



# Shaping Microtubules Into Diverse Patterns: Molecular Connections for Setting Up Both Ends

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**Microtubules serve as rails for intracellular trafficking and their appropriate organization is critical for the generation of cell polarity, which is a foundation of cell differentiation, tissue morphogenesis, ontogenesis and the maintenance of homeostasis. The microtubule array is not just a static railway network; it undergoes repeated collapse and reassembly in diverse patterns during cell morphogenesis. In the last decade much progress has been made toward understanding the molecular mechanisms governing complex microtubule patterning. This review first revisits the basic principle of microtubule dynamics, and then provides an overview of how microtubules are arranged in highly shaped and functional patterns in cells changing their morphology by factors controlling the fate of microtubule ends.** © 2011 Wiley Periodicals, Inc.

**Key Words:** microtubule, microtubule-end-binding proteins, +TIPs, cell polarity, morphogenesis

## Introduction

Cell morphology is established and maintained through the dynamic assembly and regulatory processes of molecular components, which provide a variety of spatial structures to express a given cellular function. Cells sense their surrounding environment via mechanical and chemical stimuli, such as light or forces, cell–cell and cell–extracellular matrix (ECM) interactions or gradients of signaling molecules, and they respond by developing an axis of polarity. The key element controlling cell shape is the cytoskeleton. The cytoskeleton consists of distinct filamentous systems: actin filaments, intermediate filaments, microtubules, and an emerging noncanonical cytoskeleton

composed of septins. These are all polymers, having the ability to reversibly assemble and disassemble. Intermediate filaments and septins confer cortical rigidity and actin filaments generate the driving force for cell migration and form cell shape, while microtubules serve as tracks for the directional transport of molecular components or drag ropes for the movement of organelles. Although these cytoskeletal systems have distinct roles, they interact with each other. The importance of interactions between microtubules and actin in establishing and maintaining cellular asymmetry has been described [Rodriguez et al., 2003]. In addition, accumulating evidence is revealing a novel linkage between microtubules and septin, which is discussed below.

Microtubules have an intrinsic structural polarity, which is fundamental to the directional transport mediated by motor proteins [Vallee and Sheetz, 1996; Hirokawa, 1998]. The appropriate delivery of physiologically active substances is crucial for their asymmetric distribution; therefore, the control of directionality and organization of microtubules in cells is essential to cell morphogenesis and function, and thus microtubule dynamics are a major target of signaling pathways. Following the pioneering *in vitro* studies that demonstrated the biochemical and structural properties of microtubules, recent progress, achieved by employing molecular cell biological approaches, have shed light on the molecular mechanisms underlying microtubule organization.

## Dynamic Instability

Our initial understanding of microtubule regulation came from *in vitro* analyses of purified microtubules. Microtubules are self-organized by the polymerization of  $\alpha$ - $\beta$ -tubulin heterodimers that are arranged parallel to a cylindrical axis, with  $\alpha$ -tubulin and  $\beta$ -tubulin having exposed minus and plus ends, respectively (Figs. 1A-a and 1A-b). Each tubulin subunit contains one binding site for guanine nucleotides, but only  $\beta$ -tubulin contains an exchangeably bound nucleotide [Weisenberg et al., 1968; Berry and Shelanski, 1972]. After microtubule assembly the  $\beta$ -tubulin-bound guanine triphosphate (GTP) is

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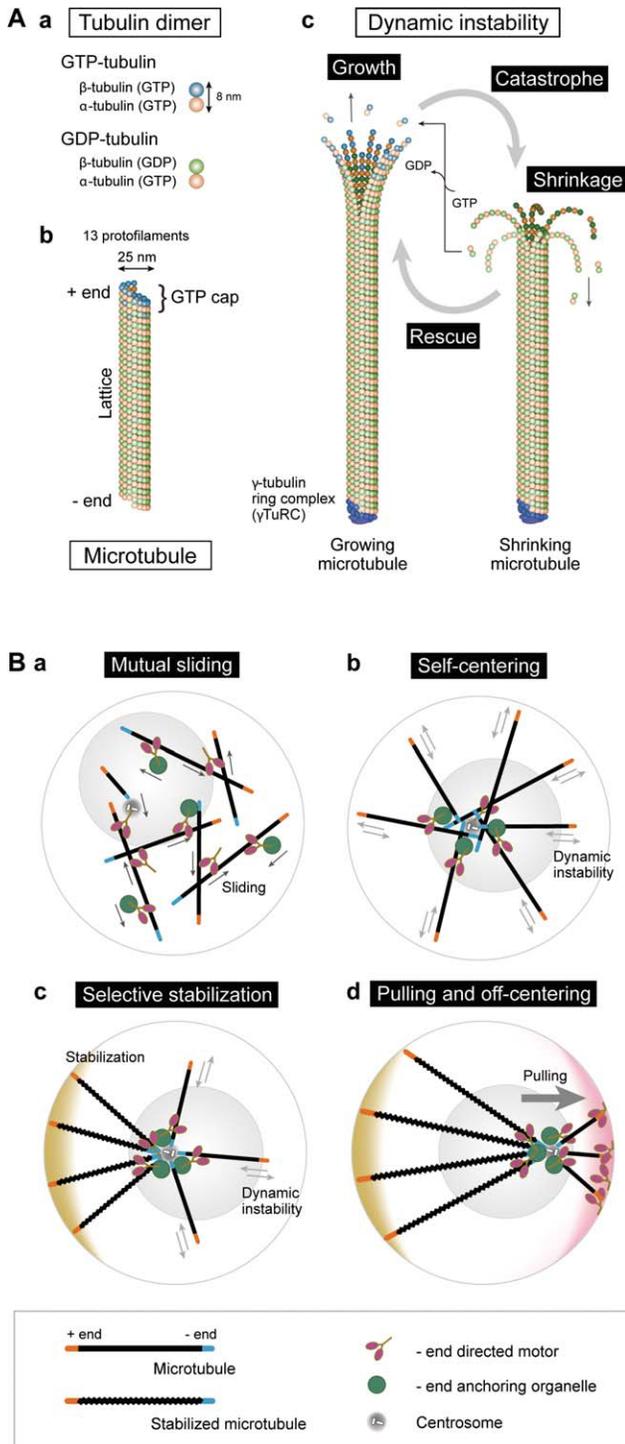
hydrolyzed to guanosine diphosphate (GDP) (Fig. 1A-c) [Jacobs et al., 1974; Weisenberg and Deery, 1976]. The hydrolysis of the nucleotide is not necessary for microtubule formation; however, the portion of microtubule carrying GTP, termed the “GTP cap” (Fig. 1A-b), is stable and displays a steady state assembly [reviewed by Howard and Hyman, 2009]. In contrast, the GDP-bound tubulins are prone to dissociate from the microtubule by increasing

the curvature of protofilaments in the microtubule and putting strain on the lattice [Elie-Caille et al., 2007].

In a population of microtubules in a steady state of assembly/disassembly, an individual microtubule interconverts stochastically between periods of slow growth and rapid shortening at the plus end, a behavior known as “dynamic instability” (Fig. 1A-c) [Mitchison and Kirschner, 1984; Hotani and Horio, 1988]. Minus ends are generally not dynamic and depolymerize continuously if the ends are not capped and stabilized. In cells, dynamic instability has a functional role in controlling the disposition of the microtubule arrays upon external stimuli: the fast disassembly provides a means for the rapid re-organization of microtubules in response to changing cellular requirements.

### Default: Self-Centering Activity of the Cytoplasm

If one looks at the pattern of microtubules in a single cultured cell that is not in contact with surrounding cells, one will generally see microtubules distributed with their minus ends clustered together around the cell center and their plus ends extending out into the cytoplasm. At the cell center, a canonical microtubule nucleator centrosome or microtubule organizing center, as well as microtubule minus end-associating organelles, such as the Golgi apparatus, centriolar satellites and nucleus, will be located near the cluster of minus ends. This radial plus end-out orientation of microtubules is established through the combination of microtubule-dependent transport of minus end-anchoring materials by a minus end directed molecular



**Fig. 1. Microtubule structure and conceptual diagrams for the microtubule patterning process.** (A) Microtubules are composed of stable  $\alpha/\beta$ -tubulin heterodimers (a) that are aligned in a polar head-to-tail fashion to form protofilaments (b). GTP bound to  $\alpha$ -tubulin is non-exchangeable and is never hydrolyzed. The cylindrical and helical microtubule wall typically comprises 13 parallel protofilaments with a diameter of 25 nm (b). Assembly and disassembly of microtubules is driven by the binding, hydrolysis and exchange of a guanine nucleotide on the  $\beta$ -tubulin (c). GTP hydrolysis occurs shortly after incorporation. It has been postulated that GTP hydrolysis changes the conformation of a protofilament to a profoundly curved structure, which makes the tubulin dimer easier to dissociate from the filament. A ‘cap’ of tubulin-GTP subunits (GTP cap) stabilizes the filament. The GDP of the disassembly products is exchanged with GTP. This stochastic assembly-disassembly cycle is termed “dynamic instability”. (B) In the non-polarized cytoplasm, motor protein-based mutual sliding of microtubules and movement of motor-associated organelles results in the self-centering of the subcellular components (a and b). Microtubules undergoing dynamic instability reach and capture the specialized sites at the cell cortex and are followed by stabilization of their entire length (c). A cortically bound form of the minus end-directed microtubule motor protein pulls the microtubule network and associated organelles to one side (d).

motor, typified by dynein, and growth of the plus ends [Rodionov and Borisy, 1997] (Figs. 1B-a and 1B-b). Even in an isolated centrosome free cytoplasm, dynamic microtubules interacting with membranous organelles and motor proteins arrange themselves into a radial array [McNiven et al., 1984]. Microtubules and purified oligomeric motors only are sufficient to organize microtubules into asters in vitro [Urrutia et al., 1991; Nédélec et al., 1997]. This ability of the microtubule-based system to find the center establishes a general coordinate system, which is then used to position organelles within the cell.

### Generation of Asymmetry in the Microtubule Pattern

A cell is polarized when it has developed a main axis of organization following a trigger by external signals in variety cell types. During this process, in numerous cell types, microtubules are dramatically reorganized [reviewed by Bartolini and Gundersen, 2006]. This reorganization can be regulated by two classes of tubulin/microtubule modulators: (1) diffusible factors that regulate the amount of functional tubulin or affecting the overall microtubule dynamics/stability and (2) localized factors that position microtubule plus and minus ends at specific sites within cells.

The diffusive factors include chaperons that regulate tubulin protein production [reviewed by Lundin et al., 2010], the conventional microtubule-associated proteins (MAPs; including MAP2, MAP4 and tau) that stabilize the entire length of the microtubule lattice [reviewed by Amos and Schlieper, 2005], the microtubule destabilizing factor stathmin/OP18 [reviewed by Cassimeris, 2002] and the microtubule severing enzymes (Spastin, Fidgetin, and Katanin) [reviewed by Roll-Mecak and McNally, 2010]. Interestingly, a subset of kinesin motor proteins, including kinesin-8, -13, and -14, not only walks on microtubule lattices, destabilizes microtubules by removing tubulin dimers from the ends, resulting in microtubule depolymerization [Wordeman, 2005; Kinoshita et al., 2006; Howard and Hyman, 2007]. In contrast, a TOG domain family protein, XMAP215, is a potent growth-promoting factor that moves with the growing microtubule plus ends where it catalyzes the addition of tubulin subunits [Brouhard et al., 2008]. These classes of molecules can regulate tubulin/microtubules throughout the cytoplasm, but occasionally they/their activities can also be localized spatially by upstream signals; for example, stathmin/OP18 is locally inactivated in motile membrane protrusions during interphase and around chromosomes during mitosis [Niethammer et al., 2004], and XMAP215 and kinesin-13s are localized to the mitotic spindle pole to stabilize and destabilize centrosomal microtubules, respectively [Lee et al., 2001; reviewed by Ems-McClung and Walczak, 2010]. Another class of diffusible factors that can regulate micro-

tubule function is enzymes that modify tubulin in microtubules post-translationally. Examples of these modifications include acetylation, polyglycylation and polyglutamylolation, tyrosination/detyrosination, and palmitoylation. These tubulin post-translational modifications specialize the function of subsets of microtubules by changing the affinity of motor proteins and MAPs to the microtubules [reviewed by Janke and Kneussel, 2010; Wloga and Gaertig, 2010].

The second class of modulators, localized factors, is of crucial importance for the generation of polarity, and is the main focus of this review (Table I). The basic concept explaining the generation of microtubule asymmetry, termed the “selective stabilization model” or “search-and-capture model,” involves local stabilization of a subset of microtubules [Kirschner and Mitchison, 1986] (Fig. 1B-c). In this model, dynamic instability allows microtubules to search stochastically the three-dimensional space within cells to find and capture specific target sites on the cell periphery that have been activated by environmental signals. The plus ends attaching to the cell cortex are stabilized at their ends by local factors, resulting in increased lifespan of the entire microtubule (Fig. 1B-c). These long-lived microtubules are a primary target for the post-translational modification [reviewed by Gundersen and Cook, 1999]. Recent studies have, however, revealed that the control of microtubule length and behavior after end-attachment is more complex; the fate of microtubule ends is differentially regulated by various microtubule end-binding proteins, including plus-end-tracking proteins (+TIPs) and the motor proteins, dynein and kinesin (Fig. 2, Table I).

Following the assembly of microtubule arrays, the entire network needs to have the ability to be pulled to one side of the cell by the tractive force. Motor proteins, which produce force directed towards either end of the microtubule (Figs. 1B-d and 2A-b), achieve this function. A cortically bound form of dynein, a minus end directed microtubule motor protein that is conserved from yeast to mammals, is indeed involved in nuclear migration, mitotic spindle orientation and cytoskeletal reorientation during wound healing [reviewed by Dujardin and Vallee, 2002; Yamamoto and Hiraoka, 2003]. Recent computer simulation approaches confirmed that the pulling force generated at the interface between the microtubule plus ends and the cell cortex is the primary driver for the movement of the nucleus and centrosome in *C. elegans* early embryos [Kimura and Onami, 2005; Kimura and Onami, 2007]. In contrast, microtubule-depolymerizing kinesins remove tubulin dimers from the ends (Fig. 2A-e), which results in the release of microtubule attachment to the cellular structure or in the generation of motive force to pull the microtubule associating material if it can remain attached to the shrinking microtubule ends.

**Table I. Representative Factors Acting at Microtubule Ends to Organize the Microtubule Network**

Human (homo sapiens:hs) or fly (Drosophila meranogaster:dm)			
End-binding proteins	MT end	Action on MT	Site of MT anchor / Receptor molecule(s)
+TIPs	EB1/MT-binding proteins	EB1 family (EB1, 2, 3)	+ Anchor Neuronal growth cone / Drebrin
			+ Anchor Neuronal dendritic spine / p140Cap, cortactin
			- Anchor Centrosome / CAP350 and FOP
		ACF7	+ Anchor Cell cortex, leading edge / Actin
		APC tumor suppressor protein	+ Guide Cell cortex, leading edge, plasma membrane / DLG1
			+ Guide Cell cortex, leading edge / IQGAP1, actin
			+ Guide Cell cortex, leading edge / mDia
			+ Anchor? Plasma membrane / AMER1, 2 (APC membrane recruitment 1, 2)
			+ Anchor? Mitotic cell cortex of <i>Drosophila</i> male germline stem cells / DE-cadherin, Armadillo, actin
			+ Anchor Mitotic kinetochore / nd
			- Anchor Mitotic SPB / nd
		CLASPs	+ Anchor Cell cortex, cell periphery in HeLa, basal cortex in epithelia / LL5 $\alpha$ and LL5 $\beta$
			+ Anchor Cell cortex, leading edge / IQGAP1
			- Anchor Golgi structure / GCC185
		CLASPs, with astrin & Kif2b	+,- Anchor Mitotic kinetochore, SPB / CENP-E (at +), nd (at -)
		CLIP-170	+ Anchor or guide? Cell cortex, leading edge / IQGAP1
		Dynein-dynactin complex	+ Guide & pull? Cell cortex, leading edge / GKAP-Dlg1
			+ Anchor Adherens junctions / $\beta$ -catenin
			+ Anchor & pull? Leading edge, cell-cell adhesion sites / Par3, through dynein light intermediate chain 2 (LIC2)
			+ Pull Mitotic cell cortex / NuMA, LGN, G $\alpha$ (hs); Mud, Pins, G $\alpha$ (dm)
			- Anchor Centrosome / Nudel, Par6
			- Anchor Nuclear pore / Bicaudal D2
		Dynein-dynactin-CLIP-170 complex	+ Pull Mitotic kinetochore / Rod-ZW10-Zwilch (RZZ) complex, NudeE/Nudel-Lis1 complex, Spindly
		MCAK/Kif2C (kinesin-13), with APC	+ Shrinkage Mitotic kinetochore / nd
		Kif2A (kinesin-13)	+ Shrinkage Mitotic SPB / DDA3
Kif2B (kinesin-13)	+,- Shrinkage Mitotic kinetochore and SPB / nd		
KLP10A, KLP59C (kinesin-13) (dm)	+,- Shrinkage Mitotic kinetochore and SPB / nd		
Kif18A (kinesin-8)	+ Shrinkage Mitotic kinetochore / nd		
CENP-E (kinesin-7)	+ Elongation Mitotic kinetochore / BubR1		
XMAP215 (Dis1/TOG/XMAP215 family)	- (also + in the cytoplasm) Anchor (at -) Mitotic SPB, Centrosome, cytoplasm / transforming acidic coiled coil (TACC)		
$\gamma$ -TuRC	- Anchor Centrosome / GCP-WD, ASP, CG-NAP (AKAP450), NLP, centrosomin, NEED1, kendrin/pericentrin		
	- Anchor <i>cis</i> -Golgi apparatus / AKAP450, GM130		
ninein	- Anchor Centrosome (mother centriole appendage), close proximity to adherens junctions in the inner pillar of organ of Corti / nd		
ninein, Ndel1, Lis1, CLIP-170	- Anchor Desmosomes in epidermis / Desmoplakin		
ninein, pericentrin, $\gamma$ -TuRC	- Anchor Myotube nuclear envelope / nd		
Nezha	- Anchor Cell adhesion / E-cadherin, p120 catenin, PLEKHA7		
Budding yeast ( <i>Saccharomyces cerevisiae</i> )			
End-binding proteins	MT end	Action on MT	Site of MT anchor / Receptor molecule(s)
+TIPs	EB1/MT-binding proteins	Bim1P (EB1 family)	+ Delivery & anchor Bud tip / Kar9-Myo2, walking along actin cables
		Kip3p (kinesin-8), with Bim1p	+ Anchor & shrinkage Bud tip / Kar9
		Kar3p (kinesin-14) & Bik1p (CLIP-170)	+ Anchor & pull Shmoo tip / mating-specific G $\alpha$ protein, Gpa1
		Stu1 (CLASP), with DASH complex	+ Anchor Mitotic kinetochore / Ndc80 complex
		Dynein, with Bik1p (CLIP-170), Kip2p (kinesin-7)	+ Slide & pull Bud cortex / Num1p through dynein intermediate chain Pac11p
		DASH complex	+ Anchor and pull Mitotic kinetochore / Ncd80, Mis12 complexes
Stu2p (Dis1/TOG/XMAP215 family)	- (also + in the cytoplasm) Anchor Centrosome and mitotic SPBs / Spc72, with yeast $\gamma$ -tubulin complex		
$\gamma$ -TuSC	- Anchor SPB / Spc110		
Fission yeast ( <i>Schizosaccharomyces pombe</i> )			
End-binding proteins	MT end	Action on MT	Site of MT anchor / Receptor molecule(s)
+TIPs	EB1/MT-binding proteins	Mai3p (EB1 family)	+ Anchor Cell end / moe1p
		EB1/MT-binding proteins: Tea1p, Tea2p (kinesin-7), Tea3p, Tea4p, Tip1p (CLIP-170)	+ Anchor Cell end / Mod5p, tea3p, bud6p, for3p
		Tip1p (CLIP-170)-Tea2p (kinesin-7) complex	+ Anchor Mitotic kinetochore / nd
		Peg1 (CLASP) & dynein	+ Anchor Cell end / nd
		Dynein	+ Pull Meiotic cell cortex / Num1/Mcp5
		DASH complex & Klp5/6 (kinesin-8)	+ Anchor & pull Mitotic kinetochore / Ndc80, Mis12 complexes
Dis1 (Dis1/TOG/XMAP215 family)	+ Anchor Mitotic kinetochore / Ndc80 complex		
Alp14 (Dis1/TOG/XMAP215 family) & Klp5/6 (kinesin-8)	+ Anchor & pull Mitotic kinetochore / nd		
Alp14 (Dis1/TOG/XMAP215 family)	- Anchor Mitotic SPB / Alp7 (TACC homologue)		
$\gamma$ -TuRC	- Anchor Mitotic SPB / Pcp1, Myo1, Msd1		

List of representative microtubule end-binding proteins involved in microtubule patterning. In vertebrates most proteins listed are conserved; therefore, only human protein nomenclature is shown (hs), except for several *Drosophila* proteins (dm). Budding yeast and fission yeast proteins are listed separately. Microtubule: MT, microtubule plus-end-tracking proteins: +TIPs, spindle pole body: SPB,  $\gamma$ -tubulin ring complex:  $\gamma$ -TuRC,  $\gamma$ -tubulin small complex:  $\gamma$ -TuSC, not determined: nd.

### Molecules Involved in Microtubule End Positioning

The representative factors acting on microtubule ends are listed in Table I. The  $\gamma$ -tubulin ring complex ( $\gamma$ -TuRC) is

well known as a minus end-capping complex that protects the microtubule minus ends from depolymerization and anchors them to the centrosome (Fig. 2B-c). Ninein is a minus end-anchoring protein, which is distinct from the

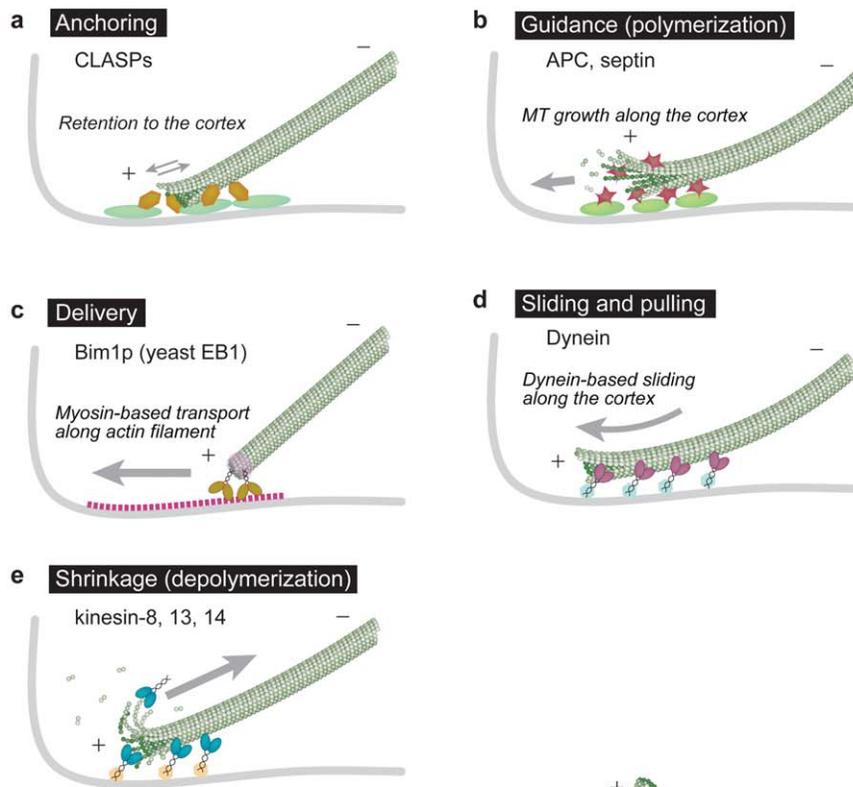
Table I. Continued

Upstream signal or event	References
Neuritogenesis	Geraldo et al. 2008
Dendritic spine formation	Jaworski et al. 2009
Radial MT organization	Yan et al. 2006
Directional migration	Kodama et al. 2003
Cdc42 and Par6-PKC $\zeta$	Etienne-Manneville et al. 2005; Mimori-Kiyosue et al. 2007
Rac1, Cdc42	Watanabe et al. 2004
LPA, Rho	Wen et al. 2004
nd	Grohmann et al. 2007
Mitotic spindle orientation	Reviewed by Yamashita 2009
Mitotic spindle organization & checkpoint	Fodde et al. 2001; Kaplan et al. 2001
Mitotic spindle organization & regulation	Louie et al. 2004
P13 kinase, ECM-integrin association	Hotta et al. 2010; Lansbergen et al. 2006; Mimori-Kiyosue et al. 2005
GSK3 $\beta$	Watanabe et al. 2009
Nucleation of noncentrosomal MTs	Efimov et al. 2007
Mitotic spindle organization & regulation	Maffini et al. 2009; Manning et al. 2010
CDC42, Rac	Fukata et al. 2002
Directional migration	Manneville et al. 2010
Cell-cell adhesion	Ligon et al. 2001
Directional migration, cell-cell adhesion	Schmoranzner et al. 2009
Mitotic spindle orientation	Reviewed by Radulescu and Cleveland 2010; Siller and Doe 2009; Wilkie and Kinch 2005
MT anchoring at the centrosome	Guo et al. 2006; Kodani et al. 2010
Centrosome centering	Splinter et al. 2010
Mitotic spindle formation and chromosome segregation	Reviewed by Kardon and Vale 2009
Aurora A, B kinases	Banks and Heald 2004
Aurora B, Polo-like kinase Plk1	Jang et al. 2008; Knowlton et al. 2009
Aurora A, B kinases	Reviewed by Ems-McClung and Walczak 2010
Moving chromatids by means of poleward flux	Rogers et al. 2004
Mitotic chromosome alignment	Stumpff et al. 2008
Chromosome congression	Sardar et al. 2010
MT nucleation and spindle formation	Brouhard et al. 2008; Lee et al. 2001
MT nucleation	Reviewed by Luders and Stearns 2007
MT nucleation	Rivero et al. 2009
Minus end anchoring in differentiated cells	Mogensen et al. 2000; Moss et al. 2007
Cortical MT organization in epidermis	Lechler and Fuchs 2007; Sumigray et al. 2011
Muscle cell differentiation	Bugnard et al. 2005
Cell-cell adhesion	Meng et al. 2008
Upstream signal or event	References
Budding, cdc42	Hwang et al. 2003; Korinek et al. 2000; Lee et al. 2000
Mitotic spindle positioning	Gupta et al. 2006
Mating-specific pheromone	Molk et al. 2006; Sproul et al. 2005; Zaichick et al. 2009
Establishment and maintenance of mitotic spindle	Ortiz et al. 2009
Nuclear migration	Reviewed by Miller et al. 2006; Yamamoto and Hiraoka 2003
Mitotic chromosome movement	Reviewed by Buttrick and Millar 2011
Anchorage of astral MTs at SPB and MT nucleation	Usui et al. 2003; Wolyniak et al. 2006
MT nucleation	Kilmartin, 1996; Kollman, 2010; reviewed by Helfant 2002
Upstream signal or event	References
End growth and mitosis	Chen et al. 2000; Chen et al. 1999
End growth, cdc42	Reviewed by Chang and Martin 2009; Hayles and Nurse 2001
Chromosome poleward movement	Goldstone et al. 2010
End growth and mitosis	Grallert et al. 2006
Nuclear migration	Saito et al. 2006; Yamashita and Yamamoto 2006
Mitotic chromosome movement	Sanchez-Perez et al. 2005, reviewed by Buttrick and Millar 2011
Kinetochores-spindle attachment	Hsu and Toda 2011
Kinetochores-spindle attachment	Garcia et al. 2002
Bipolar spindle formation	Sato et al. 2004
Anchoring of spindle MT to SPB	Flory et al. 2002; Samejima et al. 2008; Toya et al. 2007

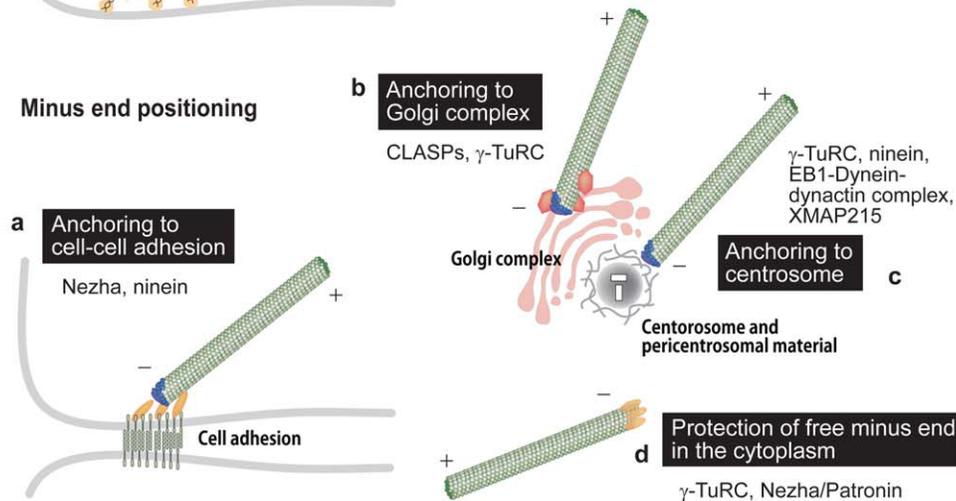
$\gamma$ -TuRC, and is localized at centrosomal and non-centrosomal sites [Mogensen et al., 2000]. Of special note is the recent discovery of a new minus end-stabilizing/anchoring molecule, Neza (also termed Patronin in *Drosophila* together with other Patronin family members) [Goodwin and Vale, 2010; Meng et al., 2008] (Fig. 2B-a).

At the plus end a large number of “microtubule plus end-tracking proteins (+TIPs)” have been identified over the past decade (Fig. 3) [reviewed by Akhmanova and Steinmetz, 2008; Mimori-Kiyosue and Tsukita, 2003; Schuyler and Pellman, 2001]. +TIPs are a diverse group of specialized MAPs that are evolutionarily conserved and that

## A Plus end positioning



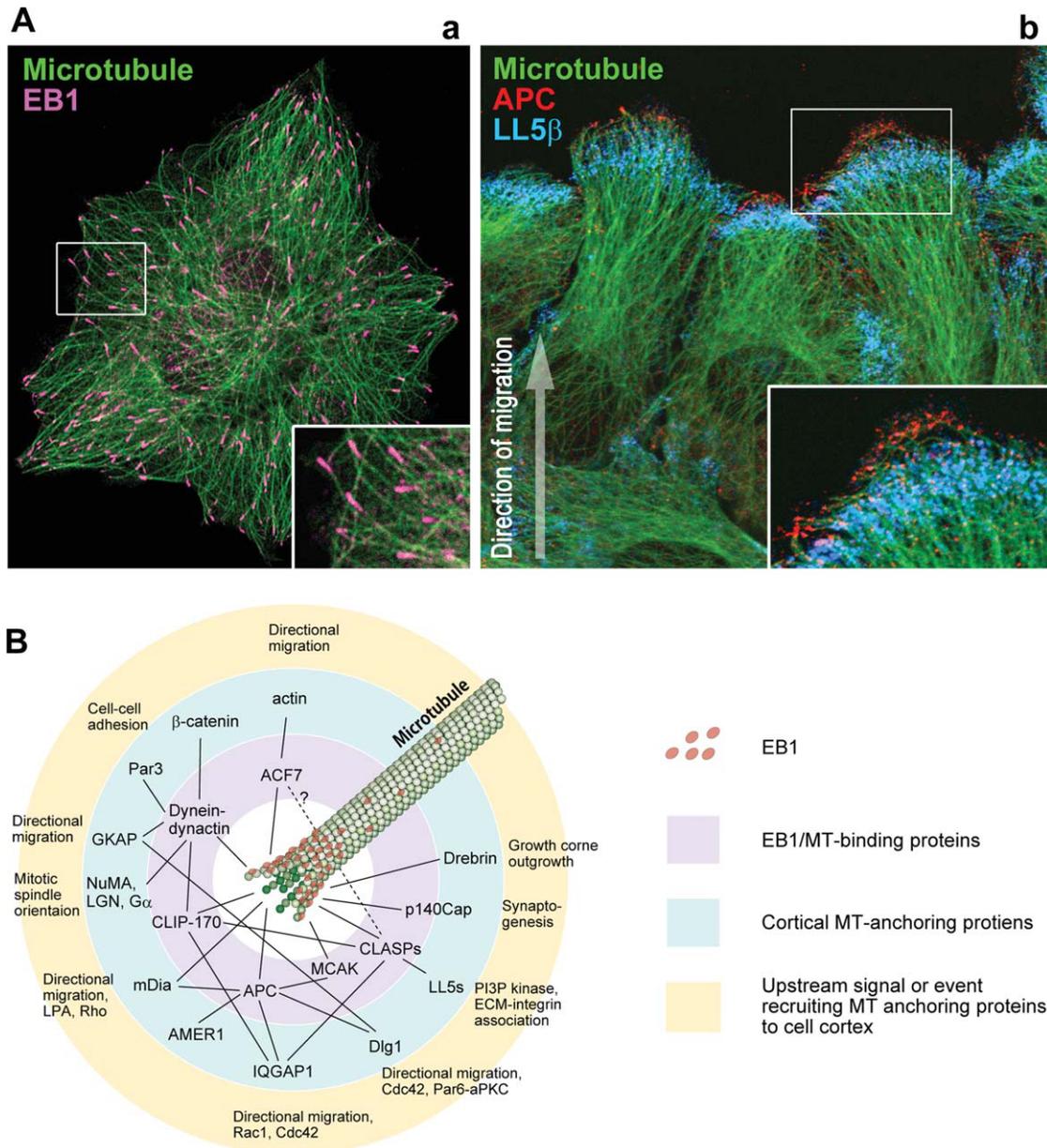
## B Minus end positioning



**Fig. 2. The fate and position of microtubule ends are differently regulated by end-binding proteins.** Examples of the mode of action of end-binding proteins at the plus end (A) and the minus end (B). Microtubule: MT,  $\gamma$ -tubulin ring complex:  $\gamma$ -TuRC.

accumulate at the ends of growing microtubules (Table I). Many +TIPs are targeted to the growing plus ends through interaction with EB1 (end-binding 1) family proteins. EB1 family proteins are autonomous plus end-binding proteins recognizing the end-specific tubulin structure independently of any binding partners [Bieling et al., 2007], probably by recognizing the GTP cap [Zanic et al., 2009], and may form a cross-bridge between adjacent protofilaments to stabilize the lattice [des Georges et al., 2008] (Fig. 3A, Table I). Thus, EB1 family proteins are core components of

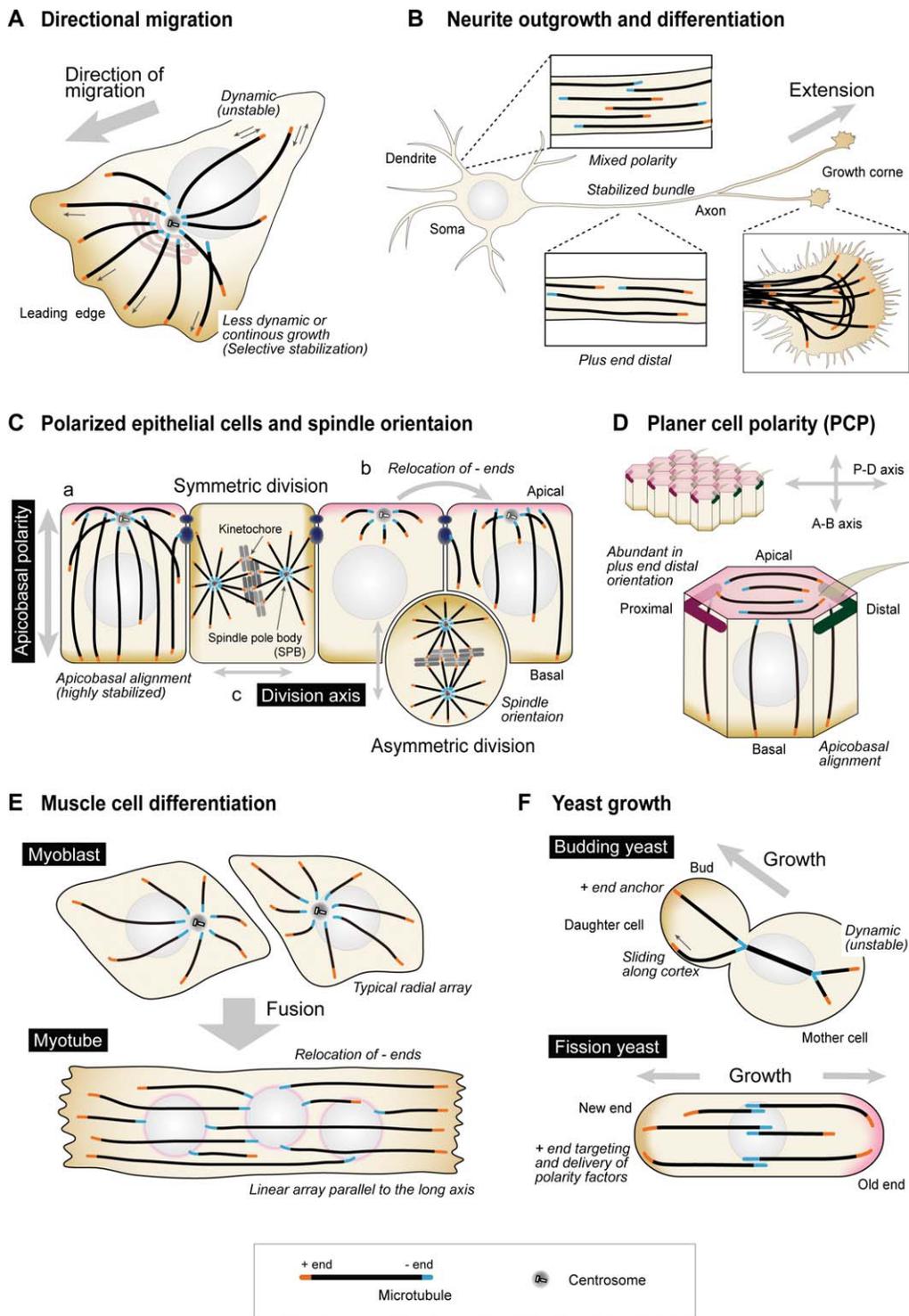
+TIP complexes (Fig. 3). In addition, XMAP215 has also been reported to autonomously bind to the plus ends [Brouhard et al., 2008]. Both EB1 family proteins and XMAP215 can act independently as microtubule growth promoters, but in some instances they are linked by SLAIN motif family proteins, which strongly stimulate processive microtubule growth in interphase cells [van der Vaart et al., 2011]. The dynein-dynactin complex can also access microtubule ends in both EB1-dependent and independent manners [Miller et al., 2006; Watson and Stephens, 2006]. It is noteworthy that



**Fig. 3. Subcellular distribution of +TIPs and molecular linkage among +TIPs.** (A) Distribution of microtubules visualized with GFP-tubulin (green) and EB1 (magenta) in HeLa cells seeded on a collagen coated cover slip (a), and microtubule (green), APC tumor suppressor protein (red) and CLASP-anchoring protein LL5 $\beta$  (cyan) in mouse NIH/3T3 fibroblasts undergoing directional migration in response to monolayer scratching (b). EB1 localizes to every growing microtubule end throughout the cytoplasm. Note that APC is accumulated in the pioneering microtubule ends in the lamellipodia extending toward the scratched area, while LL5 is concentrated at the base of the lamellipodia where many microtubule ends are terminated. (B) The molecular linkage between +TIPs at the microtubule plus-end and the upstream signal or events are shown diagrammatically. Most +TIPs bind to EB1 at the ends, and at the same time associate with the cellular structure, such as the cell cortex or mitotic kinetochores, and thereby attach the microtubule ends to these structures.

some plus end-binding proteins can also be localized at the minus end, and have roles as microtubule-anchoring and/or as microtubule-nucleating factors (Fig. 2B-b, Table I). In most cases, the factors described above exert microtubule stabilizing or growth promoting effects, and form large multi-molecular complexes that associate with cellular structures to attach microtubule ends to these structures (Fig. 3).

In contrast, microtubule-depolymerizing kinesins, including kinesin-8, -13 and -14, removes tubulin dimers from the ends and induces microtubule shortening (Fig. 2A-e). A budding yeast kinesin-8 Kip3p walks processively towards the plus end, and at the end it remains there and disassemble microtubules exclusively at the plus end, whereas the kinesin-13 family member, mitotic



**Fig. 4. Schema of polarized cell architecture and microtubule patterns.** Typical microtubule network patterns and the position of plus (orange) and minus (blue) ends in polarized cells are illustrated. Microtubule: MT.

centromere-associated kinesin (MCAK), acts at both ends [Varga et al., 2006]. Kinesin-mediated microtubule shrinkage at the plus end may generate the driving force to move organelles: budding yeast Kar3p, a minus end-directed kinesin-14 motor, localizes to plus ends tethered to the shmoo tip and microtubule depolymerization pulls the nucleus to the cell tip [Molk et al., 2006].

In certain cases, factors having different effects on microtubule ends, e.g. stabilizing and destabilizing effects, form a complex to determine appropriate microtubule length. A specific example is the complex of kinesin-13 Kif2b with CLIP-associated protein 1 (CLASP1) at mitotic kinetochores where it exhibits microtubule-depolymerizing activity to promote kinetochore microtubule

dynamics and turnover [Manning et al., 2010]. Another example is the direct association of EB1 family members with MCAK, a potent microtubule depolymerase [Lee et al., 2008]. In an *in vitro* reconstitution system, EB3, which facilitates tubulin assembly, targets MCAK to the growing microtubule ends and enhances the capacity of MCAK to induce catastrophes, resulting in increase of overall microtubule dynamicity in the system [Montenegro Gouveia et al., 2010]. In cells, overall effects exerted by +TIP complexes on microtubule ends might vary as the situation demands. Thus, the fate of microtubule ends and the resulting impact on microtubule-related events are controlled differentially and precisely at each microtubule anchor site, so that cells establish asymmetric and complex microtubule networks to carry out given functions.

### Construction and Function of Microtubule Networks in Various Processes

Examples of actual cell architectures with various microtubule organization patterns showing highlighted plus and minus ends are presented in Fig. 4. Microtubule organizing mechanisms and their biological functions during the morphogenesis of different cell types are described below.

#### Cell-to-Substrate Adhesion

The ECM provides signaling cues that regulate cell functions, and that could be the first signals adherent cells receive. The composition of the ECM, its three-dimensional organization and its stiffness are major determinants of microenvironmental signaling. The relationship between microtubule plus ends and cell-substratum adhesions was first described in migrating fish fibroblasts, in which microtubule ends targeted to focal adhesions (FAs) were visualized by vinculin staining using live cell fluorescence microscopy [Kaverina et al., 1998]. It has also been reported that fibronectin-mediated stimulation of focal adhesion kinase induces localized stabilization of microtubules by Rho signaling in migrating mouse fibroblasts [Palazzo et al., 2004]. Once attached to the basal cortex, microtubules regulate FA turnover, and thereby facilitate cell migration in concert with endocytic processes [Ezratty et al., 2005; Small and Kaverina, 2003]. Adenomatous polyposis coli (APC) tumor suppressor protein appears to be one of several factors linking FA and microtubule plus end dynamics [Matsui et al., 2008; Matsumoto et al., 2010]. On the other hand, in human MCF-10A mammary epithelial cells, the CLASP-LL5 complex anchors microtubule plus ends to non-FA cell-substratum adhesion sites composed of deposited laminin and laminin receptor integrins [Hotta et al., 2010]. Interestingly, upon epithelial-mesenchymal transition (EMT) during chicken embryo gastrulation, microtubules near the basal cortex are disrupted and the loss of the basal microtubules causes basement membrane breakdown [Nakaya et al., 2008]. This provides evidence of microtubule-ECM communication. Overall, it is likely that microtubules can be targeted

to different types of cell-substratum adhesion sites through distinct pathways to regulate cell adhesion, but the molecular linkage between the ECM and microtubules has not yet been precisely dissected and is not understood in detail.

#### Directional Migration

Directional cell migration is an important process that occurs in tissue development, chemotaxis and wound healing. During directional migration the plus ends of microtubules are stabilized near the leading edges [Waterman-Storer and Salmon, 1997] (Fig. 4A). Microtubule outgrowth from the centrosome shows no directional bias. However, dynamic instability is highly polarized; most microtubules in leading edges are stabilized with a reduced frequency of growth/shortening, while in trailing edges the dynamicity, the sum of the growth and shortening distance per unit time, is increased [Salaycik et al., 2005]. Rho family GTPases, in particular Rac1, RhoA and Cdc42, phosphatidylinositol-3,4,5-triphosphate (PIP3) signaling, and PAR (partitioning-defective) gene products are implicated in the polarization of microtubules [Wittmann and Waterman-Storer, 2001; Etienne-Manneville and Hall, 2002].

Among +TIPs, CLASPs, actin crosslinking family 7 (ACF7, also known as MACF1) and APC tumor suppressor protein localize to the cell cortex near migrating cell edges and attach EB1-positive microtubule plus ends to the cortex to facilitate directional migration (Fig. 3A-b) [Akhmanova et al., 2001; Kodama et al., 2003; Etienne-Manneville et al., 2005; Mimori-Kiyosue et al., 2007]. The molecular linkages that have been reported at the cell cortex are depicted in Fig. 3B. APC promotes persistent growth of microtubule ends and guides them to the front of the lamellipodia [Näthke et al., 1996; Kita et al., 2006]. APC remains attached to the extending microtubule ends with the help of plus end-directed motor activities [Mimori-Kiyosue et al., 2000; Jimbo et al., 2002; Jaulin and Kreitzer, 2010], which results in accumulation of APC at the ends of pioneering microtubules (Fig. 3A-b). In contrast, CLASPs, immobilized on LL5-containing cortical patches formed at the base of lamellipodia, keep the microtubule ends within this narrow area for a longer time period, although individual microtubule ends exhibit repetitive short distance growth/shortening (Figs. 2A-a and 3A-b) [Mimori-Kiyosue et al., 2005; Hotta et al., 2010]. The site of APC localization relies on the Par6-aPKC-Cdc42 complex [Etienne-Manneville et al., 2005], while the CLASP-LL5 complex requires the PI3K pathway, activated by ECM-integrin association, for localization to the basal cell cortex [Hotta et al., 2010]. The affinity of APC and CLASPs to the microtubules is partly regulated by GSK-3 $\beta$ , which phosphorylates MAPs to release microtubules and is inactivated through Rac1- or Cdc42-dependent phosphorylation, which occurs specifically at the leading

edge of migrating cells [Etienne-Manneville and Hall, 2003; Wittmann and Waterman-Storer, 2005].

In extending nerve processes, microtubule behavior and the regulatory mechanisms controlling this behavior are similar to that reported for the leading edge of other types of migrating cells. For example, the involvement of APC and CLASPs, under the control of nerve growth factor signaling and Abelson (Abl) tyrosine kinase, respectively, have been described [Lee et al., 2004; Zhou et al., 2004]. During synaptogenesis, microtubules decorated with EB1 can enter synapses and modulate spine morphology by interacting with p140Cap/SNIP, a regulator of Src tyrosine kinase, through the regulation of the actin cytoskeleton [Jaworski et al., 2009]. Microtubule orientation is unique in neurites: in axons microtubules are aligned unidirectionally, with all the plus ends pointing toward the growth cone, while microtubules are aligned nonuniformly in differentiated dendrites, with dynamic plus ends pointing both distally and toward the cell body (Fig. 4B). The precise mechanisms governing this unique microtubule organization in nerve processes are still obscure, and current knowledge has been reviewed by Conde and Caceres [2009].

### **Epithelial Cell Polarization**

Epithelial cells contain stable microtubules that are not associated with centrosomes, and these microtubules are required for epithelial polarization. At the early stage of epithelial polarization, cadherin-mediated contact interactions initiate a signaling pathway that alters microtubule organization by stabilizing microtubule ends indirectly via an as yet unknown pathway [Chausovsky et al., 2000]. A minus end-binding protein, Nezha/Patronin, may contribute to the stabilization of free minus ends in the cytoplasm [Meng et al., 2008; Goodwin and Vale, 2010] (Fig. 2B-d). Furthermore, cadherin-mediated cell–cell interactions provide extracellular cues that induce nucleus and centrosome off-centering toward cell–cell contacts, and promote orientation of the nucleus–centrosome axis toward free cell edges [Dupin et al., 2009].

Apicobasal polarization of epithelial cells involves a dramatic reorganization of microtubules (Fig. 4C-a). The radial array of microtubules focused on a centrally located centrosome is lost or greatly reduced, and a non-centrosomal apicobasal array develops (Fig. 4C-b) [Bre et al., 1987; Buendia et al., 1990], while a subset of microtubules still grow toward apical membranes [Jaulin et al., 2007]. Concomitantly, minus end-capping and end-anchoring factors, such as  $\gamma$ -tubulin, ninein and Nezha, relocate to the apical anchoring sites [Meads and Schroer, 1995; Mogensen et al., 2000; Meng et al., 2008]. At the basal sites, +TIPs, including APC and CLASP-LL5 complex, are localized to retain microtubule plus ends at the basal cortex [Reilein and Nelson, 2005; Hotta et al., 2010]. These observations are consistent with the notion that the minus and plus end-

anchoring molecules are recruited to the apical and basal region, respectively, to align microtubules along the apico-basal axis (Fig. 4C-a).

Recent studies have uncovered intriguing relationships between microtubules and septins in the formation of apicobasal microtubule arrays. Septins are filamentous guanine triphosphates (GTPases) that can bind to microtubules [reviewed by Kinoshita, 2006; Weirich et al., 2008; Spiliotis, 2010]. In epithelial cells undergoing polarization, septin 2 associated with bundled microtubules guides microtubule growth dynamics and microtubule-microtubule interactions toward the establishment of the apical microtubule meshwork [Bowen et al., 2011]. The septin tracks also facilitate post-Golgi vesicle transport by antagonizing MAP4, which has an inhibitory role in vesicle transport. This regulatory step is required for columnar-shaped epithelial morphogenesis [Spiliotis et al., 2008].

Similar to epithelial morphogenesis, microtubule alignment is important for development of the vertebrate central nervous system (CNS). The different cell types in the CNS develop from a common pool of progenitor cells. The nuclei of progenitors move between the apical and basal surfaces of the neuroepithelium in phase with their cell cycle, a process termed interkinetic nuclear migration (INM), which may have a role in regulating cell cycle and proliferation [Del Bene et al., 2008]. During INM, the plus end-directed motor dynein and the minus end-directed motor kinesin are required for apical and basal migration of the nucleus, respectively [Tsai et al., 2010; Kosodo et al., 2011].

In the mouse epidermis, which is a stratified squamous epithelium composed of proliferating basal and differentiated suprabasal keratinocytes, microtubules stereotypically reorganize as they differentiate. In basal cells microtubules form a cytoplasmic network emanating from an apical centrosome, while in suprabasal cells microtubules concentrate at cell-cell junctions. During epidermal differentiation ninein and Lis1/Ndel1, which are centrosomal proteins required for microtubule anchoring, are lost from the centrosome and is recruited to desmosomes by desmoplakin, resulting in the relocation of microtubules to the cell cortex [Lechler and Fuchs, 2007; SumiGray et al., 2011].

### **Planar Cell Polarity**

In some types of epithelia, such as the *Drosophila* wing epidermis, a global polarity cue induces a second axis within a plane, known as planar cell polarity (PCP), which is perpendicular to apical/basal polarity [Goodrich and Strutt, 2011] (Fig. 4D). Wnt signalling components, including Frizzled and Disheveled and non-classical cadherins Fat, Dachshous and Flamingo, are involved in PCP development. In the apical area of the *Drosophila* wing epidermis, microtubules are aligned along the proximal-distal axis with a small but significant excess of plus end-distal microtubules [Shimada et al., 2006; Harumoto

et al., 2010]. This characteristic alignment and asymmetry of microtubule growth is controlled in part by atypical cadherins, Dachsous and Fat, as well as by PAR-1, which appears to contribute to the distal redistribution of the core PCP mediator, Frizzled.

In mammals, motile cilia cover many organs and produce large-scale fluid flows crucial for development and physiology and that act in concert with the PCP pathway [reviewed by Wallingford, 2010; Gray et al., 2011]. Cilia are microtubule-based organelles that protrude from the cell and consist of nine outer microtubule doublets with/without an inner microtubule doublet (“9 + 2” or “9 + 0” configuration, respectively). Defects in ciliary motility cause a range of disease symptoms including bronchiectasis, hydrocephalus, and situs inversus [reviewed by Gerdes et al., 2009]. A recent finding linked Frizzled to septins in ciliogenesis as well as to collective cell movement during vertebrate embryogenesis [Kim et al., 2010]. Septins appear to be key mediators connecting microtubule systems to higher-order tissue polarities. Septin 2 also forms a diffusion barrier at the base of the ciliary membrane [Hu et al., 2010].

### **Mitotic Spindle Assembly and Orientation**

Microtubule end-binding factors play critical roles during mitotic spindle assembly and orientation along the division axis, at centrosomes, kinetochores and the cell cortex and in the spindle checkpoint that controls cell-cycle progression (Fig. 2C-c, Fig. 4C-c, Table I). For detailed discussions on the role of MAPs in mitosis and spindle orientation during asymmetric cell division, please refer to other eminent reviews Kline-Smith and Walczak, 2004; Maiato et al., 2004; and Siller and Doe, 2009, respectively.

From a biological perspectives, asymmetric cell division, in which proteins or RNA determinants are segregated differentially into two daughter cells, is essential for generating diverse cell types during development of multicellular organisms [Gonczy, 2008], for example controlling the self-renewal versus differentiation decision in skin [Fuchs, 2008], neuroblasts [Chia et al., 2008], and cancer cells [Knoblich, 2010]. Among the MAPs being highlighted in this review, cortical APC has been implicated in spindle orientation in dividing *Drosophila* male germline stem cells [Yamashita et al., 2003].

### **Muscle Cell Differentiation**

Skeletal muscle is generated by the fusion of precursor cells called myoblasts to form multinucleated syncytial myotubes, a process that requires microtubules and EB1 family proteins [Guo et al., 1986; Straube et al., 2003]. While myoblasts carry typical radial centrosomal microtubule networks, in myotubes microtubules form linear arrays parallel to the long cell axis and microtubule-nucleating material clusters (pericentriolar proteins), which include  $\gamma$ -tubulin, ninein and pericentrin, are redistributed around the nuclei (Fig.

4E). At later stages of differentiation, during myofibrillogenesis, precursors of myosin filaments display microtubule plus end directed movements to the cell membrane and form sarcomeric myosin filaments [Pizon et al., 2005].

In *Drosophila* tendon cells, a compact microtubule array, in which the microtubules are oriented in the same direction, is formed at a unique subcellular domain that connects the muscle-tendon junction and the cuticle. The *Drosophila* ACF7 homologue, Shot, and the EB1-APC1 complex are involved in the formation of this essential compact microtubule network [Subramanian et al., 2003]. In tendon cells with reduced Shot activity, EB1-APC1 dissociates from the muscle-tendon junction and the microtubule array elongates. The resulting tendon cells lose their stress resistance and elongate.

### **Yeast Growth**

Yeasts, being single-celled organisms, only carry a few microtubules, whose behavior along the growth axis is strictly controlled during progression of the cell cycle (Fig. 4F) [Hayles and Nurse, 2001; Chang and Martin, 2009]. Budding yeast and fission yeast are highly tractable model eukaryotes, and investigation of the molecular differences and similarities among these yeast species and higher eukaryotes have contributed to our understanding of cell polarity [reviewed by Gundersen, 2002].

In fission yeast, cell polarization relies largely on microtubules, which deliver polarity factors to the cell tips, where they function to recruit protein complexes involved in actin assembly. In contrast, in budding yeast, spatial cues are dependent on septins and actin. In multicellular organisms, all these cytoskeletal components may cooperate spatially within a cell to generate more complex shapes. In addition, although certain molecules, such as the EB1 family members and the dynein-dynactin complex, are highly conserved in all eukaryotic organisms, including plants, yeasts adopt unique mechanisms to target molecules to microtubule ends. For example, budding yeast dynein and Bik1p (CLIP-170), as well as fission yeast Tip1p (CLIP-170), are targeted to microtubule ends by kinesin-mediated motility [Busch et al., 2004; Carvalho et al., 2004], and Bim1p (EB1 family)-accumulated microtubule plus ends are targeted to the bud tip by myosin walking along the actin cable extending from the tip (Fig. 2A-c) [Hwang et al., 2003]. Despite minor differences, the discovery of basic modules and principles of cell morphogenesis derived from the genetic dissection of the yeast models have provided important novel insight into how more complex cells are shaped.

## **Conclusions and Perspectives**

The molecular basis for microtubule patterning is being rapidly unveiled in the modern era of molecular cell biology by

application of approaches such as cultured cell systems and in vitro reconstitution systems combined with sophisticated technologies, such as live-cell and single molecule imaging, physical manipulation and computer modeling. The fundamental concepts explaining microtubule patterning and its importance, at least at the cultured cell level, appear to be established. However, our knowledge of the upstream signals that induce the formation of microtubule-anchoring structures that have different purpose at distinct sites within cells to generate highly shaped microtubule patterns is still limited. Moreover, compared to the abundance of data from cultured cells, little is known about the detailed organization and dynamics of microtubules in mammalian cells located in their innate tissue environments, in which various physiological requirements may recruit microtubule ends to appropriate sites. On the other hand, recent progress in comprehensive genetic analysis technologies has revealed the physiological relevance of microtubule systems in various human diseases. Furthermore, tools such as embryonic stem cells or induced pluripotent stem cells are now available that are able to differentiate into a variety of cell types and tissues in vitro. With such tools in hand, the focus for the field will be to understand the biological significance of the regulation of microtubules in terms of cell differentiation, organ development and maintenance, as well as disease.

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