19-SSTR3 antibody (rabbit

polyclonal) (Santa Cruz Cat #sc-11610, discontinued); IFT88 rabbit (1:500 for IF & WB)

(GeneTex, Cat#79169); α-tubulin YL1/2 (1:1000 for IF & WB), (ThermoFisher #MA1-080017);

alpha-tubulin DM1a (1:1000 for IF & WB) (ThermoFisher #62204); rabbit monoclonal anti-p60

EPR5071, (1:250 IF), (Abcam Cat# ab111881); rabbit polyclonal anti-KATNA1, (1:100-250 IF)

(Proteintech Cat#17560-1-AP). Anti-rabbit GFP (1:250) (Life Technologies, #A11122); Anti-

mouse GFP (1:1000) (Roche, #11063100). Secondary antibodies used were: Anti-mouse

Rhodamine (1:1000) (Jackson ImmunoResearch, #715-295-150), Anti-rabbit FITC (1:1000)

(Jackson ImmunoResearch, #111-095-003), Anti-rabbit Alexa647 (1:200) (Life Technologies,

#A21245), Anti-mouse Alexa647 (1:200) (Life Technologies, #A21236), Hoescht (1:1000-2000)

(Molecular Probes, #H-3570).

Chemicals. Tubacin (Sigma-Aldrich, #SML0065) at 2 µM in DMSO; dibucaine hydrochloride,

(Sigma-Aldrich #285552) at 190 µM in DMSO. The following were used at 1µM in DMSO:

Cytochalasin D (Sigma-Aldrich #PHZ1063), Thapsigargin, (Sigma-Aldrich #T9033). BAPTA-

AM (Sigma-Aldrich #A1076). Ionomycin, 10 mM stock was a gift from the Rich Lewis

laboratory, Stanford Univ.

Generation of stable cell lines. IMCD3-SSTR3::GFP-mCherry::PACT: mCherry::PACT was

cloned from a pLV plasmid (pTS3488, created by multi-site Gateway cloning by Christian

Hoerner) onto pLV-Puro-EF1a construct using Gibson cloning. Lentivirus with the cloned

construct was generated in HEK293T and used to infect IMCD3-SSTR3::GFP (gift from

Nachury laboratory, (55)) under selection with 800 mg/mL puromycin for 4-5 days. Infected

cells were FACS-sorted into polyclonal populations by mCherry fluorescence intensity, and a

pool of low-expressing cells was selected to prevent over-expression phenotypes of a

centrosomal protein.

Katanin expression constructs: Mammalian expression constructs for turboRFP and

turboRFP::p60 (p60 domain of mouse katanin) were designed and ordered from VectorBuilder.

All constructs were amplified by transformation in DH5α and maxi-prep (Qiagen #12165).

IMCD3-SSTR3::GFP cells were transfected with each construct with ThermoFisher

Lipofectamine 3000 according to manufacturer's protocol (#L3000015). The next day, cells were

subjected to G418 selection (800ng/µL for 5-6 days). Cells were sorted by FACS into low-,

medium-, and high-expressing pools, and maintained in DMEM-F12 10% FBS + PSK and 250

ng/µL G418 to maintain transgene expression.

Transient transfection. mCherry-α-tubulin mammalian expression construct (gift from Angela

Barth) was transfected into IMCD3-SSTR3::GFP cells. Transfections were performed using

Lipofectamine 3000 transfection reagent according to manufacturer's protocol.

Immunofluorescence microscopy. Generally, fixation for immunofluorescence microscopy was

done with 100% methanol for 5 minutes at -20°C, followed by washes with 0.1% Triton X-100

in PBS at room temperature for 2 minutes, and washed 3 times in PBS. Samples were blocked

for 1 hr at RT°C or overnight at 4°C in 2% BSA, 1% goat serum, 75mM NaN$_3$. Antibodies were

diluted to the indicated concentrations in blocking buffer. Primary antibody incubations were

performed for 1 hr at RT°C or overnight at 4°C. Secondary antibody incubations were performed

for 1-2 hr at RT°C. Following each antibody incubation, samples were washed 3 times in PBS +

0.05% Tween-20 for 5 mins each at RT°C.

Images were acquired with a Zeiss Axiovert 200 inverted epifluorescence microscope and a 63x

objective, or a Leica SP8 scanning laser confocal microscope with LASX Software, using

mercury or argon lamps with white light laser excitation, and a 63x 1.4 NA oil objective.

Exposure times were constant during each experiment. For imaging of serum-starved and serum-

stimulated cells, fields of view were selected based on DAPI staining by two critieria: 1) to select

for moderate cell density, in order to avoid effects of high density on cell cycle and ciliation; and

2) to eliminate bias in % cilia quantifications from scanning by ciliary markers.

Live-cell confocal microscopy. Cells were cultured on glass-bottomed Mattek dishes and

imaged in DMEM-F12 media with 15mM HEPES without phenol red. Movies were acquired 4-

12 hr after serum stimulation with a Leica SP8 scanning laser confocal microscope using 0.5 μm

z-slices, 30-90 sec intervals, autofocus, in a 37°C incubator, and red and green channels were

acquired simultaneously. The video file was saved as .lif from LASX software and opened in

Imaris x64 8.0.2 as a 3D render for analysis of cilia disassembly dynamics and basal body

positioning.

Data analysis. Cilia counts and length measurements were performed either manually in Fiji or

Imaris x64 8.0.2 and 9.2.1, or through semi-automated detection in Imaris. Manual analysis

involved detecting ciliary membrane, marked by an enrichment of SSTR3::GFP above

background threshold, that were adjacent to a centriole (mCherry::PACT in dual-fluorescent

cells or pericentrin immunofluorescence in single- (SSTR3::GFP-expressing) or non-fluorescent

cells), to distinguish from accumulations of SSTR3+ membrane elsewhere in the cell. Manual

length measurements in Fiji were made with the line function, and in Imaris with the

Measurement tool. Generally, single z-plane images were analyzed in Fiji or Imaris, while

confocal z-stacks were analyzed in Imaris which allowed more accurate length measurement due

to the 3D render (Surpass) capability. When possible, length measurements in confocal images

were semi-automated in Imaris using the Surfaces function to create an artificial object

encompassing the ciliary membrane, and exporting Bounding Box data as a proxy for length (the

longest dimension of the object).

For live cell serum stimulation experiments, movies were visually scanned in Imaris for

examples of disassembling cilia. Images of each disassembling cilium were cropped by time

(from t0 to several mins after complete loss), and position (restricted to area of occupancy during

the that time window), and then saved in a separate file. To generate ciliary length curves, the

ciliary membrane was isolated as an artificial object using the Surface function. When possible,

the object was automatically tracked over consecutive time points with length data generated at

each time point. In cases where automatic tracking was not possible due to low signal-to-noise of

ciliary membrane fluorescence, measurements were taken manually at 15-30 minute intervals

until the initiation of ciliary disassembly, and at each time point during the disassembly event.

Matlab: Raw length measurement data from disassembling cilia movies were compiled in to an

Excel spreadsheet. A Matlab algorithm imported the data, performed smoothing and calculations

of cilium start point, and generated an output file containing disassembly rates, start and end

time, start and end length, and proportion length lost per disassembly stage. Algorithm strategy is

described in the text and Supplement.

Cilia Isolation. Cell culture: clones of IMCD3 cells, either an unsorted stably expressing GFP-

SSTR3 or FACS sorted for medium expression of GFP-SSTR3, were grown on 15cm dishes at

$3x10^6$ cells/dish in DMEM/F12 with 10% FBS and antibiotics for 24 hours. The cells were

washed 3x with HDF wash buffer, and media was replaced with DMEM/F12 and 0.2% FBS and

antibiotics (serum-starved) for 24 hours. Then all dishes were washed 3x with HDF buffer and

half received phenol-red free DMEM/F12 with 0.2% FBS (serum-starved), and the other half

received phenol red free DMEM/F12 with 10% FBS (serum-stimulated) for 24 hours. Total

serum starved time was 48 hours and total serum stimulated time was 24 hours.

Immune-capture Method. Preparation of antibody-immobilized imaging dishes: Glass in 35 mm

glass-bottomed imaging dishes (MatTek) was functionalized by plasma cleaning at 250 moor,

Low setting, 45-60 seconds. Dishes were silanized with 500 µL of 2.5% triethoxysilyl-undecanal

(TESU) in 100% ethanol, covered with Parafilm and incubated at RT°C for 1hr. Dishes were

washed 3x with 100% ethanol, then baked at 85°C for 3 hrs. Next, silanized dishes were treated

with the following series of reagents for 1hr at RT°C unless stated otherwise, with 3 PBS washes

in between steps: 1) 50mM NHS-LC- LC-biotin in water, 2) 5mg/ml neutravidin for 1hr at

RT°C, 3) 300 µg/ml biotin-Protein A 4) block with 15mM D-biotin in DMSO for 30 min, 5) anti-

rabbit SSTR3 N19 (extracellular N-terminus) antibody (100-200 µg/mL) at 37°C, followed by

one PBS wash. These protocols adapted from Dr. Nicholas Borghi (118).

Sample preparation: Culture medium was collected and subjected to centrifugation for 10 min at

1000xg at 4°C to remove large cell debris. Samples were then kept on ice until plating on treated

dishes or stored at 4°C for a maximum of 1 day. 4mL serum-stimulated or -starved medium was

incubated on a treated MatTek dish overnight at 4°C, followed by 3 gentle PBS washes. Samples

were then imaged directly, without fixation with a Leica SP8 confocal microscope.

SEM: Antibody-immobilized MatTek dishes incubated with serum stimulation medium were

fixed for SEM in 4% PFA, 2% glutaraldehyde, and 0.1M Na cacodylate. Glass bottoms were

removed, processed for imaging, and imaged with a Hitachi S-3400N VP SEM scope in the

Beckman Imaging Facility, Stanford Univ.

Filter-Spin Concentration Method. Harvest of Cilia: Deciliation of starved IMCD3 cells

(positive control): Serum-stimulated or -starved culture medium, or fresh culture medium (with

10% FBS, an additional control) was removed from 6 150cm dishes, combined and centrifuged

at 200xg at 4°C for 5 mins in the A-4-81 rotor, Eppendorf 5810R centrifuge. Cells were washed

2x with warm PBS containing 0.4% EDTA. 10 mL was added to a MatTek dish and incubated

for 10 min at 37 °C, followed by gentle up and down pipetting to remove cells from dish. An

aliquot of cell suspension was removed for cell count. Cells were centrifuged at 13000 x g for 5

mins at RT°C. The cell pellet was resuspended in 5 mL ice cold deciliation buffer (62) (112 mM

NaCl, 3.4 mM KCl,10 mM $CaCl_2$, 2.4 mM $NaHcO_3$, 2 mM HEPES, pH7.0 and a protease

inhibitor tablet [Roche]). The cell suspension was incubated at 4 °C for 15 mins with rigorous

end-over-end rotation, and then centrifuged at 1000 x g for 5 mins at 4 °C in an Eppendorf

centrifuge. The resulting supernatant was used for biochemistry and immunostaining.

Biochemistry: Half of the supernatant material from deciliated, serum starved or -stimulated cells

was centrifuged at 21,000xg for 15 min in JA25.5 rotor in Beckman Coulter Avanti J-25I

centrifuge at 4°C. The supernatant was carefully removed, and pellets were resuspended in 160

μl of sample buffer (1% SDS, 10mM Tris-HCl, pH 7.5, 2mM EDTA). Samples were boiled at

95°C for 8 mins, and equal volumes were separated by 10% PAGE and transferred to PVDF.

Blots were blocked (2% BSA, 1% normal donkey and goat serum in TBS, pH 7.4) for 1hr at

RT°C or overnight at 4°C. Membranes were blotted with YL1/2 (1:1000), mouse acetylated-

tubulin antibody (1:1000), and IFT88 rabbit antibody (1:500) in blocking buffer for 1 hr at

RT°C. Blots were washed 5x with TBST. Secondary anti-rabbit, anti-mouse, or anti-rat

antibodies labeled with either Alexa Fluor 680 (InVitrogen, #A21058) or IRDye800CW (Li-Cor

Biosciences, #926-32213), at 1:30,000 dilution were incubated with blots for 30 min at RT. Blots

were washed 5x with TBST and scanned on Licor Odyssey scanner (Li-Cor BioSciences).

Immunofluorescence: Half of the supernatant material from deciliated, serum-starved, or -starved

and -stimulated cells was concentrated using a 250ml 0.2μm PES filter unit with house vacuum

to reduce the volume to 2 mL, and finally a Millipore Ultrafree-MC filters (PVDF 0.2μm size

#UFC30GV100) to reduce the volume to ~0.5 mL. 5 μl of concentrated supernatant was pipetted

onto an acid-treated glass slide. A 22 mm acid-treated circular glass coverslip was placed on the

sample, and the slide was immediately plunged into liquid nitrogen for ~5 sec. After removing

the slide, the coverslip was removed and fixed in -20 °C 100% methanol for 5 mins.

Immunofluorescence staining was performed as described above.

Statistics. All analyses were performed in GraphPad Prism. Statistical tests used for each

analysis are indicated in the Figure legends. No explicit power analysis was used to determine

sample size. All experiments were performed with at least three biological replicates, i.e.

samples from independent cell culture passages. When used, technical replicates (i.e. repeats

from the same cell culture passage) were averaged for each biological replicate. In brief,

comparisons of mean values such as mean percent cilia across replicate experiments were

compared using an unpaired t-test. Analyses of individual measurements such as cilia length

were subjected to normality tests (Kolmogorov-Smirnoff, D'Agostino & Pearson, and Shapiro-

Wilk). If data passed all normality tests, unpaired t-test was used, if not the Mann-Whitney U test

was used. If data passed normality by some tests but not others, both types of analyses were

performed. Results were similar between parametric and nonparamentric tests unless stated

otherwise.

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Supporting Material

Figure S1. Characterization of immunostained serum stimulated cells. A) Serum starved and

stimulated cells were immunostained for pericentrin to mark the basal body (PCNT, white) and

acetylated tubulin to mark the axoneme (acTub, red). Scale bar, 10 µm. B) Serum stimulation is

accompanied by an increase in mitotic cells, inhibited by tubacin treatment. Quantifications are

based on means of 3 independent experiments with 150-200 cells analyzed per condition per

replicate. Error bars – S.E.M.

Figure S2. Schematized workflow for automated analysis of ciliary disassembly dynamics.

A) 10 control non-disassembling cilia from starved cells were imaged at 90-sec intervals over a 12

hr period and analyzed. Cumulative metrics are shown here (µm). Slight changes in length and

stochastic length fluctuations are inherently present, and used as a baseline for analysis of

disassembling cilia. Marked in yellow – maximum standard deviation of length is used as a proxy

for length measurement error, and is thus used as a threshold length for instant disassembly;

average slope of best fit line represents background decline in length over 12 hr imaging period.

B) Matlab workflow. Scale bar, 5 µm. Raw data are run through a smoothing function. Derivatives

are calculated, then normalized to background reduction (A) to identify start point of disassembly

event. Lastly, disassembly behaviors (gradual, instant, and combined) are assigned as described in

the text.

1000

1001   **Figure S3. Dynamics of dibucaine-induced ciliary shedding are consistent with serum-**

1002   **induced instant disassembly**. Starved cells were treated with 190 µm dibucaine and imaged by

1003   confocal microscopy at 30 sec intervals. A) Still images from a representative ciliary shedding

1004   show complete ciliary loss in under 30 sec. B) Length measurements from A) show instant

1005   disassembly dynamics.

1006

Figure S4. Schematics of cilia capture methods. A) Immune-capture of shed cilia. Medium

from serum stimulated cells is incubated on an imaging dish bearing immobilized antibody

against the SSTR3 membrane marker. B) Filter-spin concentration of shed cilia. Medium from

serum-stimulated cells is concentrated either by centrifugation pelleting for subsequent Western

blot or by vacuum & centrifugation filtration for immunofluorescence. Medium from cells

subjected to artificial deciliation was included as a positive control.

1013

Figure S5. tRFP-p60 overexpression reduces cytoplasmic acetylated tubulin intensity, but

does not impair overall serum-induced ciliary disassembly. A) Starved and 2 hr-stimulated

tRFP and tRFP-p60 cells were fixed and stained for acetylated tubulin (red, center column).

Scale bar, 20 μm. Insets show acet. tubulin channel alone. Inset scale bar, 10 μm. B)

Quantification of A). Mean cellular acTub intensity was normalized to cellular tRFP intensity.

Data pooled from 3 independent experiments, 80-100 cells per condition. Statistical significance

from Mann-Whitney U test. C) D) Serum starved cells pre-treated with DMSO, 2 μM Tubacin,

or 1μM CytoD were serum stimulated (6 hr). Proportion of ciliated cells was calculated by

normalizing to Starved + DMSO for each cell line (dotted line). N = 3 experiments.

1023

Figure S6. tRFP and tRFP-p60 cells exhibit similar responses to elevated $[Ca^{2+}]_i$ by

ionomycin and dibucaine, but not to thapsigargin. tRFP and tRFP-p60 cells were starved and

pre-treated with DMSO, A-B) 190 μM dibucaine (30m), 1 μM ionomycin (30m), and C-D) 5 μM

thapsigargin (Thps) (1 hr). Cilia counts are from fixed populations and normalized to respective

DMSO controls. Length measurements are from confocal z-stacks of live cells. Data from 3

independent experiments, at least 100 cells counted per condition. Statistical significance was

determined by unpaired t-test. E). Model summarizing results from Fig. 4E-F & S6C-D. Orange

bar – tRFP-p60 cells have no defect in overall ciliary disassembly, but undergo *instant*

deciliation more frequently. We make several assumptions to approximate the relative

differences in p60 and $[Ca^{2+}]_i$ levels between our experimental manipulations: 1. tRFP-p60 cells

have "*excess*" p60 compared to "*normal*" levels in tRFP control cells. 2. Thapsigargin may

produce a $[Ca^{2+}]_i$ that is physiological, but higher than the ground state (89) (labeled "*excess*" on

the figure), whereas dibucaine and ionomycin induce "*high excess*" levels of $[Ca^{2+}]_i$.

1037

1038

Supplementary Videos.

Video S1. *Primary cilium of a serum starved cell*. Imaged at 90 second intervals over 12 hrs,

45fps. The cilium undergoes rapid length fluctuations and a slight overall reduction in length at

0.003 μm/min. See Fig. 2A.1.

Video S2. *Primary cilium disassembling by gradual dynamics*. Imaged at 90 second intervals,

45fps. Cilium disassembles with an overall rate of 0.016μm/min. See Fig. 2A.2.

Video S3. *Primary cilium disassembling by instant dynamics*. Imaged at 90 second intervals,

15fps. Cilium is lost in under 90 seconds, approximate minimum rate of 4.72μm/min. See Fig.

2A.3.

Video S4. *Primary cilium disassembling by combined dynamics*. Imaged at 46 second intervals,

25fps. Cilium undergoes gradual shortening (0.029μm/min), followed by instant loss

(>5.69μm/min). See Fig. 2A.4.

Video S5. *Primary cilium shedding*. Imaged at 54 second intervals. Ciliary membrane is released

from cell surface (27:12-29:00). See Fig. 3A.

1053

A

10:17:24 - 10:18:18   10:18:18 - 10:19:13   10:19:13 - 10:20:07

B

SSTR3::GFP   mChy::tubulin   Merge

C

Merge

SSTR3::GFP

mChy::tub

D

Rel. abudance of cilia

Tubacin   −   +   −   +
         -SERUM   +SERUM

E

F

Deciliated   Starved   Stimulated

IFT88 α-tubulin

G

Deciliated (+ control)   Serum Starved   Serum Stimulated

90 —   IFT88

50 —   α- tubulin

50 —   * acet. tubulin