A hierarchy of signals regulates entry of membrane proteins into the ciliary membrane domain in epithelial cells

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Ciliopathies reveal the importance of the primary cilium to human physiology (Fliegauf et al., 2007). Cilia are found on most cells of the body, including polarized epithelial cells where the membrane of the primary cilium is an extension of the apical plasma membrane. The ciliary membrane has a unique protein composition, enriched relative to the adjacent membrane in proteins involved in cilium-dependent signal transduction (Goetz and Anderson, 2010; Patel and Honore, 2010). Some signaling proteins such as polycystin-2 and somatostatin receptor 3 are thought to possess cilium-specific targeting signals that specify selective transport (Geng et al., 2006; Berbari et al., 2008), and the ciliary membrane is thought to comprise a distinct lipid environment that may also control membrane protein content (Vieira et al., 2006; Janich and Corbeil, 2007). It is not known how or when the specialization of the ciliary membrane occurs, nor is it clear the extent to which the ciliary membrane contains or excludes other plasma membrane proteins.

The plasma membrane of polarized epithelial cells is divided into apical and basal lateral domains separated by the tight junction diffusion barrier (Mellman and Nelson, 2008). Pioneering freeze-fracture EM studies identified a structure at the base of the cilium, the “ciliary necklace” (Gilula and Satir, 1972), which was imagined to play a similar role in isolating the membrane of the primary cilium from the adjacent plasma membrane. Lacking intercellular junctions, the necklace appears more analogous to the barrier at the axon initial segment of neurons, which separates the axonal from the somatodendritic plasma membranes (Winckler et al., 1999). Recently, Septin 2 has been proposed as a component of the ciliary barrier (Hu et al., 2010), although it is unclear whether the barrier performs the same function as the tight junction or axon initial segment. Consistent with a fence is evidence of a direct vesicular

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transport components to build the primary cilium and that could circumvent a barrier if membrane proteins were delivered by this route (Rogers et al., 2004; Nachury et al., 2007; Yoshimura et al., 2007; Zuo et al., 2009). However, a recent study has demonstrated that Smoothened (Smo), a signaling protein active in the cilium, reaches the ciliary membrane by lateral movement, arguing against an entry barrier at least for this protein (Milenkovic et al., 2009).

Smo is a seven-pass transmembrane protein that functions in the Hedgehog signaling pathway and localizes to the primary cilium in the presence of Hedgehog (Zhu et al., 2003; Corbit et al., 2005; Wang et al., 2009) or when overexpressed (Rohatgi et al., 2009). Before localizing to the cilium, Smo is found on the adjacent plasma membrane and then moves laterally into the ciliary membrane without endocytosis and vectorial recycling (Milenkovic et al., 2009). Ciliary enrichment could occur by passive diffusion and retention within the cilium or by active transport facilitated by an adapter, a role recently proposed for the BBSome (Jin et al., 2010). Smo’s relocalization to the cilium is dependent on its association with β-arrestin, which binds to ciliary microtubule motor protein KIF3A (Kovacs et al., 2008). These interactions may assist Smo’s ciliary enrichment by facilitating association with the axoneme.

In contrast, podocalyxin is an apical transmembrane protein that is excluded from the primary cilium and membrane around the base of the cilium. We refer to this podocalyxin-excluding subdomain of the apical membrane as the ciliary membrane domain (CMD). Podocalyxin was first described as the major sialomucin of glomerular podocytes (Kerjaschki et al., 1984) and has been shown to play a role in apical membrane determination in epithelial cells (Meder et al., 2005). Podocalyxin’s cytoplasmic tail ends in a canonical four–amino acid PDZ-binding motif that interacts with Na+/H+ exchanger 3 regulatory factor (NHERF) proteins, NHERF1/ERM–binding phosphoprotein of 50 kD, and NHERF2 (Takeda et al., 2001; Li et al., 2002; Meder et al., 2005; Yu et al., 2007), which interact with the ERM family of actin-binding proteins (Reczek et al., 1997; Reczek and Bretscher, 1998; Yun et al., 1998; Terawaki et al., 2003). A complex of podocalyxin, NHERF2, and ezrin has been immunoprecipitated from glomerular extracts, strongly suggesting that podocalyxin can be linked to the actin cytoskeleton in kidney cells (Takeda et al., 2001). Further work in formaldehyde-fixed cells identified the PDZ-binding motif at the carboxy terminus of podocalyxin as necessary for exclusion from the CMD (Meder et al., 2005).

We investigated podocalyxin’s CMD exclusion to determine how and when apical membrane proteins can be excluded from the primary cilium. Live cell imaging was used because we found that fixation can create CMD artifacts, which may explain contradictory results in the literature. We find that the NHERF1-ERM–actin network beneath the apical plasma membrane comprises a dominant-acting selective retention matrix that effectively excludes interacting membrane proteins from entering the CMD, contributing to the specificity of the ciliary membrane.

Results

Podocalyxin exclusion from the CMD occurs after the centrosome aligns under the apical membrane but before there is a primary cilium

Elongated primary cilia appear on MDCK cells ∼1 wk after cells are seeded at high density on permeable filter supports (Sfakianos et al., 2007). Imaging MDCK cells expressing GFP-tagged canine podocalyxin (GFP-PODXL) fixed 8 d after seeding revealed that GFP-PODXL was excluded from the primary cilium and an area around its base, a region we define as the CMD (Fig. 1 A), as found for endogenous podocalyxin (Meder et al., 2005). F-actin was also excluded from this region (Fig. 1 A).

Even in cells that did not appear to have a primary cilium, GFP-PODXL and F-actin were excluded from the CMD. 4 d after seeding, few primary cilia were visible by antiacetylated tubulin staining; however, GFP-PODXL showed a pattern of exclusion from the CMD similar to that seen 8 d after seeding, a pattern matched by RFP-NHERF1 (Fig. 1 B). Thus, early stages of ciliogenesis begin several days before growth of primary cilia in MDCK cells. By analyzing the distribution of GFP-PODXL on the apical surface of live cells, we determined that the CMD is established in a majority of cells within 3 d of seeding (Fig. 1 C).

We next examined the appearance of the CMD relative to the migration of the centrosome to the apical pole. The centrosome migrates to the plasma membrane as the mother centriole matures into the basal body and extends the primary cilium (Sorokin, 1962). We found that the centrioles were positioned below the center of the apical membrane within 24 h of seeding (Fig. 1 D), well before appearance of the CMD (Fig. 1 C). Thus, appearance of the GFP-PODXL exclusion zone defined formation of the CMD as a stage of ciliogenesis between migration of the centrosome and eruption of the primary cilium.

Podocalyxin has been implicated in microvillus formation (Nielsen et al., 2007), and NHERF1 knockdown results in loss of microvilli (Hanono et al., 2006). Because the CMD appeared depleted of GFP-PODXL, RFP-NHERF1, and F-actin, we expected to see gaps in the brush border corresponding to the CMD. We used scanning EM (SEM) to visualize microvilli on the apical surface and surprisingly were not able to find any gaps in the brush border (Fig. 1 E, day 4). However, once a cilium was present, it was common to see a small region at its base that was free of microvilli (Fig. 1 E, day 4). Conceivably, the dense subapical actin network must be disassembled during ciliogenesis to allow the centrosome to dock at the apical membrane. This is consistent with recent data suggesting that ciliogenesis is facilitated by actin-severing protein gelsolin or actin polymerization inhibitor cytochalasin D (Kim et al., 2010) and basal body cortactin regulator Missing-In-Metastasis (Bershteyn et al., 2010). At day 4, the reduced F-actin in the CMD may represent loss of the subapical actin network in that region and not disassembly of microvillar actin. Gaps seen in RFP-NHERF1 and GFP-PODXL distributions likely do not indicate a complete absence of these molecules in the CMD.
The PDZ-binding motif in the cytoplasmic tail of GFP-PODXL is necessary for its exclusion from the CMD and from the cilium. It has previously been shown that the PDZ-binding motif at the end of the cytoplasmic tail of podocalyxin is necessary for its restricted distribution in the apical membrane (Meder et al., 2005). This motif has also been shown to bind to members of the NHERF family (Takeda et al., 2001; Li et al., 2002; Meder et al., 2005; Yu et al., 2007). Consistent with these findings, deletion of the four-amino acid PDZ-binding motif of GFP-PODXL...
Figure 2. **GFP-PODXL<sup>Δ4</sup>** and GFP-GPI are found in the CMD and cilia of live MDCK cells, but fixation can create the appearance of CMD exclusion. (A) Live cells expressing GFP-PODXL<sup>Δ4</sup> or GFP-GPI were imaged 4 d after seeding and, in contrast to GFP-PODXL, failed to show exclusion from the CMD. Images were collected with microscope settings identical to Fig. 1 C. GFP-PODXL day 4 image from Fig. 1 C is shown for comparison. (B) Paraformaldehyde-fixed...
GPI–expressing cells (77/219 fixed and 64/194 live). Images in A, B, and E are projections of z stacks. Error bars represent standard deviation between 4–expressing cells had similar numbers of cilia that could be detected using the two methods (24/77 fixed and 34/126 live), as did GFP-PODXL (GFP + cilium). Scoring GFP-PODXL–expressing cells, 54/188 fixed cells were ciliated, but only 4/144 live cells had a GFP-positive cilium. In contrast, cilia were identified by antiacetylated tubulin (ciliated); in live cells, cilia were identified as GFP-positive projections from the center of the apical membrane after seeding on filters. (F) Cilia longer than 2 µm extending from GFP-positive cells were counted in five fields in each of two experiments. In fixed cells, (E) Cells expressing GFP-PODXL, GFP-PODXL 4, or GFP-GPI (green) were fixed and stained with acetylated tubulin (white) to image primary cilia 12 d after seeding on filters. (F) Cilia longer than 2 µm extending from GFP-positive cells were counted in five fields in each of two experiments. In fixed cells, cilia were identified by acetylated tubulin (ciliated); in live cells, cilia were identified as GFP-positive projections from the center of the apical membrane (GFP + cilium). Scoring GFP-PODXL–expressing cells, 54/188 fixed cells were ciliated, but only 4/144 live cells had a GFP-positive cilium. In contrast, GFP-PODXL4–expressing cells had similar numbers of cilia that could be detected using the two methods (24/77 fixed and 34/126 live), as did GFP-GPI–expressing cells (77/219 fixed and 64/194 live). Images in A, B, and E are projections of z stacks. Error bars represent standard deviation between experiments. Bars, 10 µm.
We first added only the four–amino acid PDZ-binding motif from podocalyxin to the carboxy terminus of GFP-CEACAM1 (GFP-CEACAM1-DTHL). GFP-CEACAM1-DTHL was not retained outside the CMD (Fig. 5, A and B), and its mobility measured by FRAP was similar to GFP-CEACAM1 (Fig. 5, C and D). In contrast, replacement of the last 62 amino acids of GFP-CEACAM1 with those of PODXL (GFP-CEACAM1-PODXL) was sufficient to exclude the construct from the CMD (Fig. 5, A and B) and to reduce its mobile fraction in the apical membrane (Fig. 5, C and D). Subsequent deletion of the PDZ-binding motif from the cytoplasmic tail of GFP-CEACAM1-PODXL (GFP-CEACAM1-PODXLΔ4) eliminated these effects (Fig. 5, A–D). Finally, immunoprecipitation (IP) of the podocalyxin and CEACAM1 constructs confirmed that GFP-CEACAM1-PODXL interacted with NHERF1 similarly to GFP-PODXL, whereas the constructs that were not excluded from the CMD did not (Fig. 5 E). Together, these results indicate that the NHERF1-dependent retention activity associated with the podocalyxin cytoplasmic tail can be transferred to another protein autonomously. Although the activity required more than just the last four residues comprising the canonical PDZ-binding motif, these motifs have previously been shown to be context dependent (Maday et al., 2008).

We also determined whether the properties of podocalyxin’s cytoplasmic tail are unique, we tested the cytoplasmic domains of other NHERF1-binding membrane proteins for their ability to alter the distribution and mobility of GFP-CEACAM1. Cystic fibrosis transmembrane conductance regulator (CFTR) and Csk-binding protein (CBP) are both membrane proteins reported to be immobilized by their interactions with NHERF1.
We transferred the ERM-binding domain of NHERF1 to GFP-CEACAM1 and found that it acquired the membrane distribution and mobility of GFP-PODXL (Fig. 6, A–D). Similarly, addition of the actin-binding domain of ezrin to GFP-CEACAM1 (GFP-CEACAM1-ezrin) resulted in CMD exclusion and significantly reduced mobile fraction, as judged by FRAP (Fig. 6, A–D).

Retention of GFP-CEACAM1-NHERF1 should be independent of endogenous NHERF1 because the construct can interact with ERMs directly using its NHERF1 ERM-binding domain, unless the retention matrix itself is dependent on NHERF1. To test this, we used shRNA to knock down expression of NHERF1 in our GFP-CEACAM1-NHERF1 cell line. Despite a nearly complete knockdown of endogenous NHERF1 (Fig. 6 B), CMD exclusion was not affected (Fig. 6, A and C). Endogenous NHERF1 was also not required to restrict the lateral mobility of GFP-CEACAM1-NHERF1 (Fig. 6, D and E). Thus, the retention matrix itself does not require NHERF1, which appears to act only as an adapter that restricts lateral movement of interacting membrane proteins by linking them to ERMs and actin.

A link to ERMs or actin results in CMD exclusion even with NHERF1 knockdown

In an additional set of experiments, we asked whether the direct fusion of domains from either NHERF1 or its presumptive binding partner ezrin would substitute for podocalyxin’s PDZ binding motif deletion or NHERF1 knockdown. We generated cell lines that highly expressed either GFP-CEACAM1-PODXL or GFP-CEACAM1-PODXLΔ4 and stained the cells for endogenous podocalyxin (Fig. 5, F and G). Cells expressing high levels of GFP-CEACAM1-PODXL did not show CMD exclusion of either GFP-CEACAM1-PODXL or endogenous podocalyxin, whereas neighboring cells without GFP-CEACAM1-PODXL excluded endogenous podocalyxin from the CMD. High expression of GFP-CEACAM1-PODXLΔ4 did not affect the distribution of endogenous podocalyxin. We conclude that the selective retention mechanism is saturable and that there is not an additional barrier to endogenous podocalyxin’s entry to the CMD or cilium.
Figure 5. CEACAM1 can be excluded from the CMD by adding tails from NHERF1-binding proteins. (A) GFP-CEACAM1–based constructs differ in their exclusion from the CMD 4 d after seeding. Images were collected with identical microscope settings to Fig. 1 C. (B) Cells were scored for GFP exclusion from the CMD as in Fig. 1 C. Only 5/169 cells appeared to exclude GFP-CEACAM1 from the CMD, and GFP-CEACAM1-DTHL (13/135), GFP-CEACAM1-PODXL (13/135), and GFP-CEACAM1-CFTR (12/148) were similar, whereas GFP-CEACAM1-PODXL (146/253) and GFP-CEACAM1-CFTR (94/111) were excluded from the CMD in most cells. (C) FRAP measurements indicated that GFP-CEACAM1 constructs that were excluded from the CMD were also less mobile in the apical membrane. (D) There was no significant difference between FRAP measurements of GFP-CEACAM1 and GFP-CEACAM1-DTHL after 120 s; however, there were significant differences between GFP-CEACAM1-PODXL and GFP-CEACAM1-PODXLΔ4, GFP-CEACAM1-CFTR and GFP-CEACAM1-CFTRΔ4, and GFP-CEACAM1-CBP and GFP-CEACAM1-CBPΔ4 (P < 0.005). (C and D) Each FRAP value is a mean of measurements from eight cells. Error bars represent standard deviation between measurements. (E) Cells expressing GFP constructs were grown on
Figure 6. CEACAM1 can be excluded from the CMD independently of NHERF1 by adding domains that bind more directly to the cytoskeleton. (A) Addition of NHERF1’s ERM-binding domain or ezrin’s actin-binding domain is sufficient to exclude GFP-CEACAM1 from the CMD 4 d after seeding. NHERF1 was knocked down in GFP-CEACAM1-NHERF1 cells (GFP-CEACAM1-NHERF1 shRNA), and exclusion was similar to control cells (GFP-CEACAM1-NHERF1 vector). Images were collected with identical microscope settings to Fig. 1 C. (B) GFP-CEACAM1-NHERF1 shRNA and GFP-CEACAM1-NHERF1 vector cell lysates were blotted with anti-NHERF1 and antiezrin antibodies. Molecular mass is indicated in kilodaltons. (C) Cells were scored for GFP exclusion from the CMD as in Fig. 1 C. 113/199 cells expressing GFP-CEACAM1-NHERF1 appeared to exclude the construct from the CMD, and similar results were seen for GFP-CEACAM1-ezrin (105/185). After shRNA knockdown of NHERF1, GFP-CEACAM1-NHERF1 was excluded from the CMD in 193/393 cells, a similar ratio to cells only treated with vector (125/232). Error bars represent standard deviation between experiments. (D) FRAP measurements indicated that GFP-CEACAM1 was less mobile in the apical membrane after addition of an ERM- or actin-binding domain, and this was independent of NHERF1 knockdown. (E) There are significant differences in the FRAP measurements between GFP-CEACAM1 and both GFP-CEACAM1-NHERF1 (**, P < 0.005) and GFP-CEACAM1-ezrin (*, P < 0.05) after 120 s. No significant difference was seen in the FRAP of GFP-CEACAM1-NHERF1 after shRNA knockdown of NHERF1. GFP-CEACAM1 data are from Fig. 5 and are included as a reference. (D and E) Each FRAP value is a mean of measurements from eight cells. Error bars represent standard deviation between measurements. Images are projections of z stacks. Bars, 10 µm.
we asked whether we could cause ciliary retention of a nonciliary protein by adding a microtubule-binding element to its cytoplasmic domain. We thus generated a GFP-CEACAM1 construct fused to microtubule-associated protein tau (GFP-CEACAM1-tau). The 352–amino acid tau protein was a much larger addition to GFP-CEACAM1 than our ERM- or actin-binding domains but did not interfere with apical trafficking of the fusion protein at low expression levels. Before ciliogenesis, GFP-CEACAM1-tau was evenly distributed across the apical membrane (Fig. 8 A), and its mobility was not significantly different from GFP-CEACAM1 by FRAP (Fig. 8 B). Once a primary cilium developed, however, GFP-CEACAM1-tau appeared concentrated in the cilium relative to GFP-CEACAM1 (Fig. 8 C). These data show that a protein can be enriched in the cilium simply by association with axonemal microtubules. Thus, selective retention in the cilium, perhaps via microtubule motors such as KIF3A, may contribute to the ciliary enrichment of selected membrane proteins.

Discussion

The ciliary membrane represents a distinct, differentiated microdomain that, in epithelial cells, exists as a subregion of an already distinct apical surface. How the specificity of the ciliary membrane is generated and maintained is only now becoming clear, and our results add a fundamental new mechanism to the process. We have found that PDZ-dependent interactions of membrane proteins such as podocalyxin with NHERF1, ezrin, and actin comprise an effective retention matrix that is necessary and sufficient to impede the passive diffusion of membrane proteins from the apical surface into the CMD and membrane of the primary cilium. This retention mechanism can even prevent...
the ciliary localization of membrane proteins such as Smo, which are normally concentrated in the cilium. Although the ciliary membrane may also be a specialized lipid environment (Vieira et al., 2006; Janich and Corbeil, 2007), this does not appear to contribute to the exclusion of apical membrane proteins. Nor does a diffusion barrier act to prevent the entry of passively diffusing proteins or of Smo, which moves laterally from its site of insertion in the plasma membrane to the cilium (Milenkovic et al., 2009). Consequently, we propose that a hierarchy of mechanisms exist that control the biogenesis of the ciliary membrane, including selective retention outside of the CMD, nonselective or selective transport from bulk plasma membrane into the CMD, and selective retention of a subset of proteins after arrival in the cilium. The latter two mechanisms likely involve specific adapters or motors such as the BBSome (somatostatin receptor 3; Jin et al., 2010), β-arrestin (Smo; Kovacs et al., 2008), and KIF3A (Crumbs3 and Smo; Fan et al., 2004; Sfakianos et al., 2007; Kovacs et al., 2008).

It seems clear why proteins involved in signaling might be selectively transported to or retained within the ciliary membrane. Why bulk plasma membrane proteins need to be excluded is less clear but may reflect the need to maintain sufficient space for signaling proteins or to prevent entry of proteins that might interfere with signaling. In this regard, it is important to note that diffusion barriers may also play an important role, although one apparently not relevant to the membrane proteins studied here. Recently, Septin 2 has been proposed to impede the movement of Smo and other ciliary membrane proteins into and out of cilia (Hu et al., 2010), a mechanism that may apply only to one apparently not relevant to the membrane proteins studied here. Fixing and permeabilizing MDCK cells can create the appearance of CMD exclusion for some apical markers, including selective retention outside of the CMD, nonselective or selective transport from bulk plasma membrane into the CMD, and selective retention of a subset of proteins after arrival in the cilium. The latter two mechanisms likely involve specific adapters or motors such as the BBSome (somatostatin receptor 3; Jin et al., 2010), β-arrestin (Smo; Kovacs et al., 2008), and KIF3A (Crumbs3 and Smo; Fan et al., 2004; Sfakianos et al., 2007; Kovacs et al., 2008).

Although it was previously demonstrated that podocalyxin needs its PDZ-binding motif for cilium exclusion (Meder et al., 2005), we have defined the mechanism responsible for this effect. We found that NHERF1 is the PDZ domain protein required for podocalyxin’s CMD exclusion in MDCK cells, immobilizing and retaining it in the nonciliary portions of the apical plasma membrane. NHERF2 has also been shown to bind podocalyxin (Takeda et al., 2001; Li et al., 2002) and be excluded from the CMD (Meder et al., 2005), but a functional role for NHERF2 in CMD exclusion has never been demonstrated. We predict that it could serve the same function as NHERF1 but is not endogenously expressed at high enough levels in MDCK cells to sequester a large fraction of podocalyxin outside the CMD. We also show that the addition of a NHERF1-interacting sequence from either CFTR or CBP is sufficient to cause GFP-CEACAM1 CMD exclusion, demonstrating that our findings are not exclusive to podocalyxin. We expect that all apical membrane proteins that bind to NHERF1 or are otherwise linked to the actin cytoskeleton are excluded from the CMD.

By monitoring the appearance of a GFP-PODXL–free subregion of the apical domain, we were able to identify early stages of ciliogenesis. Imaging GFP-PODXL and γ-tubulin revealed that the centrioles migrate to the future position of the primary cilium before GFP-PODXL is excluded from a central subdomain of the apical membrane. Phalloidin staining shows that F-actin is depleted from the CMD after MDCKs have been grown on filters for 4 d (Fig. 1 A); however, SEM images of 4-d-old cells do not show a corresponding lack of microvilli (Fig. 1 E), suggesting that the cleared F-actin was part of the subapical terminal web. Once a primary cilium grows days later, a small region without microvilli is present at the base of the cilium (Fig. 1 E), indicating that the basal body may continue to locally break down F-actin even after extending a cilium. The early loss of NHERF1 and podocalyxin from the CMD must represent a signal acting at the membrane to clear these proteins, but that signal does not appear to eliminate microvilli in the CMD.

Our experiments have also identified an experimental artifact that is particularly relevant to studies of the primary cilium. Fixing and permeabilizing MDCK cells can create the appearance of CMD exclusion for some apical markers, including CEACAM1 and GFP-GPI. Live cell imaging avoids this issue; however, the expression of exogenous proteins also has drawbacks when investigating retention mechanisms. Once binding sites are saturated, remaining protein is free from retention. We demonstrated this principle by expressing high levels of GFP-CEACAM1-PODXL, a construct that binds to NHERF1, which caused endogenous podocalyxin to enter the CMD (Fig. 5, F and G).
Competition for NHERF1 binding by exogenous protein expression has also been documented using CFTR (Haggie et al., 2006). To avoid saturating NHERF1-binding sites in our studies of CMD exclusion, we only used cells expressing low levels of exogenous protein (Fig. 5 E, compare GFP-PODXL band with endogenous podocalyxin band).

We have been able to enrich GFP-CEACAM1 in the primary cilium simply by adding the microtubule-associated protein tau to its cytoplasmic tail. This result demonstrates that anchoring a membrane protein to microtubules is sufficient to achieve selective localization in the cilium without the need for direct ciliary transport or a diffusion barrier at the base of the cilium. GFP-CEACAM1-tau is homogenously distributed across the apical membrane before the growth of the primary cilium and is mobile according to our FRAP measurements. Although microtubules are found throughout the cell, few are apparently close enough to the apical membrane to allow GFP-CEACAM1-tau to bind. Once the cilium grows, GFP-CEACAM1-tau can freely diffuse into the ciliary membrane, where it binds to microtubules of the axoneme. We do not expect this direct link to represent a physiological mechanism for cilium enrichment, but an indirect scaffolding system like the one that connects podocalyxin to actin can be envisioned.

Smo has been shown to be delivered to the apical membrane before concentrating in the cilium in response to Hedgehog (Milenkovic et al., 2009). Part of this mechanism is association of β-arrestin with Smo and KIF3A (Kovacs et al., 2008), which would link Smo to microtubules. This complex could transport Smo to the distal tip of the cilium, immobilize Smo by binding it to microtubules, or sequester it in the ciliary membrane by rendering it unable to cross a possible Septin 2 barrier back into the apical membrane. Other ciliary proteins might be retained in the ciliary membrane by the BBSome. The BBSome is a good candidate for a ciliary retention complex because it localizes to the cilium (Nachury et al., 2007), recognizes ciliary localization domains (Jin et al., 2010), and can indirectly link to microtubules through the dynein–dynactin complex (Kim et al., 2004).

We have found that primary cilium enrichment or exclusion of apical plasma membrane proteins can be mediated by cytoskeletal retention. Protein components that fall into this class are not dependent on a diffusion barrier for their localization. That GFP-PODXL can freely enter the CMD and cilium after dissociation from the NHERF1-ERM-actin retention matrix indicates that a cilinal fence does not restrict podocalyxin diffusion. Thus, it is now apparent that entry into, or exclusion from, the CMD involves a hierarchical interplay of several elements: (a) signals for selective inclusion within the CMD; (b) a possible barrier that impedes exit from (or less likely, entry into) the CMD; and (c) a retention matrix that prevents movement to the cilium by immobilizing nonciliary proteins in the plasma membrane.

Materials and methods

Cell culture
MDCK II and GP2-293 cells were maintained in Dulbecco’s MEM with low glucose supplemented with 10% FBS, 2 mM l-glutamine, penicillin and streptomycin at 37°C, and 5% CO₂. For microscopy experiments, cells were seeded at a density of 5 × 10⁵ for each 12-mm polycarbonate filter (Transwell; Corning). Medium was replaced daily for cells on filters.

Antibodies
The antibodies used in this study were rabbit anti-γ-tubulin (TS192; Sigma-Aldrich); mouse antiacetylated tubulin (clone 6-11B-1; Sigma-Aldrich); rabbit anti-GFP (A11122; Invitrogen); mouse anticentrin (610602; BD); rabbit anti-GFP conjugated to Alexa Fluor 647 (Invitrogen); Alexa Fluor 488, 546, and 647 goat anti-mouse IgG and goat anti-rabbit IgG (Invitrogen); goat anti-mouse (IRDye 800CW; LI-COR Biosciences); and goat anti-rabbit (IRDye 680; LI-COR Biosciences). Anti-gp135 antibody was provided by G. Ojakian (State University of New York Downstate Medical Center, Brooklyn, NY).

Microscope
A confocal microscope with integrated photomultiplier detectors (SPS; Leica) was used to acquire images for this study. Objective lenses were a 100× 1.47 NA HCX PL APO oil immersion objective and a 63× 1.40 NA HCX PL APO oil immersion objective. Application Suite software (Leica) was used to manage images.

Immunofluorescence microscopy
Cells on filters were fixed by incubation in 4% paraformaldehyde (Electron Microscopy Sciences) for 15 min at room temperature or in methanol for 20 min at −20°C. Cells were permeabilized with 0.05% saponin (Riedel-de Haën) and 2% BSA (Sigma-Aldrich) in Dulbecco’s PBS with calcium and magnesium (Invitrogen). Primary and secondary antibody incubations were 1 h, and filters were washed with permeabilization buffer after each incubation. Alexa Fluor 647–conjugated phalloidin (Invitrogen) was included in the secondary incubation. Filters were mounted in SlowFade Gold (Invitrogen).

Live cell microscopy
Cells grown on filters were washed twice with cell culture medium before filters were cut from their supports and placed cell side down on a 22 mm glass bottom dish (WillCo Wells). A slice hold down (SHD-26GH/15; Warner Instruments) was placed on top of the filter, and cell culture medium was added to the dish. Cells were imaged in a 37°C chamber with 5% CO₂.

Images used to quantify CMD exclusion were acquired with a 100× objective and 2× digital zoom; images for quantitation of cilia used 3× digital zoom. To quantitate CMD exclusion, three fields of cells were scored in each of two experiments. To quantitate cilia (live and fixed), five fields of cells were scored in each of two experiments. Only cells with a mean fluorescence intensity and peak fluorescence intensity within a standard range were scored.

FRAP measurements were made using a 63× objective and 10× digital zoom. Application Suite software was used to automate the bleach of a 750-nm-diameter circle, acquisition of postbleach images, and quantitation of fluorescence recovery. The region bleached was never in the center or at the edge of the cell. To calculate recovery, the fluorescence intensity of the bleached region in the first image acquired after bleaching (time 0) was subtracted from all intensity measurements. Values were then normalized to prebleach intensity of the bleached region and scaled to the intensity of a nearby region of apical membrane to account for photo-bleaching during image acquisition. Traces in figures are means of FRAP calculations from at least eight cells from at least two experiments.

To visualize GFP-Smo on the cell surface, cells on filters expressing GFP-Smo constructs were washed twice with 4°C Dulbecco’s PBS with calcium and magnesium (Invitrogen). PBS was completely aspirated from the apical chamber, and 200 μl Alexa Fluor 647–conjugated anti-GFP antibody in PBS was added to the apical chamber. Cells were incubated on ice for 5 min before being washed twice with 4°C PBS with calcium and magnesium. Filters were cut from their supports, placed on an ice-cold glass bottom dish, and weighed down with a slice anchor before an addition of 4°C PBS with calcium and magnesium to the dish. Cells were quickly imaged at room temperature. The brightness of images in Figs. 2 D, 3 C, and 7 B was increased using Photoshop CS4 (Adobe).

SEM
Samples were fixed in one-half Karnovsky’s fixative (2% paraformaldehyde/2.5% glutaraldehyde in 0.1 M sodium cacodylate buffer, pH 7.4) overnight and postfixed in 1% OsO₄ for 1 h. Cells were dehydrated through a graded series of EtOH and infiltrated with hexamethyldisilazane. They were then air dried, mounted on stubs, and sputter coated with 10 nm AuPd. Samples were viewed on a microscope (XL30 ESEM; FEI).
Generation of fluorescent protein fusion constructs

GFP-GPI (Keller et al., 2001) was subcloned into pQCXIN for this study. This pQCXIN GFP-GPI plasmid became the basis for our other transmembrane GFP constructs, as cDNAs could be inserted downstream of the GFP with a stop codon upstream of the GPI linkage sequence. Sequences for canine PODXL (GenBank accession no. AY970669) and CEACAM1-1L (GenBank accession no. DQ75212) were relied on to select their signal sequences and silently add restriction enzyme sites. These edited sequences were synthesized and inserted downstream of GFP in pQCXIN GFP-GPI by Blue Heron Biotechnology.

GFP-PODXLΔ4 was made by replacing the distal tail of GFP-PODXL with synthesized oligonucleotides corresponding to the PODXL tail without its last four amino acids. GFP-CEACAM1-DTHL was made by inserting the last four codons of PODXL to the end of GFP-CEACAM1’s sequence using oligonucleotides.

GFP-CEACAM1-PODXL and GFP-CEACAM1-PODXLΔ4 were created by cutting the last 62 codons from the tail of GFP-CEACAM1 and replacing them with the corresponding tail fragment of either GFP-PODXL or GFP-PODXLΔ4.

To facilitate the creation of other constructs, we created a GFP-CEACAM1 construct with the stop codon deleted (GFP-CEACAM1-NS), which allowed us to insert synthesized oligonucleotides at the end of the CEACAM1 sequence. Oligonucleotides corresponding to the carboxy-terminal 32 amino acids of CTRF (GenBank accession no. NM_000492) were added to GP-GPI 5′-3′EcoRI with synthesized oligonucleotides corresponding to the PODXL tail without the last four codons. GFP-CEACAM1-CFTR was created to allow for the insertion of an shRNA sequence into the vector by modifying the HindIII sites at positions 2872 and 4282 using site-directed mutagenesis. These edited sequences were synthesized, annealed, and then ligated to the LTRH1 vector between the BglII and HindIII sites.

NHERF1 knockdown with shRNA

LTRH1-puro (Barton and Medzhitov, 2002; Sfakianos et al., 2007) was modified to allow for the insertion of an shRNA sequence into the vector by mutating the HindIII sites at positions 2872 and 4282 via site-directed mutagenesis. Oligonucleotides targeting NHERF1 mRNA (Yu et al., 2007) were synthesized, annealed, and then ligated to the LTRH1 vector between the BglII and HindIII sites. Retroviral vectors were produced and cells were infected as described for GFP constructs. 1 d after infection, cells were selected with 8 µg/ml puromycin. To determine the degree of protein knockdown in shRNA-expressing cells, a 10-cm plate of confluent cells was washed twice with 4°C PBS with calcium and magnesium, completely aspirated, and placed on ice before treatment with 300 µl of M-PER Mammalian Protein Extraction Reagent (Thermo Fisher Scientific). After 2 min, supernatant from the plate was applied to a column (QIAshredder; QIAGEN) and centrifuged at 13,000 g for 1 min. The flow-through was analyzed by Western blotting after addition of NuPAGE LDS Sample Buffer (Invitrogen) and 2% mercaptoethanol and incubation at 95°C for 1 min.

IP of GFP constructs

IP protocol is based on Cheeseeman and Desai (2005). For each IP, 160 µl of resuspended Affi-Prep Protein A Support (Bio-Rad Laboratories) bead slurry (~110 µl bead volume) was used to make anti-GFP beads. Volumes were scaled up to prepare beads for many reactions at once. Beads were washed twice with PBST (PBS and 0.1% Tween 20), resuspended in 500 µl PBST with 80 µg/ml anti-GFP antibody, and rotated for 1 h at room temperature. Beads were then washed twice with PBST and twice with sodium borate buffer, pH 9.0 (0.2 M sodium borate and 0.2 M boric acid), resuspended in 500 µl sodium borate buffer with 33 mM dimethyl pimelimidate, and rotated for 30 min at room temperature. To neutralize residual dimethyl pimelimidate, beads were washed once in neutralization buffer (0.2 M ethanolamine and 0.2 M NaCl, pH 8.5), rotated for 1 h in neutralization buffer, resuspended in 500 µl of neutralization buffer, and stored at 4°C.

Two 245-mm tissue culture plates were confluent monolayers of cells were washed in 4°C PBS with calcium and magnesium and then placed on ice. Plates were scraped into 10 ml lysis buffer (100 mM NaCl, 300 mM sucrose, 3 mM MgCl2, 10 mM Pipes, pH 6.8, 0.5% Triton X-100, and complete EDTA-free protease inhibitors [Roche]) centrifuged at 12,000 g, 300 mM sucrose, 3 mM MgCl2, 10 mM Pipes, pH 6.8, 0.5% Triton X-100, and complete EDTA-free protease inhibitors [Roche]) centrifuged at 12,000 g, and 2-mercaptoethanol was added to 2% final concentration before incubation at 4°C. Supernatant was collected, and the protein concentration was measured by bichinchnic acid assay. 20 µg of cell lysate was added to a 100-µl bead volume of anti-GFP beads that had been washed twice with PBS/0.1% Tween and twice with lysis buffer. Lysate and beads were incubated overnight at 4°C with rotation. After overnight incubation, beads were washed five times with lysis buffer, and proteins were eluted by incubation in 100 µl of 4% SDS and 40 mM Tris, pH 8.0, at 70°C for 15 min. Eluate was mixed with NuPAGE LDS Sample Buffer (Invitrogen), and 2-mercaptoethanol was added to 2% final concentration before incubation at 95°C for 1 min and Western blot analysis.

Western blot

Protein samples in NuPAGE LDS Sample Buffer were separated by electrophoresis using NuPAGE 4–12% Bis-Tris gels (Invitrogen). Proteins were transferred to polyvinylidene fluoride membrane using the iBlot transfer system (Invitrogen). Membranes were blocked for 1 h with PBS/0.05% Tween 20/1% BSA. Primary antibodies in PBS/0.05% Tween 20/0.5% BSA were applied to membranes overnight at 4°C. Membranes were washed with PBS/0.05% Tween 20/0.5% BSA before a 1-h incubation with secondary antibodies (LiCOR Biosciences). After a final wash with PBS/0.05% Tween 20/0.5% BSA, antibody signals were visualized using a scanner (Odyssey; LiCOR Biosciences) and analyzed with Odyssey software version 3.0. Image levels were adjusted using Photoshop CS4.

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